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MOLECULAR UNDERSTANDING OF OSMOSIS AND A MULTISCALE FRAMEWORK TO INVESTIGATE CONFINED FLUID PROPERTIES

BY

ANJAN V. RAGHUNATHAN

DISSERTATION

Submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy in Mechanical Engineering in the Graduate College of the University of Illinois at Urbana-Champaign, 2010

Urbana, Illinois

Doctoral Committee:

Professor Narayana R. Aluru, Chair
Professor John G. Georgiadis
Professor Umberto Ravaiolli
Assistant Professor Emad Tajkhorshid
Abstract

Understanding the fluid structure and behavior in nanoscale confinements is of major importance in a wide variety of applications including biological and engineering devices. A critical biological application in which the physics at the nanoscale is important is osmosis. Critical functions of life as well as technology to develop better water filtration systems depends on a fundamental understanding of osmosis. In this thesis, first, a molecular understanding of osmosis in uncharged and charged semi-permeable membranes is developed using Molecular Dynamics (MD) simulation studies. Specifically, we identify key inter-molecular forces that initiate osmosis in uncharged and charged membranes and explain the significance of various inter-molecular forces as the system evolves to a steady-state. We also investigate the effect of size-asymmetric electrolytes on osmosis through uncharged semi-permeable membranes.

Second, we develop a multiscale framework to investigate fluids in confinement. Since the atomistic simulations are extremely computational, they become intractable at very large length scales. Also, the classical continuum theory breaks down at the atomistic level. Towards the goals of bridging the two scales, we formulate a semi-classical framework to predict the concentration and potential profiles of LJ fluids confined in channels of widths ranging from $2\sigma_{ff}$ to $100\sigma_{ff}$ ($\sigma_{ff}$ is the fluid-fluid LJ parameter). The semi-classical framework utilizes the Nernst-Planck equation coupled with a theoretical potential formulation to obtain the accurate concentration and potential profiles in a channel. The results obtained from the semi-classical framework are then compared with results obtained from MD simulations in the channel.
To my family.
I would like to thank my advisor, Prof. Aluru, for his continuous guidance, patience and input that helped me to thread the path necessary to reach my goals. His insights into the research project, asking fundamental and focussed questions, helped make my journey through understanding nanofluidic and multiscale fluid phenomena that much more enticing. I would also like to thank Professors John Georgiadis, Emad Tajkhorshid, Umberto Ravaioli and Victoria Coverstone for their unflinching support and help during the course of my problem formulation and the useful discussions that I have had with them.

I would also like to acknowledge the National Science Foundation (NSF) and the Center for Advanced Materials for Purification of Water with Systems (water-CAMPWS) for their financial support as well as inputs for collaborative research that made it possible to work towards the cause of developing better water filtration systems.

Finally, I am also very grateful for the constant support I received from the Computational Multiscale Nanosystems group throughout these years that I have pursued my graduate studies.
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Chapter 1

Introduction

Understanding the transport of fluids in confinements ranging from the macroscale to the nanoscale is of importance in a wide variety of biological and engineering applications. Study of the functional characteristics and transport properties of fluids in the continuum scale is known by the classical theory for fluid transport. The study of the fluid structure and transport properties in nanoscale confinements is broadly known as the field of Nanofluidics.

An important phenomenon that is related to the transport of fluid in nanoscale confinements is osmosis. Osmosis, a primary passive mode of “pumping” water, is an essential ingredient to life. It is a complex phenomena in which a solvent, in this case water, is driven by its free energy gradient through a semi-permeable membrane towards a solute-rich reservoir. Osmosis has been studied extensively because of its impact in a variety of areas including separation of metal ions from water using Reverse Osmosis (RO) membranes[14]. RO membranes are critical in filtering toxic wastes, particularly the small solutes like the metal ions that cannot be filtered through other methods of filtration.

Osmosis is also pervasive in biological systems, where the distribution of nutrients and the release of metabolic waste products is controlled by osmosis [39]. Aquaporin, a water channel present in plants, depends on water in its local environment and utilizes the osmotic pressure for many critical functions. In humans, the method by which nitrogenous waste is removed from kidneys is based on osmosis and the physiology of most aquatic organisms is dominated by methods of maintaining some form of osmoregularity in relation to the changing environment.

A molecular description of osmosis is of fundamental importance to understand and
mimic biological functions. Further, a molecular understanding of osmosis and the critical molecular interactions that initiate osmosis would help in developing an insight into the methods that can be used to increase the speed of water transport during osmosis. This could help in developing more efficient and better filtration membranes that use lesser energy to filter water through RO membranes.

Recent studies on osmosis using molecular dynamics (MD) include the understanding of the mechanism of solvent transport through small pores using hard-sphere atoms (see e.g., [31]). There have also been several MD studies of hard-sphere Lennard-Jones (LJ) atoms (see e.g., [43]) to understand osmosis and more recently these studies have been extended to water transport driven by an osmotic salt gradient through carbon nanotube arrays [28]. Studies were also performed to understand the effect of electrolyte on osmosis, but these were performed in leaky membranes where both water and ions go through the pore [16]. Inspite of the vast literature on osmosis, several aspects of the osmotic phenomenon remain unanswered including a molecular understanding (which molecular interactions initiate osmosis, what molecular interactions are significant at steady-state, etc.) of osmosis and the dependence of osmosis on the charge of the membrane.

In the first part of this thesis, we report on the varying osmotic flux through uncharged, positively charged and negatively charged semi-permeable membranes using molecular dynamics simulations. Our results indicate that the osmotic flux through a negatively charged membrane is highest, followed by positively charged and uncharged membranes. Next, we try to provide a fundamental understanding of osmosis in uncharged and charged semi-permeable membranes. Specifically, we identify the key inter-molecular forces that initiate osmosis in uncharged and charged membranes and explain the significance of various intermolecular forces as the system evolves to a steady-state. Further, we investigate the effect of size-asymmetric electrolytes on osmosis through an uncharged semi-permeable membrane (only water is transported through the membrane pore). For an uncharged pore, the osmotic flux when the chambers are filled with a KCl solution is found to be higher compared to that
of when the chambers are filled with an NaCl solution \((J_{KCl} > J_{NaCl})\). Similar observations were made with salt solutions of KF and LiCl, i.e., \(J_{KF} > J_{LiCl}\). The differential affinity of the cation and the anion of the size-asymmetric electrolyte towards the pore effects the osmotic flux through the pore as well as the water orientation in the pore.

In the second part of this thesis, we try to formulate a theoretical framework that would bridge both scales — the continuum fluid behavior (in a macroscale confinement of the fluid) with the nanofluidic behavior in atomistic confinements. The success in understanding fluids and flow at a molecular level has also driven interest in the fields related to designing micro and nanofluidic channels for applications in lab-on-a-chip, energy storage and conversion, water purification, and nanomanufacturing \([59, 46, 62]\). Computational analysis plays an important role in design and optimization of these micro and nanofluidic devices and numerous studies have already been performed to model and predict the static and dynamic properties of fluids in micro and nanochannels \([30]\). Continuum or classical theories are generally accurate in predicting properties and transport of bulk fluids where nanoscale confinement and interfacial behavior are not significant. When the fluid is under strong confinement, i.e., a bulk description of the fluid is not valid, atomistic molecular dynamics (MD) simulations \([15]\) can be used to understand the fluid behavior. There are many examples where both the interfacial behavior as well as the bulk behavior of the fluid can be important. For example, hybrid micro-nanochannels, where ion selective nanochannels are connected to microscale solution chambers, require proper understanding of both the bulk and confined behavior of the fluid. Another example where both the macroscale and the atomistic features become important is in electroosmosis through channels with an electric-double layer (EDL) \([49]\). In this case, the strong density gradients of the electrolyte produced in the atomic scale are coupled to the macroscopic behavior in ways that are difficult to be captured by classical constitutive relations or other average descriptions.

In micro and nanofluidic devices where both the interfacial behavior and the macroscopic behavior of the fluid are important, the use of a classical continuum theory to resolve the
physics in the entire device can be inaccurate, while the use of MD simulations may not be possible because of computational limitations. Hence, it is of fundamental interest to develop methods that combine the atomistic features to the existing continuum theory. Approaches that seek to accomplish this are broadly described as multiscale models [3]. Multiscale models aim at providing a “bridge” between the atomistic and continuum theories, either by simultaneously simulating them in different regions of the domain or by incorporating the atomistic physics that is missing in the classical theories [67].

The multiscale simulations developed to understand flow under confinement can be categorized into coupled continuum methods [35, 50], involving either a heterogeneous domain decomposition or a corrected continuum theory, and coarse-grained methods, which involve reducing the degrees of freedom in a microscopic Hamiltonian [42, 26]. A hydrodynamic model used for this purpose is the Dissipative Particle Dynamics (DPD) approach [22, 18], which considers a “cluster” of atoms as a particle interacting with other such cluster particles with a distinct dissipative field of interaction. DPD suffers from the drawback that the results of the simulation depends on the optimally chosen time step. Further, the integration scheme to be chosen is a non-trivial task and could lead to artifacts in the predicted results [63]. Also, the boundary conditions applied in DPD are not well defined and ongoing studies involve finding approaches to improve the applied boundary conditions [47]. Other approaches to study fluids under confinement involve theoretical predictions, e.g., using the integral DFT theory [57] to predict the fluid dynamics in the system by solving modified continuum equations with a predicted density. Though the mathematical framework of DFT is formally exact, a precise expression of the intrinsic Helmholtz energy as a functional of the molecular density profile is unknown for most systems of practical interest [69]. Further details of confined fluid theories including DFT can be found in [20, 69] and references therein.

Towards the goal of developing a multiscale framework to investigate fluids in confinement, we describe a novel interatomic potential based semi-classical theory to predict the
concentration and potential profiles of LJ fluids and electrolytes confined in channels of widths ranging from $2\sigma_{ff} - 100\sigma_{ff}$ ($\sigma_{ff}$ is the fluid-fluid LJ parameter). Both uncharged and charged channel wall cases have been considered. For each of the channels studied, comparisons are made with MD simulations to analyze the accuracy of the proposed formulation. The results obtained from the formulation are found to be in good agreement with the MD simulation data. To our knowledge, this is the first semi-classical theoretical formulation that while preserving the atomistic physics close to the wall, quickly and accurately predicts the concentration and potential for a wide range of channel widths. Hence, the proposed semi-classical formulation is a robust, fast and accurate method that can be used to predict the atomistic details at various length scales ranging from the nanoscale to the macroscale.

![Simulation hierarchy for various critical length scales](image)

Figure 1.1: Simulation hierarchy for various critical length scales [64].

The rest of the thesis is organized as follows: a brief overview of MD simulations and their application to simulating fluid in confined nanochannels is given in Chapter 2. Chapter 3 focuses on the molecular understanding of osmosis in charged and uncharged pores. The effect of different electrolytes present in the bath attached to the semi-permeable membrane
is also studied in chapter 3. Chapter 4 outlines the novel interatomic potential based semi-classical theory for LJ fluids and test cases that prove the validity of the framework. Finally, the concluding remarks on the understanding of osmosis and the new multiscale framework is presented in chapter 5.
Chapter 2

Nanopore Simulations using Molecular Dynamics

There have been several numerical and experimental methods developed in the last decade to understand fluid structure and transport at the nanoscale. For example, the fluidity of sub-nanometer to nanometer thin film confined between surfaces has been studied both by experiments and by atomistic simulations [25, 7]. Another example of a numerical simulation to study nanofluidics is the investigation of the electroosmotic transport of water through nanoscale capillary for desalination applications[48]. Water and electrolyte transport through nanometer scale pores present in cell membranes have been studied using Molecular Dynamics (MD) simulations [19] and Brownian dynamics simulations [24]. For water and other fluids in a confinement, the classical fluid mechanics theory can be used to predict the static and transport properties in the region that is at a significant distance away from the wall. Investigation of the behavior of water in nanoscale confinements indicates that the water (or any other fluid’s) structure at the interfacial region close to the wall, specifically within 1–2 nm of the wall, cannot be predicted using the classical fluid mechanics. These are problems which can be investigated better using atomistic MD simulations.

Making a note that MD simulations are computationally expensive and cannot be applied to large length scale systems, in this chapter, we discuss MD simulations and its application to investigating fluids in nanoscale confinement. An overview of an MD simulation is given along with the description of important thermodynamic ensembles. The various equilibrium and non-equilibrium properties that can be extracted from MD are also mentioned. The aspects of MD simulations, important for nanopore simulations will also be discussed.
2.1 Molecular Dynamics simulations

In a Molecular Dynamics (MD) simulation, a system is represented by $N$ interacting particles [15]. The motion of the $N$ particles is described by the Newton’s law. At any time, the state of the system is given by $(r_i, v_i)$, where $r_i$ is the position of the particle $i$ and $v_i$ is the velocity of the particle $i$ in the system. An ensemble average is computed using the trajectories and velocities of the atoms from the MD simulation run to obtain the system observables, e.g., the concentration and the velocity distribution in a confined fluid setup. The statistical averages are computed after the system has achieved an equilibrium state (for an equilibrium MD simulation), or in the case of a non-equilibrium MD simulation, the statistical average is computed after the system has achieved steady-state.

Algorithm 1 A simple MD algorithm

1: Input: $N$ interacting particles, force field parameters, time step $\Delta t$ and total steps $n_{MD}$
2: Set $r_i$ and $v_i$ for $i = 1...N$ and time $t = t_0$, $n = 1$
3: repeat
4: Calculate force $F^t_i$ on each atom
5: Update $v_i^{t+\Delta t}$ and $r_i^{t+\Delta t}$
6: Store trajectory. If necessary, perform on-the-fly data analysis
7: Set $t = t + \Delta t$, $n = n + 1$
8: until $n > n_{MD}$
9: Analysis of the MD simulation data (density distribution, velocity distribution e.t.c.)

Algorithm 1 outlines the steps involved in a Molecular Dynamics simulation. A brief description of the steps involved in a Molecular Dynamics simulation is given below:

1. **Initialization**: The number of particles $N$ in the system is decided and the ensemble on which the simulation is run is selected. The details on ensembles is given in the following section. Particles are assigned coordinates $(r_i)$ at random or at lattice positions. The velocities $(v_i)$ are assigned from a Maxwellian distribution at the given temperature [15]. The temperature of the system is monitored using the following relation [15]:

$$ T = \frac{k_B N}{N} $$
\[ k_B T(t) = \sum_{i=1}^{N} \sum_{\alpha=1}^{3} \frac{mv_{\alpha,i}^2(t)}{N_f} \] (2.1)

where, \( k_B \) is the Boltzmann constant, \( N \) is the number of particles in the system, \( \alpha \) is the directional component, \( v \) is the velocity, \( N_f \) is the number of degrees of freedom and \( m \) is the mass of the particle.

2. **Force Calculation:** Depending on the existing force fields for atoms in the system one would calculate the forces on each particle in the system at a particular time \( t \). The force acting on a particle \( i \) is computed by \( F_i = -\partial U/\partial r_i \), where \( U \) is the potential energy of the system given by

\[ U = \sum_i u_1(r_i) + \sum_i \sum_{j>i} u_2(r_i, r_j) + \sum_i \sum_{j<i} \sum_{k>j<i} u_3(r_i, r_j, r_k) + \ldots \] (2.2)

where, \( u_1 \) is the potential energy due to external fields and the remaining terms, modeled by intermolecular potentials, represent the particle interactions (e.g., \( u_2 \) is the pair potential and \( u_3 \) is the three-body potential and so on).

Typically, the three-body and higher-order potentials are truncated in Equation (2.2). The functional form and the parameters of the interaction potentials are called the force field, and are the most important inputs to the MD simulation. Force calculation is the most time consuming step in the MD simulation (time required to calculate the forces on \( N \) particles in the system scales as \( O(N^2) \)). However, there are efficient algorithms that would ensure that this force calculation is done in the order of \( O(N (ln N)) \) (details of the interaction potentials and some efficient evaluation algorithms are given in section 2.3).

3. **Integrating the equations of motion:** Having computed the forces on all particles in the system, the Newton’s equation of motion is integrated over the given time interval (\( \Delta t \)) to obtain the new coordinates of the particles in the system. The most
commonly used time marching algorithm in MD simulation is the velocity Verlet algorithm [2]. The new position \((r(t + \Delta t))\) and velocities \((v(t + \Delta t))\) obtained from the Verlet algorithm are:

\[
r(t + \Delta t) = 2r(t) - r(t - \Delta t) + \frac{f(t) \Delta t^2}{m} \quad (2.3)
\]

\[
v(t) = \frac{r(t + \Delta t) - r(t - \Delta t)}{2 \Delta t} + O(\Delta t^2) \quad (2.4)
\]

where \(r\) is the coordinate of the particle, \(f(t)\) is the force on the particle at time \(t\), \(\Delta t\) is the time step in the MD simulation, \(v\) is the velocity of the particle and \(m\) is the mass of the particle. The time step \(\Delta t\) for a MD simulation is optimized for both speed and accuracy of the simulation. For the current work, MD simulations have been carried out with time steps of 1 and 2 fs (femto seconds). The use of Cartesian coordinates rather than internal coordinates leads to efficient integration of the equations of motion from a simple form of the inertial terms [53]. If the temperature of the system is to be maintained at a certain value, the update algorithm is modified depending on which thermostat is used. Two of the commonly used thermostats are the Berendsen [6] and the Nosé-Hoover thermostat [44].

4. **Output and/or data analysis:** Once the system configuration at a new time step is known, the various properties (e.g., fluid density and velocity distributions) of the system can be computed. Some of these calculations are performed on-the-fly during the simulation, while in many cases, these calculations are performed after the simulation has finished. To obtain the various properties and observables of the system, the trajectory obtained from the MD simulation is analyzed. For example, the diffusion coefficient (obtained from the Green-Kubo [13] relation), can be computed using the velocity data obtained from the MD simulation (Equation (2.5)),
\[ D = \int_{0}^{\infty} dt < v(0).v(t) > \] (2.5)

where, \( D \) is the self-diffusion coefficient of a particle, \( v \) is the velocity of the particle (obtained from each time step in MD) and \( t \) is the time. Other nanofluidic properties of interest include the density profile, velocity profile, ionic flux etc. They will be discussed in detail in chapters 3 and 4.

Clearly, the main elements necessary for an accurate MD simulation are, (a), the correct force field parameters and reasonable models, (b), accurate and efficient potential and electric field calculations and (c), correct data analysis algorithms. Significant progress over the years on these three aspects of MD simulations [1] have ensured that MD has become an important tool in the study of nanofluidic transport.

### 2.1.1 Thermodynamic ensembles used in MD simulations

In a conventional MD simulation the energy \( E \) and momentum \( P \) are constants of motion. A set of thermodynamic parameters are maintained constant in a MD simulation to depict a real life experiment. Such a set of parameters that are maintained constant over time are together known as an ensemble of the system. There are many ensembles in which one could perform a MD simulation. However the ensemble is chosen with regards to the one that is closest to the real life experiment that is being modeled. The various commonly used ensembles are:

- **Micro-canonical Ensemble (NVE)**

  In this ensemble the number of particles \( N \), the volume of the system \( V \) and the energy of the system \( E \) are maintained constant during the simulation of the system [15]. This is the most popular choice of an ensemble for the MD simulation. This ensemble cannot be used to simulate an open system.
• **Canonical Ensemble (NVT)**

The number of particles $N$, the volume of the system $V$ and the temperature of the system $T$ are maintained in this ensemble [15]. This kind of an ensemble is useful for simulating isolated and isothermal systems. Clearly, this ensemble cannot be used to simulate systems that involve a thermal gradient. This ensemble is commonly used in Monte Carlo simulations. While simulating in this ensemble, a thermostat (like the Nosè-Hoover [44] or Berendsen [6]) is used to maintain the temperature of the system.

• **Isobaric-Isothermal Ensemble (NPT)**

As the name suggests the number of particles ($N$), the pressure ($P$) and the temperature ($T$) of the system are kept constant in these simulations. These are more realistic simulations of a system that is open to the atmosphere.

• **Grand Canonical Ensemble ($\mu$VT)**

When the chemical potential $\mu$ of the system is maintained along with the volume ($V$) and the temperature ($T$), the system is simulated in the Grand Canonical Ensemble. This type of system is common in real life when one has an open reservoir bath connected to an experimental setup involving a membrane immersed in a solution. This system is allowed to exchange particles as well as energy with the surrounding based on the chemical potential of the system. It is straightforward to simulate such a system using the Monte Carlo method. The deterministic simulation of such systems can be performed using a grand canonical molecular dynamics simulation. However, maintaining the chemical potential by inserting or deleting of particles within the system could affect the dynamics of the system. Thus, care should be taken to ensure that there is no artificial effect on the dynamics of the system, either by reducing the insertion/deletion steps or keeping the reservoirs far away from the pore or channel that is simulated. The present work involves an open system and more details on grand canonical molecular dynamics are discussed in chapter 3.
2.2 MD Interaction Potentials: Theory and calculations

To obtain the forces of interaction between various atoms and molecules in an MD simulation, the inter-atomic and intermolecular potentials between these atoms and molecules is to be calculated. The total intermolecular potential \( u(R) \) can broadly be categorized as bonded and non-bonded interactions. The bonded interactions are usually short-ranged, while the non-bonded interactions include both the short-ranged interactions (e.g., the van der Waals interaction) and long-ranged interactions (Coulombic interactions).

The most common intramolecular bonded interactions include covalent bond interaction potentials \( u_{\text{bond}} \), which represent the high frequency vibrations along the chemical bond, the angular bond potential arising from the bending between two adjacent bonds \( u_{\text{angle}} \), the dihedral potential due to the torsional motion of the bond \( u_{\text{dihedral}} \) and the planar orientation of one atom relative to three others \( u_{\text{improper}} \). Equation (2.10) lists the bonded interaction potentials commonly occurring in MD simulations.

\[
\begin{align*}
\text{\( u_{\text{bond}} \)} &= \sum_{\text{bonds,}\alpha} K_{\alpha}^{\text{bond}} (r_{\alpha} - r_{0\alpha})^2 \\
\text{\( u_{\text{angle}} \)} &= \sum_{\text{angles,}\beta} k_{\beta}^{\text{angle}} (\theta_{\beta} - \theta_{0\beta})^2 \\
\text{\( u_{\text{dihedral}} \)} &= \sum_{\text{dihedrals,}\gamma} K_{\gamma}^{\text{dihed}} (1 + \cos(n_{\gamma} \psi_{\gamma} + \delta_{\gamma})) \\
\text{\( u_{\text{improper}} \)} &= \sum_{\text{improper,}\delta} k_{\delta}^{\text{impr}} (\phi_{\delta} - \phi_{0\delta})^2 
\end{align*}
\]

(2.10)

where, \( r_{\alpha} \) is the bond length, \( r_{0\alpha} \) is the associated equilibrium bond length, \( K_{\alpha}^{\text{bond}} \) the respective bond spring constant; \( \theta_{\beta} \) the angle between two bonds, \( \theta_{0\beta} \) the associated equilibrium bond angle and \( k_{\beta}^{\text{angle}} \) the relative spring constant for the angle; \( \psi_{\gamma} \) is the angle of rotation around a bond, \( K_{\gamma}^{\text{dihed}} \) the rotational spring constant proportional to the energy barrier for
rotation and \( n_\gamma \) the number of maxima (or minima) in one full rotation with \( \delta_\gamma \) the angular offset; \( \phi_\delta \) is the improper torsional angle, \( \phi_{0\delta} \) the associated equilibrium value and \( k_\delta^{impr} \) the associated angle spring constant.

The van der Waals interaction between atoms \( i \) and \( j \) is modeled using the Lennard-Jones 6-12 potential. The form of the LJ interaction potential is given by:

\[
u_{LJ}(r) = \sum_{i=1}^{N} \sum_{i \neq j} 4\epsilon_{ij} \left( \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{6} \right)
\]

where, \( \epsilon_{ij} \) is the energy parameter and \( \sigma_{ij} \) is the distance parameter.

Figure 2.1 shows the variation of the LJ potential for an Argon atom with the force field obtained from GROMOS [21]. As can be observed in the potential plot, the LJ potential consists of an attractive part \((r^{-6})\) and a repulsive part \((r^{-12})\). The main parameters involved in deciding a particle’s LJ parameters are the energy parameter \( \epsilon \) and the spatial parameter \( \sigma \). The determination of these parameters is through empirical forms as well as comparing properties like the diffusion coefficient of the species with experimental values. Since this interaction is a short range interaction, there is no \( O(N^2) \) computational expense as special neighbourlist [15] algorithms make sure that the computation is performed fast.

![Figure 2.1: Plot of the Lennard-Jones interaction [27] between a pair of atoms with a strongly repulsive and an attractive part. The parameters \( \sigma \) and \( \epsilon \) are the distance and energy parameters, respectively. Note that this is a short range interaction.](image)
2.2.1 Electrostatics computations in Molecular Dynamics simulations

The electrostatic contribution $U_{elec}$ accounts for the interaction between the atom’s partial charges $q_i$ and $q_j$, $r_{ij}$ is the separation between them, $\epsilon_0$ is the permittivity of free space and $\epsilon_r$ is the relative dielectric constant of the medium in which the charges are placed. The calculation of the Coulombic forces is the most time consuming part of the MD simulation. This is because electrostatic interactions are long range, unlike the Lennard-Jones interactions. Efficient methods have been developed (like the Particle Mesh Ewald Method [11]) that use fast summation methods to calculate this electrostatic interaction between the particles in MD when the simulation is performed with periodic boundary conditions.

The Coulomb interaction between particles that are computed in MD is computationally expensive and of the order of $O(N^2)$. However, efficient algorithms to calculate the electrostatic summation have been developed. The two important fast electrostatic summation algorithms are described below:

- **Particle based techniques:** Among the particle methods, the most common method used for electrostatic summation calculation is the Particle Mesh Ewald (PME) method [11]. The derivation of the energy formulation for PME is given in [15]. The final form for the electrostatic energy of charges present in a three dimensionally periodic system calculated from PME is:

$$u_{coul} = \frac{1}{2V} \sum_{k \neq 0} \frac{4\pi}{k^2}|\rho(k)|^2 \exp(-k^2/4\alpha) - (\alpha/\pi)^{1/2} \sum_{i=1}^{N} q_i^2 + \frac{1}{2} \sum_{i \neq j}^{N} q_i q_j \frac{erfc(\sqrt{\alpha} r_{ij})}{r_{ij}}$$

(2.12)

where, $V$ is the volume of the simulation box, $k$ is the reciprocal space vector, $q_i$ is the charge on atom $i$, $r_i$ is the coordinate of the charge $i$, $\rho(k) = \sum_{i=1}^{N} q_i \exp(ik \cdot r_i)$ and $\alpha$ is the parameter that defines the Gaussian width. The Gaussian width is optimized for
computational efficiency. The first term in the Ewald sum calculation is the Fourier sum. The second term is the correction to the self interaction energy between a charge and its periodic image. The third term is the real space summation of the potential due to the charges in the system. The above formula reduces the computational cost for the electrostatic potential calculation to $O(N \ln N)$.

- **Multipole techniques:** Multipole methods like the Fast Multipole Method (FMM), consider a group of particles at a large distance from a particle to be a “big cluster”. The interaction of this cluster with the particle then does not need to be calculated by explicit particle-particle interactions. Clustering the system into bigger and bigger groups helps speed up the calculation of the electrostatic interaction potential ($O(N)$). This algorithm was first formulated by Appel et al. [4] and later refined by Greengard and Rokhlin [17]. Details of the algorithm can be found in [4], [17].

### 2.2.2 Molecular models for water simulations

A large number of “hypothetical” models for water have been developed in order to mimic its structural characteristics [65]. The basis for the prediction of the structure of water is that if the (known) model can successfully predict the physical properties of water, then the (unknown) structure of water can be determined. The molecular models for water involve positioning the electrostatic sites and the Lennard-Jones sites, which may or may not coincide with one or more of the charged sites. Generally, each model is developed to match well a certain set of physical structures or parameters (e.g., the density anomaly, radial distribution function, or other critical parameters). Various models for water (SPC/E, TIP3P, TIP4P, etc) are used in literature [66]. The validity of the water models and hence the structure of liquid water in confinements are based on how successfully they predict some standard physical properties of bulk liquid water. Figure 2.2 shows the water models that are used with three, four and five site models. Some of the common models and their estimates of
Table 2.1: Properties of the SPC/E, TIP3P and TIP4P water models and experimental value (bulk) at 25°C.

<table>
<thead>
<tr>
<th>Model</th>
<th>Dipole Moment</th>
<th>Dielectric constant</th>
<th>Self Diffusion($10^{-5}cm^2s^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SPC/E [33]</td>
<td>2.35</td>
<td>71</td>
<td>2.49</td>
</tr>
<tr>
<td>TIP3P [40]</td>
<td>2.35</td>
<td>82</td>
<td>5.19</td>
</tr>
<tr>
<td>TIP4P [40]</td>
<td>2.18</td>
<td>53</td>
<td>3.19</td>
</tr>
<tr>
<td>Experiment [29]</td>
<td>2.95</td>
<td>78.4</td>
<td>2.27</td>
</tr>
</tbody>
</table>

water properties, e.g., the dielectric constant and dipole moment, are given in Table 2.1 along with experimental bulk values for water at 25°C.

Figure 2.2: Four different water models [8]: (a) SPC/E (b) PPC (c) TIP4P and (d) TIP5P; For SPC/E model the parameters are: $l_1 = 1Å^0$, $\theta = 109.47^0$, $q_1 = 0.4238e$ and $q_2 = -0.8476e$

The commonly used water model is the Simple Point Charge Extended (SPC/E) [5] and it will be used in the current work. For the SPC/E model, the H-O-H angle is 109.47° and the charge on the hydrogen and oxygen atoms are 0.4238 e and −0.8476 e, respectively. SPC/E is a rigid water model where the H-O-H angle is fixed. The bond length between hydrogen and oxygen atoms in the water molecule is 0.16 nm. The SPC/E model predicts the water properties like diffusion coefficient and dielectric constant to reasonable accuracy.
Rigidity of the H-O-H angle makes this a non-polarizable model for water. There have been recent advances in developing polarizable water models [61]. However, these models are computationally more expensive and cannot be used in calculating transport properties such as the ionic mobility or conductivity, since that would require large amounts of statistical data from the MD simulations.

### 2.2.3 Static and dynamic properties computed from MD simulations

From the trajectory of the MD results, the density and velocity profiles of atoms can be obtained from the equilibrium molecular dynamics simulation. The density and the velocity profiles of the system averaged over the entire equilibrium simulation is obtained from the “binning” method [2]. The simulation box is divided into bins and the number of particles as well as the average velocity is counted within the bins. The statistical average over the simulation time gives the density and the velocity profiles from the MD simulation.

Dynamic properties of the atoms in the system can also be calculated from MD. A common dynamic property is the velocity autocorrelation function [9]. The self-diffusion coefficient of an atom in the system can be obtained from the velocity autocorrelation function. Other autocorrelation functions like the dipole autocorrelation function and hydrogen bonding autocorrelation function provide fundamental understanding of the atomistic time varying properties of confined fluids. In non-equilibrium MD simulations with an applied field, the mobility and conductivity of atoms can also been calculated. Bell et al. [38] have calculated the mobility and conductivity of ions in an electrolytic solution from non-equilibrium MD simulations.
2.3 Molecular Dynamic Simulations in confined channels/pores

Molecular Dynamics simulations can be used to calculate the equilibrium and non-equilibrium properties of fluids in the nanopore. Since the surface-to-volume ratio of the nanopore is very high, the fluid-surface interaction has a significant influence on the fluid transport. The energy barrier developed in the nanopore could influence the pore properties such as the selectivity and permeability of ions through them. Recent study of water and ion permeation through nanopores using MD simulations have been discussed in [60] and references therein. A description of the nanochannel system investigated is given below along with details of the observables that are extracted and analyzed from the MD simulations on nanochannels.

It is important to define the wall properties and geometry of the nanopore to be simulated in MD. Review of some of the different nanopore simulations on cylindrical, slit and channel pores in MD is found in [60]. One way to implement the wall structure in MD involves a non-atomistic approach. Channel walls would have no atomistic detail and the interaction parameter between the wall and the fluid is defined using a 9-3 LJ function of the distance from the wall [12]:

\[
V_{\text{wall}}(z) = 4 \epsilon' [\left(\frac{\sigma'}{z}\right)^9 - \left(\frac{\sigma'}{z}\right)^3]
\]  

(2.13)

Here, \( z \) is the distance of the fluid atom from the wall surface, and the parameters \( \epsilon' \) and \( \sigma' \) are the Lennard-Jones parameters.

It is necessary to explicitly define the atoms in the channel wall for nanochannels as the interfacial region could influence the nanofluidic transport through them. Channel wall atoms consist of Lennard-Jones atoms with or without charges on them.

Periodic boundary conditions are normally applied to MD simulation of nanopores/nanochannels. To simulate an infinitely long pore, periodic boundary conditions are applied only to direc-
tions perpendicular to the wall normal of the pore [50]. In this setup, the pore mouth region and pore wall-bath interactions are assumed to have little or no effect on the dynamics of the system. However, the pore mouth region becomes important in cases where there exists energy barriers near the mouth region that could affect the water and ion transport through the pore. To analyze such systems, a reservoir can be attached to either side of the nanopore[10]

The schematic of a sample nanochannel system simulated in MD is shown in Figure 2.3.

![Figure 2.3](image.png)

Figure 2.3: One of the nanochannel setup’s used in the present work. The channel is filled with a Lennard-Jones fluid.

### 2.3.1 Fluid properties in nanoscale confinement

In fluids confined in nanochannels or nanopores, the critical length scale of the channel approaches the size of the fluid molecules and the surface to volume ratio is orders of magnitude higher than that of macroscopic systems. This would indicate that the fluidic static and transport properties can be significantly influenced by the geometric confinement and
the surface effects can dominate the fluid structure and transport in the channel. Specifically, the geometric confinement and surface effects can effect the microscopic properties including the fluid concentration distribution inside the channel. These properties of the fluid inside the channel can be dramatically different from that in the bulk region. The difference in the static and dynamic properties in the channel can results in the difference in the fluid transport behavior in the nanoscale confinement as compared to a macroscopic system. This results in (a), the breakdown of the classical continuum theories at these length scales (close to the interface) and (b), a difference in the transport properties of the fluid, e.g., the diffusion coefficient and the viscosity, as compared to that in the bulk.

From the discussion above, we understand that MD simulations become a critical tool to study the fluid phenomenon in nanoscale confinements. One such fluid phenomenon at the nanoscale that is of extreme importance in the fields related to cellular biology and water filtration is Osmosis. The next chapter would discuss MD simulations used to understand osmosis at a fundamental and molecular level.
Chapter 3

Molecular Understanding of Osmosis in Semi-Permeable Membranes

The previous chapter provided a general description of the Molecular Dynamics (MD) simulation and its application to studying fluids in confinement. In this chapter, we provide a molecular understanding of osmosis through membranes. MD simulations are used to study osmosis through nanoporous semi-permeable membranes. We use MD to understand the mechanism of single-file osmosis of water through a semi-permeable membrane with an uncharged, positively and a negatively charged nanopore. The osmotic flux of water through uncharged and charged pores is computed using MD simulations and the physical mechanism explained using molecular interactions. Further, the molecular mechanisms governing osmosis is explained. The observed osmotic flux dependence on the nanopore charge are explained by computing all the molecular interactions involved and identifying the molecular interactions that play an important role during and after osmosis. Finally, the molecular interactions governing steady-state osmosis is also analyzed. This study helps in a fundamental understanding of osmosis and in the design of advanced nanoporous membranes for various applications of osmosis.

3.1 A theoretical understanding of osmosis

Osmosis is a complex phenomena in which a solvent is driven by its free energy gradient through a semi-permeable membrane towards a solute-rich reservoir. In all living matter, osmosis is a primary passive mode of “pumping” water which is an essential ingredient to life. Osmosis has been studied extensively because of its impact in a variety of areas including
separation of metal ions from water using reverse osmosis (RO) membranes. Osmosis is also pervasive in biological systems, where the distribution of nutrients and the release of metabolic waste products is controlled by osmosis [39]. Aquaporin, a water channel present in plants, depends on water in its local environment and utilizes the osmotic pressure for many critical functions. One major cellular function that depends on osmosis is the maintenance of the water pressure in the biological intra- and extracellular regions to avoid the rupture of the cell. In humans, the method by which nitrogenous waste is removed from kidneys is based on osmosis and the physiology of most aquatic organisms is dominated by methods of maintaining some form of osmoregularity in relation to the changing environment.

There have been several molecular dynamics (MD) studies of hard-sphere LJ atoms (see e.g., [43]) to understand osmosis and more recently these studies have been extended to water transport driven by an osmotic salt gradient through carbon nanotube arrays [28]. Despite the vast literature on osmosis, several aspects of the osmotic phenomenon remain unanswered including a molecular understanding of osmosis and the dependence of osmosis on the charge of the membrane. In this chapter, using MD simulations, we first compute the osmotic flux through uncharged, positively charged and negatively charged semi-permeable membranes. We then try to answer the following main questions.

- What molecular interactions initiate osmosis?
- Is there a dependence of osmosis on the polarity of the pore embedded in the semi-permeable membrane?
- What are the key inter-molecular forces that initiate osmosis in uncharged and charged membranes
- What molecular interactions are significant at steady-state osmosis?
- Is there a dependence of osmosis on the electrolyte present in the solvent region?
Can this study be used to design a better filtration membrane, that has a faster water flux through the nanopore?

3.2 Osmosis through uncharged and charged pores

To study the effect of osmosis through uncharged and charged pores using an MD simulation, the system simulated needs to consist of a bath with a high concentration of electrolyte attached to a bath with a low concentration of electrolytes with a semi-permeable membrane in the middle. Since we apply a periodic boundary in all directions, there is a need for a special setup for the MD simulation. The electrolyte that is present as solute in this study is potassium chloride (KCl). The simulation details of this special MD setup is given below followed by the results obtained for this MD setup.

3.2.1 Simulation Details

Figure 3.1: A schematic (left) and a snapshot (right) of the MD simulation system for osmosis. The high solute concentration chamber is denoted by $CH_h$ and the low solute concentration chamber is denoted by $CH_l$.

Figure 3.1 shows a snapshot of the MD simulation system. The system consists of two square membranes that are 3.3 nm long in the $x$- and $y$- directions. The thickness of the membrane is 1.5 nm in the $z$-direction. The two square membranes separate the two KCl solutions of different concentrations. The membrane atoms are located in a face centered...
cubic fashion in the $xy$-plane. Each membrane consists of a semi-permeable pore of diameter 0.9 nm at the center of the membrane. The *steric* hinderance of the pore ensures that the membrane is truly semi-permeable, i.e., only water molecules can pass through the pore and the potassium and chloride ions do not go through the pore.

Figure 3.1 also shows the dimensions of the solution chambers connecting each membrane. Two membranes are connected back-to-back as shown in Figure 3.1 and periodic boundary conditions are applied to the system in all the three directions [43]. For charged pore simulations, the pore wall is assigned discrete charges on the atoms to produce a net charge density of $\pm 0.12 \, \text{C/m}^2$. The membrane and the pore wall atoms are modeled as Lennard-Jones (LJ) atoms with parameters for carbon [68]. Further, these atoms are frozen to their original lattice positions to ensure that the membrane does not move during the MD simulation run. Water is modeled by the well known SPC/E model. The potassium ($\text{K}^+$) and chloride ($\text{Cl}^-$) ions are modeled as single site LJ atoms with a unit charge present at the center of the atom[32, 33].

MD simulations were performed using Gromacs 3.1.4 [36]. The MD simulation was performed in the canonical (NVT) ensemble. A Berendsen thermostat was used to maintain the temperature of the fluid at 300K. The electrostatic interactions were computed by using the Particle Mesh Ewald method [11]. The LJ cutoff distance and the real space cutoff distance for electrostatic calculations was 1 nm. The low and high solute chambers were initially filled with a KCl solution of 0.3 M and 1.85 M concentrations, respectively. The number of ions in the two chambers does not change during the simulation as the membrane pores are permeable only to water. The hydrostatic pressure of the two chambers was calculated from the force exerted on the membrane wall atoms. Water was allowed to enter the pore during a 1 ns equilibration run. Thereafter, the simulation was run a further 200 ps to ensure that the pressure in the two chambers is the same ($\approx 40$ bar). Two different initially equilibrated configurations were simulated in MD for 4 ns while keeping the initial number of water and solute molecules the same in both the simulations. The trajectory was
saved every 0.1 ps and the calculation of the mean force for post-processing analysis was carried out on-the-fly during the MD simulation run. Simulation results described later were obtained after averaging over the two production runs of 4 ns each. Three simulations with pore wall surface charge densities of 0, 0.12 and -0.12 C/m² were performed. The osmotic flux variation in all the three cases was calculated.

### 3.2.2 Results: Osmotic flux vs Pore polarity

![Graph showing water occupancy in chambers over time for different membrane pore polarities](image)

Figure 3.2: Variation of the water occupancy in the two chambers with time for the three membrane pore polarities of 0, 0.12 and -0.12 C/m². Low solute chamber drains, while the high solute chamber accumulates water molecules.

During osmosis the water molecules transports from the low solute chambers to the high solute chamber through the nanopore. The number of water molecules accumulated in the high solute chamber ($CH_h$) of 1.85 M KCl and the decrease in the number of water molecules in the low solute chamber ($CH_l$) of 0.3 M KCl with time are shown in Figure 3.2.
The osmotic flux is initially dominant leading to an increase or decrease in the number of water molecules in $CH_h$ and $CH_l$, respectively. As shown in Figure 3.2, the water occupancy in each chamber saturates after about 2 ns indicating that a steady-state has been reached.

The number of water molecules accumulated in $CH_h$ and the decrease in the number of water molecules in $CH_l$ is dependent on the membrane polarity. From Figure 3.2 it is observed that the osmotic flux in the negatively charged pore ($J_-$) is higher as compared to the osmotic flux in the positively charged pore ($J_+$. Also, the osmotic flux in the uncharged pore ($J_0$) is the lowest, i.e., $J_- > J_+ > J_0$.

To understand these results, we computed the total mean force acting on a water molecule in the axial direction ($z$-direction) as an average over time along the centerline of the pore from the summation of the LJ (12-6) interaction and the electrostatic interaction, which is computed using the Ewald summation [11]. Figure 3.3 shows the mean force on a water molecule for the uncharged pore. A positive mean force moves the water molecule in the direction of $CH_l$ to $CH_h$ and a negative mean force moves the water molecule in the direction of $CH_h$ to $CH_l$. We note that the mean force due to ion-water interactions is asymmetric at the ends of the pore region, i.e., the mean force is higher near the pore mouth connected to $CH_h$ compared to the mean force near the pore mouth connected to $CH_l$. The tendency for the ions in the reservoir to “pull” the water molecules towards them to maintain their hydration shell is dominant in $CH_h$ compared to $CH_l$. Thus, a higher mean force on water is observed near the pore mouth connected to $CH_h$. The asymmetry in the mean force on water due to ion-water interactions causes water to move from $CH_l$ to $CH_h$. The asymmetry in the mean force on water due to the water-water and wall-water interactions is not as significant (see Figure 3.3 (inset)). From this discussion, we can conclude that osmosis in uncharged pores is primarily initiated by ion-water interactions.

When the pores are charged, in addition to the ion-water asymmetry (see Figure 3.3) near the pore mouth regions, the mean force on the water molecules due to the water-wall electrostatic interactions is also found to be asymmetric as shown in Figure 3.4. The asymmetry
Figure 3.3: Mean force on water (averaged over 1.5 ns) due to ion-water interactions in the positive, negative and uncharged pores. Inset: Mean force on a water molecule (averaged over 1.5 ns) in the axial direction along the centerline of the uncharged pore due to water-water and wall-water interactions. A positive mean force means that water is driven from the low solute chamber to the high solute chamber and vice versa. The first 1.5 ns represents about 75 % of the osmosis duration.
in other interactions (e.g. water-water) is negligible, though some of these interactions can be different in charged pores when compared to the uncharged pores. The effect of ion-water asymmetry on osmosis in charged pores is similar to that of in an uncharged pore.

In addition to ion-water asymmetry, Figure 3.4 indicates that the net mean force on a water molecule in the axial direction due to water-wall electrostatic interactions is higher near the pore mouth connected to $CH_l$ compared to the mean force near the pore mouth connected to $CH_h$. The positive mean force near the pore mouth connected to $CH_l$ moves the water molecules from $CH_l$ to $CH_h$. Since the positive mean force is much higher compared to the negative mean force, the net water movement (osmosis) is from the low solute chamber to the high solute chamber. From the above discussion, in the case of charged pores, we can infer that the osmosis is primarily caused due to the asymmetry in ion-water and water-wall electrostatic interactions, while in the case of uncharged pores the osmosis is primarily due to the asymmetry in the ion-water interactions. As a result, the osmotic flux in positively and negatively charged pores is found to be higher compared to the osmotic flux in the uncharged pore.

### 3.2.3 Mean force analysis

The flux in the negatively charged pore ($J_-$) is higher compared to the flux in the positively charged pore ($J_+$). This can be explained from Figure 3.4 by noting that the mean force on water (near the pore mouth connected to $CH_l$) due to water-wall electrostatic interactions is higher in the negatively charged pore compared to the positively charged pore. Note that the mean force near the pore mouth connected to $CH_h$ in both positively and negatively charged pores is similar, so the asymmetry is higher in the case of a negatively charged pore. The higher mean force near the pore mouth connected to $CH_l$ in the negative pore can be explained by comparing the dipole orientation of water in the two charged pores.

The inset in Figure 3.4 shows the time averaged dipole orientation of water with respect to the $z$-axis along the centerline of the pore. The dipole orientation is calculated by using
Figure 3.4: Mean force on a water molecule (averaged over 1.5 ns) in the axial direction along the centerline of the pore due to water-wall electrostatic interactions. Inset: Dipole orientation of water (averaged over 1.5 ns) in the positive and negatively charged pores along the centerline axis. $\theta$ is the angle between the H-O-H dipole and the positive $z$-axis.

Table 3.1: Probability for the water-chain to be broken in the pore (averaged over 1.5 ns).

<table>
<thead>
<tr>
<th></th>
<th>Uncharged</th>
<th>Positively Charged ($\sigma=0.12$ C/m$^2$)</th>
<th>Negatively Charged ($\sigma=-0.12$ C/m$^2$)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.8</td>
<td>0.36</td>
<td>0.056</td>
</tr>
</tbody>
</table>

the angle made by the angle-bisector of H-O-H with the positive $z$-axis. A positive $<\cos(\theta)>$ value implies that the water enters the pore in a single-file with the hydrogen atoms first. The water orientation during osmosis through the pore is opposite in the positive and negative pores. In the negative pore, water molecules enter with hydrogen atoms first, while the oxygen atoms enter first in the positively charged pore. Since the LJ interactions of the hydrogen atoms are negligible, in the negatively charged pore they tend to go closer to the pore wall, giving rise to a higher electrostatic interaction with the wall. Thus, the water molecules in the negative pore experience a higher mean force due to wall-water electrostatic interaction compared to a positively charged pore.
3.2.4 Water-chain stability in the pore

The osmotic flux through the nanopore can also be understood qualitatively by computing the probability of the water-chain to be broken in the pore. The probability of the single-file water chain being broken in the pore during osmosis was calculated for the uncharged and charged pores by dividing the number of times the water chain is broken during the 1.5 ns simulation time with the total number of steps at which statistics were collected (every 2.5 ps). The probability for the water-chain to be broken is highest in the uncharged pore and lowest in the negative pore, as shown in Table 3.1. A lower probability for the single-file water chain to be broken also suggests a higher osmotic flux.

![Figure 3.5: Mean force on water in the axial direction along the centerline of the pore due to (a) water-water and (b) ion-water interactions, during (averaged over 1.5 ns) and after (averaged over 2 to 4 ns) osmosis in the uncharged pore. At steady-state, the asymmetric ion-water mean force is counter-balanced by the asymmetric water-water mean force.](image)

3.2.5 Steady-state behavior

During osmosis the total mean force on water molecules is unbalanced across the pore. As time progresses, an increase in the number of water molecules in the $CH_h$ chamber leads to a more negative mean force on the water molecules in the pore mouth region connected to $CH_h$. A steady-state is reached when the positive mean force acting on the water molecules is balanced by the negative mean force. In the case of an uncharged pore, we observe
that (see Figure 3.5) during steady-state the net mean force on water due to water-water interactions (about -700 KJ/mol/nm) is balanced by the net mean force on water due to ion-water interactions (about 700 KJ/mol/nm). Note that at steady-state the ion-water asymmetry across the pore is lower compared to the ion-water asymmetry during osmosis and the asymmetry in other interactions (e.g. water-wall interactions) across the pore is still negligible at steady-state. In the case of charged pores, we observe that during steady-state the net negative mean force on water due to water-water interactions is balanced by the net positive mean force on water due to wall-water electrostatic and ion-water interactions.

The above study, when repeated on a larger semi-permeable pore of 1.2 nm diameter, yielded similar observations of the osmotic flux variation, indicating that the mechanism of water transport does not change as long as the pores are strictly semi-permeable.

![Figure 3.6: Hydrostatic pressure variation on the chamber walls (CH₁ and CH₂) over time. Pressure increases in CH₂ during osmosis and then saturates to a constant pressure difference (between CH₂ and CH₁) of 74 bar.](image)

Steady-state osmosis can be described by using the van’t Hoff equation, \( \Delta \Pi = RT \Delta C \), where \( R \) is the gas constant, \( T \) is the absolute temperature and \( \Delta C \) is the average solute concentration difference between the two chambers. By substituting the corresponding solute
concentrations into the van’t Hoff equation, the pressure difference between the two chambers is estimated to be 70 bar. We also computed the hydrostatic pressure in the two chambers using MD and Figure 3.6 shows the variation of the hydrostatic pressure with time in both the chambers. At steady-state, the pressure difference between the two chambers is about 74 bar, which matches reasonably well with the prediction from the van’t Hoff equation. From a molecular point of view, our results seem to suggest that at steady-state the asymmetry in water-water interactions is the primary contribution to the pressure difference between the two chambers.

From the discussion above we conclude that for single-file water transport through semi-permeable nanopores, using MD simulations, it is found that the osmotic flux in charged pores is higher compared to the osmotic flux in an uncharged pore. While ion-water interactions initiate osmosis in uncharged pores, both ion-water and wall-water electrostatic interactions initiate osmosis in the charged pores. During steady-state the mean force due to water-water asymmetry is primarily balanced by the mean force due to the ion-water (and wall-water in the case of charged pores) asymmetry. In the case of charged pores, water orientation near the mouth of a nanopore is found to be important and is shown to influence the osmotic flux.

### 3.3 Effect of size-asymmetric electrolyte on osmosis

From the above study we concluded that in uncharged pores, osmosis is primarily initiated by the ion-water interaction. If the ion-water interaction is significant in osmosis, then the next question that arises is: What is the effect of having different kinds of electrolytes in the chambers on the osmotic flux of water through the semi-permeable membrane? Recent studies were performed to understand the effect of electrolytes on osmosis. However, these were performed in leaky membranes where both the water molecules and ions go through the pore [16]. Using detailed MD simulations similar to that used for polarity effect studies,
we investigate the effect of size-asymmetric electrolytes on osmosis through an uncharged semi-permeable membrane.

An example of a size-asymmetric electrolyte is KCl, where the ion radius and the solvation radius of the potassium and chloride ions are different from each other. For an uncharged pore, the osmotic flux dependence of KCl, NaCl, KF and LiCl solutions, with the same concentration gradient of the solute in all cases, have been studied. The influence of the cation and anion affinity towards the pore on the osmotic flux through the pore has also been investigated. Similar to the earlier study, the mean force analysis is also carried out to explain the electrolyte dependence of osmosis. The effect of the ionic hydration analysis indicates a strong correlation between the ionic hydration and the cation and anion affinity to the pore.

### 3.3.1 Simulation Details

The MD simulation system (see Figure 3.7 for a snapshot), is similar to that used for the uncharged semi-permeable membrane studied earlier. Similar to the earlier setup, each membrane consists of a semi-permeable pore of diameter 0.9 nm. The membrane and the pore atoms are modeled as Lennard-Jones (LJ) atoms with parameters for carbon [68] and are frozen to their lattice positions.

MD simulations were performed using Gromacs 3.1.4 [36] in the NVT ensemble, with the temperature of the fluid maintained at 300 K using a Berendsen thermostat. The rest of the simulation details is the same as that given in section 3.2.1.

### 3.3.2 Results: Asymmetric electrolytes vs osmotic flux

The MD simulations were performed for four different size-asymmetric electrolytes (KCl, KF, NaCl and LiCl, having different bare and hydrated radii). The osmotic flux variation in all the simulations was calculated from the MD simulation by tracking the number of
water molecules in the chambers every 0.1 ps. At the start of the simulation, osmosis is dominant leading to the accumulation of water molecules in the high solute chamber ($CH_h$) and decrease in the number of water molecules in the low solute chamber ($CH_l$). However, the increase in the number of water molecules in $CH_h$ leads to an increase in the hydrostatic pressure developed that tends to drive the water molecules in the direction opposite to that of osmosis. At steady-state, the hydrostatic pressure developed between $CH_h$ and $CH_l$ ($\approx 74$ bar) balances the osmosis through the pore.

Figure 3.8 shows the variation of the number of water molecules with time in $CH_l$ and $CH_h$ chambers for KCl and NaCl solutions. We observe that the osmotic flux is higher when a KCl solution is used instead of an NaCl solution. In addition, the osmotic equilibrium is reached faster (in about 2 ns) when a KCl solution is used compared to the time required (close to 3 ns) with an NaCl solution.

The dependence of the osmotic flux on the type of the salt can be explained by understanding the affinity of an ion (cation/anion) to a nanopore. The affinity of an ion to the nanopore mouth is defined as the closest approach of an ion to the pore mouth. For example, if a cation is closer to the pore mouth compared to an anion, this is referred to as
Figure 3.8: Variation of the water occupancy in the two chambers during osmosis for NaCl and KCl electrolytes.

cation affinity and vice versa. In the case of a KCl salt, we observed cation affinity (i.e. K$^+$ ions are closer to the pore mouth compared to the Cl$^-$ ions) which led to a higher osmotic flux compared to an anion affinity in the case of an NaCl salt (the Cl$^-$ ion was found to be closer to the pore mouth compared to the Na$^+$ ion) which led to a lower osmotic flux. These observations and the inferences obtained from them are explained in more detail below.

### 3.3.3 Effect of the ion affinity on osmosis

The affinity of an ion towards a nanopore is primarily determined by two molecular interactions, namely, the ion-water interactions and the ion-nanopore interactions. Ion-water interactions determine the hydrated radius of an ion and are computed by accounting for the LJ and electrostatic interactions between the ion and the water molecules. Ion-nanopore interactions are computed by accounting for the LJ interaction between the ion and the carbon atoms of the nanopore. In a KCl solution, the LJ parameter, $\sigma_{K^+\cdot C} = 0.311$ nm, is smaller than the LJ parameter, $\sigma_{Cl^-\cdot C} = 0.365$ nm, implying that the $K^+$ ion can go
Figure 3.9: The variation in the PMF of ions in the (a) KCl and (b) NaCl solutions along the centerline of CH$_i$ chamber. The CH$_i$-nanopore interface is at an axial distance of 1.5 nm.
Table 3.2: The hydration # at the pore-$CH_h$ interface region for different salt solutions in the chamber during osmosis. Also listed are the LJ carbon-ion parameters and the ion with a higher affinity to the pore.

<table>
<thead>
<tr>
<th>Salt</th>
<th>Ion</th>
<th>Hydration #</th>
<th>(\sigma_{\text{ion-C}}) (nm)</th>
<th>Affinity to pore</th>
</tr>
</thead>
<tbody>
<tr>
<td>KCl</td>
<td>K$^+$,Cl$^-$</td>
<td>7, 5.75</td>
<td>0.311, 0.365</td>
<td>K$^+$</td>
</tr>
<tr>
<td>NaCl</td>
<td>Na$^+$,Cl$^-$</td>
<td>5.85, 6.5</td>
<td>0.3645, 0.365</td>
<td>Cl$^-$</td>
</tr>
<tr>
<td>KF</td>
<td>K$^+$,F$^-$</td>
<td>7.25, 5.95</td>
<td>0.311, 0.37</td>
<td>K$^+$</td>
</tr>
<tr>
<td>LiCl</td>
<td>Li$^+$,Cl$^-$</td>
<td>5.9, 6.5</td>
<td>0.41, 0.365</td>
<td>Cl$^-$</td>
</tr>
</tbody>
</table>

closer to the pore mouth compared to the Cl$^-$ ion. In addition, the hydrated radius of a K$^+$ ion (0.36 nm) is smaller than that of the Cl$^-$ ion (0.39 nm), implying again that the K$^+$ ion can go closer to the pore mouth region without significantly affecting its hydration shell as compared to a Cl$^-$ ion. These observations are confirmed from PMF analysis shown in Figure 3(a). In the low solute chamber ($CH_l$), the PMF valley (see Figure 3.9(a)) for the K$^+$ ion in the centerline region is closer to the pore mouth compared to that of the Cl$^-$ ion. We also observed that near the pore mouth, the hydration number for the K$^+$ ion is higher than that of the Cl$^-$ ion. All the above observations imply a higher affinity of the K$^+$ ion towards the pore mouth.

We also observed that the water molecules close to the pore mouth orient with their oxygen atoms pointing towards the K$^+$ ion and hydrogen atoms pointing towards the pore mouth. In fact, water molecules enter the pore with the same orientation i.e., with their dipole vector oriented in the direction from $CH_l$ to $CH_h$. In the case of an NaCl solution, the LJ parameter, \(\sigma_{Na^+_a-C} = 0.3645\) nm, is similar to the LJ parameter, \(\sigma_{Cl^-_a-C} = 0.365\) nm and thus the \(Na^+_a\) and Cl$^-$ interactions with the carbon pore are similar. However, a smaller hydrated radius of the Cl$^-$ ion (0.39 nm) as compared to the \(Na^+_a\) ion (0.42 nm), implies that the Cl$^-$ ion can go closer to the pore mouth region without breaking its hydration shell as compared to the \(Na^+_a\) ion. This is also evident from the PMF valley observed for Cl$^-$ ion close to the pore mouth in $CH_l$, as shown in Figure 3.9(b).
3.3.4 Water dipole orientation effects

The water dipole orientation in the pore is in a direction opposite to that observed in the KCl solution case, i.e., from $CH_h$ to $CH_l$. It was also observed that in the case of a KF solution (see Table 3.2), the K$^+$ ion is closer to the pore mouth and the water flux and water orientation were comparable to that of in a KCl solution. In an LiCl solution, the Cl$^-$ ion is closer to the pore mouth as compared to the Li$^+$ ion (which has higher hydration radius and strength of hydration shell as observed from the parameters given in Table 3.2). In this case, the osmotic flux and the water orientation are similar to those observed in the case of an NaCl solution.

3.3.5 Mean force analysis

The above observations can be understood from a mean force analysis of the various ions and water molecules across the pore. Our earlier discussion on osmosis through semi-permeable membranes have shown that in an uncharged pore, the asymmetry in the ion-water interaction across the axis of the pore initiates osmosis, while the water-water and wall-water interactions are symmetric and do not contribute much to osmosis. When the chambers were filled with a KCl solution, the ion-water mean force asymmetry across the pore (“pulling” water from the pore to $CH_h$) is found to be higher than that of when the chambers were filled with an NaCl solution (see Figure 3.10). This salt-dependence of osmotic flux can also be understood from the hydration number of the ion with a higher affinity to the pore in the high solute chamber.

As shown in Table 3.2, when the chambers are filled with a KCl solution, the ion with higher affinity to the pore (K$^+$) has a hydration number of 7, while in the case of an NaCl solution, the ion with higher affinity to the pore (Cl$^-$), has a slightly lower hydration number of 6.5. Thus, a K$^+$ ion “pulls” more water molecules from the pore in the case of a KCl solution as opposed to the Cl$^-$ ion in the case of an NaCl solution, i.e., $J_{KCl} > J_{NaCl}$. Similar
conclusions can be drawn by investigating the ion-water mean force, hydration number and osmotic flux when the chambers are filled with KF and LiCl solutions (see Table 3.2).

![Figure 3.10: Comparison of the ion-water mean force (kJ/mol/nm) when the chambers contain either KCl or NaCl solutions.](image)

To summarize the discussion presented in this section, the size-asymmetric electrolyte dependence of osmosis through a semi-permeable pore was studied using MD simulations. The osmotic flux through the pore is influenced by the differential cation and anion affinity to the pore. Simulation results indicate that the higher ion-water mean force asymmetry across the pore in the KCl or KF solutions (as compared to the NaCl or LiCl solution) gives rise to a higher osmotic flux through the pore. These results were also understood from the hydration numbers of the ions close to the pore mouth. The water orientation in the pore also exhibited a size-asymmetric electrolyte dependence, depending on the cation/anion affinity to the pore.
Chapter 4

Interatomic potential based semi-classical theory for confined LJ fluids

In this chapter, we formulate a semi-classical (inter-atomic) potential based theory to predict the concentration and potential profiles of LJ fluids confined in channels of widths ranging from $2\sigma_{ff} - 100\sigma_{ff}$ ($\sigma_{ff}$ is the fluid-fluid LJ parameter). For each of the channels studied, comparisons are made with MD simulations to analyze the accuracy of the proposed formulation. The results obtained from the semi-classical theory are found to be in good agreement with the MD simulation data. To our knowledge, this is the first semi-classical theory that while preserving the atomistic physics close to the wall, quickly and accurately predicts the concentration and potential profiles for a wide range of channel widths. This semi-classical theory can predict both the physics close to the interface, which cannot be explained using standard continuum theory, and the continuum theory in the bulk. Hence, the formulation is defined as a semi-classical formulation. The potential used in this formulation is the inter-atomic LJ potential between the atoms present in the channel. We illustrate in the following sections that the proposed formulation is a robust, fast and accurate method that can be used to predict the atomistic details at various length scales ranging from the nanoscale to the macroscale. It should be noted that the initial framework for the semi-classical formulation was developed by Dr. J. H. Park in the CMN group. I have contributed to making the framework accurate, including developing a better form for the soft-core potential for the LJ fluid, and more accurate MD simulations with which to compare the results with. The more accurate results I obtained from this theory are described in what follows.
4.1 Theoretical details of the semi-classical framework

Figure 4.1: Molecular representation (top) and a continuum representation (bottom) of a Lennard-Jones fluid confined between two channel walls.

We derive the semi-classical formulation for a LJ fluid confined between two solid walls that are infinite in the $y$- and $z$- directions (see Figure 4.1). Therefore, it is reasonable to assume a one-dimensional variation of the concentration of the fluid across the channel while deriving the semi-classical theory. For the derivation of the theory, we assume that the average concentration of the LJ fluid inside the channel, $c_{\text{avg}}$, and the wall-atom concentration, $c_{\text{wall}}$, are given. Our goal is to calculate the concentration and potential profile across the channel using the proposed formulation. If the total potential profile, $U$, in the channel is known, the fluid concentration, $c$, inside the channel can then be obtained by solving the
well known 1-D steady-state Nernst-Planck equation [58], i.e.,

$$\frac{\partial}{\partial x} \left( \frac{\partial c}{\partial x} + \frac{c}{RT} \frac{\partial U}{\partial x} \right) = 0$$  \hspace{1cm} (4.1)$$

where $R$ is the gas constant, $T$ is the temperature of the LJ fluid and $U$ is the total potential. Dirichlet boundary conditions are applied on both the channel wall boundaries, i.e., on $\Gamma_1 (x = 0)$ and $\Gamma_2 (x = L)$, (see Figure 4.1),

$$c(x = 0) = c_0$$
$$c(x = L) = c_L$$  \hspace{1cm} (4.2)$$

The concentration of the LJ fluid at the channel walls is zero, i.e., $c_0 = c_L = 0$. Hence, in order to solve Equation (4.1), an additional constraint has to be applied on the fluid concentration $c(x)$ inside the channel. Assuming that there is no mass transfer into or out of the channel, the average concentration of the LJ fluid atoms inside the channel will always be maintained. Hence, we impose a constraint on the concentration profile in the channel to ensure that the average concentration of the LJ fluid atoms inside the channel is $c_{avg}$, i.e.,

$$\frac{1}{L} \int_0^L c(x) dx = c_{avg}$$  \hspace{1cm} (4.3)$$

Typically, for large channels the concentration in the central part of the channel is close to the bulk value. In this case $c_{avg}$ is specified to be the bulk concentration of the fluid, $c_{bulk}$. For smaller channels, the average concentration is typically smaller than the bulk concentration and this is discussed further in the results section. To summarize, given the total potential profile $U(x)$ in the channel, one could obtain the concentration profile across the channel by solving Equation (4.1) with boundary conditions and constraints given by Equations (4.2) and (4.3).
4.1.1 Models for the total potential $U(x)$

The total potential at a point $x$ inside the channel, $U(x)$, depends on the concentrations of the wall and fluid atoms inside the channel as well as on the inter-atomic LJ force field of the wall and fluid atoms. $U(x)$ can thus be obtained by a summation of the fluid-fluid and the wall-fluid potential, i.e.,

$$U(x) = U_{\text{wall-fluid}}(x) + U_{\text{fluid-fluid}}(x).$$

(4.4)

The wall-fluid potential

The wall-fluid potential can be calculated from the integration of the contribution of a continuous distribution of wall atoms as was originally discussed by W. A. Steele [55, 56]. The wall-fluid potential at a point $x$, $U_{\text{wall-fluid}}(x)$, can be obtained by accounting for the interaction of an atom at a position $x$ with all the wall atoms in the neighborhood of $x$ by using the 12-6 LJ [34] wall-fluid inter-atomic potential, i.e.,

$$u_{\text{LJ}}^{\text{wf}}(r) = \left[ \frac{C_{12}^{\text{wf}}}{r^{12}} - \frac{C_{6}^{\text{wf}}}{r^{6}} \right]$$

(4.5)

where $C_{12}^{\text{wf}} = 4\epsilon_{\text{wf}}\sigma_{\text{wf}}^{12}$ and $C_{6}^{\text{wf}} = 4\epsilon_{\text{wf}}\sigma_{\text{wf}}^{6}$. $\epsilon_{\text{wf}}$ and $\sigma_{\text{wf}}$ are the wall-fluid LJ energy and distance parameters, respectively. In the pair-wise LJ interaction, the potential is negligible beyond a certain cut-off distance which is defined as $R_{\text{cut}}$. Let $N_w$ be the number of wall atoms within a sphere of radius $R_{\text{cut}}$ from the point $x$. The total wall-fluid potential at the point $x$ using a molecular representation is then given by:

$$U_{\text{wall-fluid}}(x) = \sum_{i=1}^{N_w} u_{\text{LJ}}^{\text{wf}}(x - x_i)$$

(4.6)
where \( x_i \) is the location of the wall atom \( i \). Representing the wall atoms by a density, \( c_{\text{wall}}(x_i) \), we can approximate the wall-fluid potential at the point \( x \) by

\[
U_{\text{wall-fluid}}(x) = \sum_{i=1}^{N_l} u_{LJ}^{wf}(x - x_i)c_{\text{wall}}(x_i)\Delta\Omega_i
\]

(4.7)

where \( N_l \) denotes the number of radial wall layers that represent the wall atoms within the sphere of radius \( R_{\text{cut}} \), \( c_{\text{wall}}(x_i) \) is the density of the wall atoms in the \( i \)th radial layer and \( \Delta\Omega_i \) is the volume of the \( i \)th radial layer.

Figure 4.2: The shaded region in the figure (top) is the volume circumscribed by the sphere of radius \( R_{\text{cut}} \) located at the point \( x \) with the channel wall. Figure (bottom) also shows the disk layer of thickness \( dx' \) and radius \( \sqrt{R_{\text{cut}}^2 - (x - x')^2} \) used for the purpose of integration of Equation (4.8) in the circumscribed volume.
A continuum approximation for the discrete summation given in Equation (4.7) is given by:

\[ U_{\text{wall-fluid}}(x) = \int_{\Omega} u_{\text{LJ}}^w(x - x')c_{\text{wall}}(x')d\Omega \]  

(4.8)

where \( \Omega \) is the volume of the wall atoms circumscribed by the sphere of radius \( R_{\text{cut}} \). The circumscribed volume is shown as the shaded region in Figure 4.2. To evaluate the integral in Equation (4.8), we assume that the circumscribed volume is composed of circular disks located at \( x' \) with a thickness \( dx' \) (see Figure 4.2). The wall-fluid potential at \( x \) due to a circular disk can be expressed as:

\[ dU_{\text{wall-fluid}}(x) = \left[ \int_0^{S_1} u_{\text{LJ}}^w(S)c_{\text{wall}}(x')2\pi sds \right] dx' \]  

(4.9)

where \( S = \sqrt{s^2 + (x - x')^2} \) and \( S_1 = \sqrt{R_{\text{cut}}^2 - (x - x')^2} \). Since \( R_{\text{cut}} \) is used only for computational efficiency in molecular simulations, a more accurate treatment is:

\[ dU_{\text{wall-fluid}}(x) = \left[ \int_0^\infty u_{\text{LJ}}^w(S)c_{\text{wall}}(x')2\pi sds \right] dx' \]  

(4.10)

Assuming the walls are infinitely thick, the total wall-fluid potential can be rewritten as:

\[ U_{\text{wall-fluid}}(x) = \int_{-\infty}^0 dU_{\text{wall-fluid}} dx' \]  

(4.11)

If the wall-fluid potential at the point \( x \) is influenced by both walls, then

\[ U_{\text{wall-fluid}}(x) = \int_{-\infty}^0 dU_{\text{wall-fluid}} dx' + \int_0^\infty dU_{\text{wall-fluid}} dx' \]  

(4.12)

If the wall-atom concentration \( c_{\text{wall}} \) is assumed to be uniform, the total wall-fluid potential...
\[ U_{\text{wall-fluid}} \text{ is then given by:} \]

\[
U_{\text{wall-fluid}}(x) = c_{\text{wall}} \int_{-\infty}^{0} \int_{-\infty}^{\infty} \left[ \frac{C_{12}^{\text{ff}}}{\sigma_{f}^{12}} - \frac{C_{6}^{\text{ff}}}{\sigma_{f}^{6}} \right] 2\pi s ds dx' + c_{\text{wall}} \int_{0}^{\infty} \int_{0}^{\infty} \left[ \frac{C_{12}^{\text{ff}}}{\sigma_{f}^{12}} - \frac{C_{6}^{\text{ff}}}{\sigma_{f}^{6}} \right] 2\pi s ds dx' \]  

\[(4.13)\]

Simplifying Equation (4.13), the final expression for \( U_{\text{wall-fluid}} \) at the position \( x \) is given by:

\[
U_{\text{wall-fluid}}(x) = \frac{2\pi C_{12}^{\text{ff}} c_{\text{wall}}}{90} \left[ \frac{1}{x^9} + \frac{1}{(L-x)^9} \right] - \frac{2\pi C_{6}^{\text{ff}} c_{\text{wall}}}{12} \left[ \frac{1}{x^3} + \frac{1}{(L-x)^3} \right] \]  

\[(4.14)\]

**The fluid-fluid potential**

In an atomistic approach, the fluid-fluid potential at a position \( x \), \( U_{\text{fluid-fluid}}(x) \) can be obtained by summing the inter-atomic fluid-fluid potential \( (u_{\text{ff}}^{LJ}) \) over all the fluid atoms surrounding the position \( x \). The inter-atomic fluid-fluid potential \( u_{\text{ff}}^{LJ} \) is given by:

\[
u_{\text{ff}}^{LJ}(r) = \left[ \frac{C_{12}^{\text{ff}}}{r^{12}} - \frac{C_{6}^{\text{ff}}}{r^{6}} \right] \]  

\[(4.15)\]

where \( C_{12}^{\text{ff}} = 4\epsilon_{f f} \sigma_{f f}^{12} \) and \( C_{6}^{\text{ff}} = 4\epsilon_{f f} \sigma_{f f}^{6} \). \( \epsilon_{f f} \) and \( \sigma_{f f} \) are the fluid-fluid LJ energy and distance parameters, respectively. Assuming that the LJ potential is negligible beyond a certain cutoff distance \( R_{\text{cut}} \) from the point \( x \), \( U_{\text{fluid-fluid}} \) is given by:

\[
U_{\text{fluid-fluid}}(x) = \sum_{i=1}^{N_f} u_{\text{ff}}^{LJ}(x - x_i) \]  

\[(4.16)\]

where \( N_f \) is the number of fluid atoms within the sphere of radius \( R_{\text{cut}} \) from the point \( x \). Representing the fluid atoms by a density, \( c(x_i) \), we can approximate the fluid-fluid potential at a point \( x \) to be:

\[
U_{\text{fluid-fluid}}(x) = \sum_{i=1}^{N_m} u_{\text{ff}}^{LJ}(x - x_i) c(x_i) \Delta\Omega_i' \]  

\[(4.17)\]
where $N_m$ denotes the number of fluid layers representing the fluid atoms within the sphere of radius $R_{cut}$, $c(x_i)$ is the density of the fluid atoms in the $i^{th}$ radial fluid layer and $\Delta \Omega'_i$ is the volume of the $i^{th}$ radial layer.

Similar to the calculation of the wall-fluid potential, the calculation of the potential from the fluid atoms can also be performed by using a continuum approach. The continuum approximation for the discrete summation given in Equation (4.17) is:

$$U_{fluid-fluid}(x) = \int_{\Omega'} u_{LJ}^{ff}(r)c(x')d\Omega'$$

(4.18)

where $r = |x - x'|$, $\Omega'$ is the volume circumscribed by the sphere of radius $R_{cut}$ within the channel (excluding any volume that might be circumscribed on the channel walls).

For the fluid layers within a distance of $\sigma_{ff}$ from the point $x$, if we assume that $c$ approximately obeys the Boltzmann distribution, then $c$ has the form of $\exp\left(-u_{LJ}^{ff}/K_B T\right)$ ($K_B$ is the Boltzmann constant). This indicates that the variation of $r$ in the integrand of Equation (4.18) is of the order of $O(r^{-23})$. This very high degree of $r$ in the integrand will lead to numerical singularities when evaluating Equation (4.18) for $r \to 0$. Hence, to calculate the fluid-fluid potential, we introduce a truncated soft-core LJ potential, $u_{LJ}^{t}(r)$, that consists of a modified functional form for the repulsive core of the 12-6 LJ potential. We define the functional form for $u_{LJ}^{t}(r)$ in a similar fashion to that used by Mezei [41] for free energy calculations of dense LJ fluids. The expression for $u_{LJ}^{t}$ is given by:

$$u_{LJ}^{t}(r) = \begin{cases} 
0 & r \leq R_{crit} \\
2 - \left(\frac{r}{R_{min}}\right)^2 & R_{crit} < r \leq R_{min} \\
\left(c_{12}^{ff} - c_{6}^{ff}\right) & R_{min} \leq r \leq R_{cut}
\end{cases}$$

(4.19)

where $R_{min}$ is the distance within which the modified soft-core repulsion term exists and $R_{crit}$ is the distance within which the interaction potential is assumed to be zero.

The form closest to the truncated LJ fluid-fluid potential given above was originally
Figure 4.3: A fluid layer located at $x'$ is shown in the figure (top), along with the volume circumscribed by the sphere of radius $R_{cut}$ on this layer. The circular disk of radius $\sqrt{R_{cut}^2 - r^2}$ and thickness $dx'$ of this circumscribed volume is shown in the figure (bottom). The fluid-fluid potential due to this fluid layer on the point $x$ is computed by integrating along the radius ($s$) and the thickness ($r$) of the layer.

used by Dr. J. H. Park from the form given by Mezei [41], for developing the semi-classical framework. The form used by Dr. J. H. Park included the inner squared term given in Equation (coarsegraineqn). However, the power of the squared term was not accurate enough to obtain good comparisons for the multiscale and MD simulations. I have extended the same form used as shown in Equation (4.19) to obtain results that are in better comparison with MD simulations.

It can be observed from Equation (4.19) that $u_{LJ}^i(r)$ consists of a soft-core repulsive term and a zero potential region within an “inner” core close to $r = 0$. Additionally, $u_{LJ}^i$ is not singular at the point $r = 0$. In this paper, we use $R_{min} = 0.939\sigma_{ff}$ and $R_{crit} = 0.29\sigma_{ff}$.
Figure 4.4: The comparison between the inter-atomic 12-6 LJ fluid-fluid potential $u_{LJ}^{ff}$ and the truncated soft-core LJ potential $u_{LJ}^{t}$ used in the semi-classical formulation. The plot in the inset shows the variation of the attractive part of the potential in more detail.

These parameters were determined by matching the fluid-fluid potential for a large channel (e.g., in this paper we have used a $11\sigma_{ff}$ channel) with the fluid-fluid potential obtained from molecular dynamics simulations. Figure 4.4 shows the comparison of $u_{LJ}^{ff}$ with $u_{LJ}^{t}$ given by Equation (4.19) for these $R_{min}$ and $R_{crit}$ values.

Substituting $u_{LJ}^{t}$ instead of $u_{LJ}^{ff}$ in Equation (4.18) we obtain the total fluid-fluid potential given by,

$$U_{\text{fluid-fluid}}(x) = \int_{\Omega'} u_{LJ}^{t}(r) c(x') d\Omega'$$

(4.20)

As shown in Figure 4.3, Equation (4.20) is integrated by assuming circular disks of thickness $dx'$ spanning the region $\Omega'$. The total fluid-fluid potential can thus be rewritten as:

$$U_{\text{fluid-fluid}}(x) = \int_{x-R_{cut}}^{x+R_{cut}} \left[ \int_{0}^{\sqrt{R_{cut}^2-r^2}} u_{LJ}^{t}(r, s) c(x') (2\pi s) ds \right] dx'$$

(4.21)

It should be noted that the limits of integration for $x'$ in Equation (4.21) will change when the point $x$ is closer than $R_{cut}$ from one of the channel walls. Details regarding further
simplification of Equation (4.21) are provided in the Appendix.

4.1.2 Implementation of the semi-classical framework

The semi-classical formulation to compute the concentration of a LJ fluid sandwiched between two channels is given by Equation (4.1), with boundary conditions given by Equations (4.2) and (4.3). The total potential, $U$, needed in Equation (4.1) is given by Equation (4.4). The contributions of the wall-fluid and fluid-fluid interactions to the total potential are computed by Equations (4.14) and (4.21), respectively. Since the fluid-fluid potential, $U_{\text{fluid-fluid}}$, is a function of the concentration of the fluid, $c$, Equation (4.1) is nonlinear, and an iterative scheme needs to be used to find the self-consistent concentration and potential.

The implementation of the semi-classical theory is summarized in Algorithm 2. The input parameters needed for the implementation are the wall-fluid and the fluid-fluid LJ parameters, the average fluid concentration inside the channel $c_{\text{avg}}$, the concentration of the wall atoms, $c_{\text{wall}}$, and the length of the channel, $L$. The initial concentration of the fluid is assumed to be uniform throughout the channel with a value of $c_{\text{avg}}$. Given the concentration of the wall atoms, the wall-fluid potential can be computed using Equation (4.14). Note that the wall-fluid potential needs to be computed only once as it does not depend on the concentration of the fluid. Using the initial guess for the fluid concentration, the fluid-fluid potential is computed using Equation (4.21). Equation (4.1) is then solved to find the new fluid concentration. Since Equation (4.1) is highly nonlinear, to obtain proper convergence we use a relaxation parameter, $\alpha$, as shown in Step 8 of Algorithm 2, to obtain the concentration during the iterative process. In this paper, we use $\alpha = 0.65$. The iterative process is repeated until a self-consistent solution is obtained.

The proposed semi-classical formulation can be easily applied to other geometries, e.g., nanopores. In addition, for geometries where the total potential varies not just along one-dimension but along two- or three-dimensions, can be extended by considering a multi-dimensional form of Equation (4.1).
Algorithm 2 The algorithm for the semi-classical theory

1: Input: LJ force field parameters for the wall \((\sigma_{wf}, \epsilon_{wf})\) and the fluid atoms \((\sigma_{ff}, \epsilon_{ff})\), relaxation parameter \(\alpha\), average concentration of the fluid, \(c_{avg}\), concentration of LJ wall atoms, \(c_{wall}\), and the channel width, \(L\).

2: Set the initial guess, \(c^0 = c_{avg}\).

3: Set counter \(n = 1\) and tolerance, \(tol\) (typically, \(tol = 1 \times 10^{-3}\)).

4: repeat

5: Calculate \(U_{wall-fluid}^n\) and \(U_{fluid-fluid}^n\) from concentration \(c^{n-1}\) using Equations (4.14) and (4.21).

6: \(U^n = U_{wall-fluid}^n + U_{fluid-fluid}^n\)

7: Using \(U^n\), solve Equation (4.1) with boundary conditions given by Equations (4.2) and (4.3) to obtain \(c_{new}^n\).

8: Perform relaxation step: \(c^n = c^{n-1} + \alpha(c_{new}^n - c^{n-1})\)

9: \(n = n + 1\)

10: until \(|c^n - c^{n-1}| < tol\)

11: The converged concentration \((c^n)\) and potential profile \((U^n)\) across the channel are obtained.

4.2 The semi-classical framework and MD:

Simulation details

Equation (4.1) is normalized with respect to the channel width \((x^* = x/L)\), the thermal energy \((U^* = U/RT)\), and the bulk fluid concentration \((c^* = c/c_{bulk})\). The normalized equation is given by:

\[
\frac{\partial}{\partial x^*} \left( \frac{\partial c^*}{\partial x^*} \right) = \frac{\partial}{\partial x^*} (c^* P_s) \tag{4.22}
\]

Here, the non-dimensional parameter, \(P_s\), is defined as the pseudo Peclet number and is given by:

\[
P_s = -\frac{L}{RT} \frac{dU}{dx} \tag{4.23}
\]

Various numerical techniques can be used to solve Equation (4.22) and in this study we have used the finite volume method (FVM) [23]. In Equation (4.22), \(P_s\) is highly non-linear close to the channel wall since the gradient of the potential can be high close to the channel wall region. The variation of \(P_s\) in a channel of width \(L = 7\sigma_{ff}\) is shown in Figure 4.5. It can
Figure 4.5: The pseudo Peclet number $P_s$ across a channel of width $7\sigma_{ff}$ (only half the channel is shown).

Table 4.1: Parameters for the Lennard-Jones potential.

<table>
<thead>
<tr>
<th>Interaction</th>
<th>$C_6$ (kJ nm$^6$ mol$^{-1}$)</th>
<th>$C_{12}$ (kJ nm$^{12}$ mol$^{-1}$)</th>
<th>$\sigma$ (nm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>O-O</td>
<td>$0.26187 \times 10^{-2}$</td>
<td>$0.26307 \times 10^{-8}$</td>
<td>0.317</td>
</tr>
<tr>
<td>O-Si</td>
<td>$0.62337 \times 10^{-2}$</td>
<td>$0.76929 \times 10^{-5}$</td>
<td>0.3277</td>
</tr>
<tr>
<td>Si-Si</td>
<td>$0.14738 \times 10^{-1}$</td>
<td>$0.22191 \times 10^{-4}$</td>
<td>0.3385</td>
</tr>
</tbody>
</table>

be observed from the figure that $P_s$ is small in the center of the channel but has a significant non-linear variation close to the channel wall. This non-linear variation in $P_s$ indicates that numerical stabilization techniques need to be used to solve Equation (4.22). In this study, we have used the exponential numerical scheme to solve a convection-diffusion equation first proposed by Spalding [54, 45].

The results obtained from the semi-classical theory are compared with the results from MD. MD simulations are performed for a LJ fluid confined in a nanochannel as shown in Figure 4.1(top). The dimensions of the channel wall in the $y$- and $z$- directions are both 4.4 nm. The channel walls are made up of LJ atoms with the parameters of silicon obtained from
the GROMOS force field [37]. The density of the channel walls is $c_{\text{wall}} = 80$ atoms/nm$^3$. The walls consisted of 6-layers of silicon atoms with an inter-layer spacing of 0.195 nm. The fluid inside the channel has the LJ parameters of the water-oxygen atoms from the SPC/E force field [32]. The bulk concentration of the LJ fluid inside the channel is $c_{\text{bulk}} = 32$ atoms/nm$^3$. Table 4.1 gives the LJ force field used for the wall (silicon) and fluid (water-oxygen) atoms in our simulations studies. The time step for the NVT MD simulation was 2 fs and the LJ cutoff distance was 1.38 nm. The temperature of the fluid was maintained at 300 K during the simulation using a Nose-Hoover thermostat [44], with a time constant of 0.5 ps. The MD simulation was performed using GROMACS [37]. The range of channel widths used in the MD simulations were from $2\sigma_{ff}$ to $40\sigma_{ff}$.

### 4.3 Results: Comparison of the semi-classical theory with MD

![Figure 4.6](image_url)

Figure 4.6: Comparison of the density profile across a $11\sigma_{ff}$ channel obtained from MD simulation and the semi-classical theory.
4.3.1 Comparison of the concentration and potential profiles

The accuracy of the semi-classical formulation was investigated by comparing the concentration and potential profiles obtained for different channel widths with those from MD simulations. The comparison of the concentration profiles for 11σ_{ff} channel is shown in Figure 4.6. The average concentration used in the boundary condition given by Equation (4.3) in the semi-classical formulation was the bulk fluid concentration, \( c_{\text{avg}} = c_{\text{bulk}} = 32 \text{ atoms/nm}^3 \) (corresponds to 55M). The concentration profiles obtained from the MD simulation and the semi-classical formulation are found to be in good agreement. Both approaches predict a “bulk-like” region in the channel center and the well-known “layering” of fluid near the wall. A total of 11 fluid concentration peaks are observed and their magnitude diminishes while approaching the channel center. The location of the peaks is approximately σ_{ff} from each other. The concentration of the first peak from the channel wall is located between 0 and σ_{ff}, the second peak is located between σ_{ff} and 2σ_{ff}, and so on till the center of the channel, making up the 11 peaks. The formation of the 11 peaks can be explained by investigating the total potential and its two components — wall-fluid and fluid-fluid potential as shown in Figure 4.7. From the total potential it can be deduced that typically, the valley in the potential corresponds to the peak in the concentration, i.e., there are 11 valleys in the total potential corresponding to the 11 peaks in the concentration profile.

The total potential, \( U \), has a valley in the region within σ_{ff} from the channel wall. As shown in Figure 4.7 the wall-fluid potential, \( U_{\text{wall-fluid}} \), also has a valley there while the fluid-fluid potential, \( U_{\text{fluid-fluid}} \), has a positive peak. Thus, it can be deduced that the first valley in the total potential (corresponds to the first peak in the concentration) is primarily due to \( U_{\text{wall-fluid}} \), while the \( U_{\text{fluid-fluid}} \) acts to diminish this valley. Furthermore, the magnitudes of valleys in \( U_{\text{fluid-fluid}} \) become less significant as we approach the center of the channel. These valleys are responsible for the remaining 9 peaks in the concentration profile. The wall-fluid potential also influences these peaks, but in a less significant manner and only within 4σ_{ff}
from the channel wall. The valleys in the fluid-fluid potential do not exactly correspond with the valleys in the total potential because of the contribution from the wall-fluid potential.

It is observed that there is difference in the first peak of the concentration obtained from MD and the semi-classical formulation. The first peak obtained from MD simulation is 105 atoms/nm$^3$ while that from the semi-classical formulation is 175 atoms/nm$^3$. This difference originates from the small difference in the total potential, $U$, within a distance $\sigma_{ff}$ from the channel wall as shown in Figure 4.7. This difference in $U$ is due to both the $U_{\text{wall-fluid}}$ and the $U_{\text{fluid-fluid}}$. Within $\sigma_{ff}$ from the wall, the valley of the $U_{\text{wall-fluid}}$ potential from the semi-classical formulation has a smaller magnitude as compared to the MD data. If the difference in $U$ is dominated by $U_{\text{wall-fluid}}$, then the first peak in the concentration from the
Figure 4.8: Comparison of the density profile across a $7\sigma_{ff}$ channel obtained from MD and the semi-classical formulation.

The semi-classical formulation will be smaller than that from the MD simulation—contrary to the observation in the concentration profile. However, the $U_{\text{fluid-fluid}}$ potential is also found to influence this difference. $U_{\text{fluid-fluid}}$ from the semi-classical formulation is lower than the $U_{\text{fluid-fluid}}$ data from MD at the position of the first concentration peak ($\approx 0.9\sigma_{ff}$ from the wall). The combined effect of the $U_{\text{fluid-fluid}}$ (with a difference of $-0.4K_BT$ in potential as compared to MD) and $U_{\text{wall-fluid}}$ (with a difference of $0.05K_BT$ in potential as compared to MD) results in the magnitude of total potential, $U$, being larger for the semi-classical formulation, i.e., a more negative potential. Assuming that the concentration and the total potential obey the Boltzmann distribution, the first concentration peak observed from the semi-classical formulation is higher than that from the MD simulation. The difference in the $U_{\text{fluid-fluid}}$ potential could be due to the truncated soft core potential introduced in Equation (4.19). Though the truncated potential works well for bulk systems, it may not capture all the features in the interfacial region, leading to the deviation in $U_{\text{fluid-fluid}}$. Especially closer to the wall, i.e., $<0.7\sigma_{ff}$ from the wall, the deviation between the semi-classical and MD data in $U_{\text{fluid-fluid}}$ is significant. However, this deviation has a negligible influence on the
converged solution (concentration) because the concentration itself is negligible in this region due to the large value in $U_{\text{wall-fluid}}$ and subsequently in $U$.

Figure 4.9: Comparison of (a), the total potential, (b), the wall-fluid potential and (c), the fluid-fluid potential, across a $7\sigma_{ff}$ channel from MD and semi-classical simulation.

Further comparisons of the concentration and potential profiles were performed on channels with smaller widths. The concentration profiles obtained from MD and the semi-classical formulation are in good agreement in the case of the $7\sigma_{ff}$ wide channel. Since there is no “bulk” region in this case, the value of $c_{\text{avg}}$, which is also used in the semi-classical formulation, will be less than the bulk concentration, $c_{\text{bulk}}$. To enable proper comparison with MD simulations, $c_{\text{avg}}$ was evaluated from the total number of atoms in the channel in the MD simulation divided by the volume of the channel region. In this channel, the volume of the channel is found to be $430 \ \text{nm}^3$ ($7\sigma_{ff} \times 4.4 \times 4.4$) and the number of fluid atoms in the channel in MD was 1285. Hence, the average fluid concentration is evaluated as $c_{\text{avg}} = 30 \ \text{atoms/\text{nm}^3}$. 

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Figure 4.8 shows the comparison of the concentration profile obtained from both approaches. Consistent with the observations in the $11\sigma_{ff}$ channel, 7 concentration peaks are observed in the $7\sigma_{ff}$ channel. The total potential, wall-fluid and the fluid-fluid potential are shown in Figure 4.9. The difference in the first peak in the concentration profile can again be explained using the wall-fluid and fluid-fluid potential, as was done in the case of the $11\sigma_{ff}$ channel.

4.3.2 Comparison in very small channels

![Figure 4.10: The concentration profile in a $3\sigma_{ff}$ channel obtained from MD and semi-classical simulation.](image)

The concentration and potential profiles obtained from MD and the semi-classical formulation compare reasonably well even in smaller channels for widths ranging from $2\sigma_{ff}$ to $6\sigma_{ff}$. The comparison of the concentration profile in the $3\sigma_{ff}$ channel is shown in Figure 4.10. Similar to the $7\sigma_{ff}$ channel, to make proper comparison between MD and results, the value of $c_{avg}$ for the $3\sigma_{ff}$ channel was calculated from the number of atoms used in the MD simulation and the value is 26 atoms/nm$^3$. The semi-classical theory shows a good
agreement with the MD data except for the first peak. The magnitude of the peak closer to the wall is higher with the semi-classical formulation compared to the MD data. Again, this difference can be explained from the potentials in the channel. The comparison of the total potential, wall-fluid and fluid-fluid potential obtained from MD and semi-classical formulation are shown in Figure 4.11. Similar to the observation for the $11\sigma_{ff}$ case, the wall-fluid potential from the semi-classical formulation is higher at the first concentration peak as compared to the MD data and the fluid-fluid potential from the semi-classical formulation is lower than MD data at the same location. Higher difference in fluid-fluid potential leads to a lower value for the first valley of the combined total potential. Hence, the corresponding concentration peak is overestimated by the semi-classical formulation. The considerable
deviation of the fluid-fluid potential even closer to the wall ($< 0.7\sigma_{ff}$) and its negligible impact on the calculated concentration profile is similar to that observed and explained for the $11\sigma_{ff}$ channel. In addition, we also observe that the concentration peak at the center of the channel is much diminished as compared to the peak at the center in the $7\sigma_{ff}$ channel. This observation is because of two reasons. First, the region available for the fluid molecules is typically the region $\sigma_{wf} < x < L - \sigma_{wf}$. In the $3\sigma_{ff}$ case, this region is about $\sigma_{ff}$. Hence, there does not exist enough room in the central region for the formation of a significant fluid layer. Second, the wall-fluid potential from channel walls on either side overlap, i.e., the wall-fluid potential at the center of the channel is considerable due to the contribution from the channel walls on either side (see Figure 4.11(b)). This wall-fluid potential overlap also prevents the formation of a significant concentration peak at the center of the channel. From the above discussion, it can be concluded that the semi-classical formulation is quite successful in predicting the fluid concentration in the channel even when the size of the central region is only about $\sigma_{ff}$.

![Figure 4.12: The concentration profile in a $2\sigma_{ff}$ channel obtained from MD and the semi-classical simulations.](image)

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As we further shrink the size of the channel width to $2\sigma_{ff}$, we still observe a good match for the concentration profile (see Figure 4.12). The concentration was much smaller than the bulk concentration and using the procedure outlined earlier, $c_{avg} = 16 \text{ atoms/nm}^3$ was obtained and used in the semi-classical formulation. Consistent with the trend in bigger channels, one would expect two concentration peaks in the $2\sigma_{ff}$ channel. However, the number of peaks obtained is one and not two. The reason for this is apparent from the analysis of the total potential, wall-fluid potential and fluid-fluid potential (see Figure 4.13). The wall-fluid potential overlap from the channel wall on either side becomes even larger than that in the case of the $3\sigma_{ff}$ channel. Thus, there is no attractive region (negative potential region) in the wall-fluid potential throughout channel (see Figure 4.13(b)). Equation (4.14) still predicts a reasonable match for the wall-fluid potential with the MD data. Unlike in the higher channel width cases, as there exists only one valley in the wall-fluid potential, it contributes to only one concentration peak. The fluid-fluid potential has no valley and thus does not contribute to the formation of another concentration peak. The semi-classical formulation has successfully captured this phenomenon and reasonably matches the concentration profile obtained from the MD simulation. There still exists a difference in the fluid-fluid potential calculated from MD and the semi-classical formulation very close to the channel wall. The reason that this deviation does not affect the obtained concentration profiles is the same as explained in the $3\sigma_{ff}$ channel case. It should be noted that a more accurate calculation of the wall-fluid potential in all these channel widths would involve accounting for the discreteness of the channel wall. Also, $2\sigma_{ff}$ was the smallest channel through which fluid atoms enter in an MD simulation. In a $1\sigma_{ff}$ channel, fluid atoms hardly enter the channel, since there is a strong repulsion by the LJ potential from both walls.

### 4.3.3 Predictions in large channels

The concentration profile obtained from the semi-classical formulation and MD are in good match for a relatively large channel of width $20\sigma_{ff}$, as shown in Figure 4.14(a). For an even
larger channel, e.g., a $100\sigma_{ff}$ channel, the MD simulation is computationally expensive. However, even for such a big channel, the atomistic features in the interfacial region can be quite significant. Although a lot of work has gone in developing a model or formulation to capture the atomistic features with a very low computing cost for very large channels, it has yet to be successful. The semi-classical formulation that has been proposed here has been successful in this regard. Figure 4.14(b) shows the concentration obtained from the semi-classical formulation for this large channel. As shown in the figure (inset), both the “layering” of the fluid very close to the wall as well as the “bulk” concentration at the center of the channel are captured using the semi-classical formulation. The number of
Figure 4.14: The concentration profile of the LJ fluid in a (a), 20σ_{ff} wide channel obtained from MD and semi-classical formulation, and (b), in a 100σ_{ff} wide channel obtained from the semi-classical simulation. The inset in (b) shows the “layering” in the concentration profile close to the channel wall region.

concentration peaks that can be observed is much smaller than 100, since the peaks diminish to the “bulk” concentration within a distance of 10σ_{ff} from the channel wall. It is apparent that using a relatively inexpensive computations for the semi-classical theory, one could obtain the concentration and potentials in 100σ_{ff} or even higher channel widths. Hence, the semi-classical formulation can be used for fast computations involving very large channels without any loss in the atomistic detail close to the wall-fluid interface.

To summarize, an interatomic potential based semi-classical theory, , has been proposed to predict the concentration and potential profiles of a LJ fluid confined between two channel walls. The proposed semi-classical formulation solves the Nernst-Planck equation, using a potential obtained from an atomistic description. While the wall-fluid potential was cal-
culated from the 12-6 LJ potential, the fluid-fluid potential is evaluated by introducing a truncated soft core LJ atomistic potential. It is observed that the concentrations and potentials predicted by the are in good agreement with the MD simulations for all the channel widths studied - ranging from $2\sigma_{ff}$ to $20\sigma_{ff}$ - thus validating the accuracy of the semi-classical formulation. The semi-classical formulation can be further improved by developing more advanced models for the wall-fluid and coarse-grained approaches for the fluid-fluid potential. This formulation provides a means to capture the underlying atomistic physics in the interfacial region without resorting to computationally intensive atomistic simulations. Further, the semi-classical formulation was used to capture the interfacial behavior in a very large $100\sigma_{ff}$ channel, for which MD simulation is computationally much more expensive. The ease of implementation and the robustness of the approach make it unique to ascertain the static fluid properties at scales ranging from the macroscale to a few atomic diameters.
Chapter 5

Conclusions

In this thesis, first, we studied the osmosis in single-file water transport through semi-permeable nanopores using MD simulations. We found that the osmotic flux in charged pores is higher compared to the osmotic flux in an uncharged pore. While ion-water interactions initiate osmosis in uncharged pores, both ion-water and wall-water electrostatic interactions initiate osmosis in the charged pores. During steady-state the mean force due to water-water asymmetry is primarily balanced by the mean force due to the ion-water (and wall-water in the case of charged pores) asymmetry. In the case of charged pores, water orientation near the mouth of a nanopore is found to be important and is shown to influence the osmotic flux.

Second, the size-asymmetric electrolyte dependence of osmosis through a semi-permeable pore was also studied using MD simulations. The osmotic flux through the pore is influenced by the differential cation and anion affinity to the pore. Simulation results indicate that the higher ion-water mean force asymmetry across the pore in the KCl or KF solutions (as compared to the NaCl or LiCl solution) gives rise to a higher osmotic flux through the pore. These results were also understood from the hydration numbers of the ions close to the pore mouth. The water orientation in the pore also exhibited a size-asymmetric electrolyte dependence, depending on the cation/anion affinity to the pore.

Third, an inter-atomic potential based semi-classical theory has been proposed to predict the concentration and potential profiles of a LJ fluid confined between two channel walls. The proposed formulation solves the Nernst-Planck equation, using a potential obtained from an atomistic description. While the wall-fluid potential was calculated from the 12-
6 LJ potential, the fluid-fluid potential is evaluated by introducing a truncated soft core LJ atomistic potential. It is observed that the concentrations and potentials predicted by the semi-classical theory are in good agreement with the MD simulations for all the channel widths studied - ranging from $2\sigma_{ff}$ to $20\sigma_{ff}$ - thus validating the accuracy of the formulation. The formulation can be further improved by developing more advanced models for the wall-fluid and coarse-grained approaches for the fluid-fluid potential. The semi-classical approach provides a means to capture the underlying atomistic physics in the interfacial region without resorting to computationally intensive atomistic simulations. Further, the semi-classical formulation was used to capture the interfacial behavior in a very large $100\sigma_{ff}$ channel, for which MD simulation is computationally much more expensive. The ease of implementation and the robustness of the approach make it unique to ascertain the static fluid properties at scales ranging from the macroscale to a few atomic diameters.

An extension of the semi-classical theory for LJ fluids (described in Chapter 4) was also attempted towards the goal of predicting the structure, concentration and potential profiles of a Coulombic system, specifically, water molecules confined between uncharged walls. Two approaches were attempted to extend this framework. First, water was assumed to be a dielectric medium. The correlation between the dielectric constant of water and its concentration was developed using a series of periodic bulk MD simulations. To my knowledge this approach has not been used previously to calculate water electrostatic potential in channels to compare with explicit water MD simulations. However attempt at this approach failed as I was not able to obtained accurate results for the dielectric constant and concentration profiles in sub-micron water layers accurately.

A second approach used develop the framework for water was to first obtain an empirical water-water \textit{single-site} inter-molecular electrostatic potential from bulk MD simulations of water, $u_{elec}^{wt-wt}$ \cite{51}. Further, the continuum approximation of the total electrostatic water-
water potential in a channel \( U_{\text{water-water}}^{\text{Elec}} \) was obtained using:

\[
U_{\text{water-water}}^{\text{Elec}}(x) = \int_{\Omega'} u_{\text{elec}}^{\text{wt-wt}}(r)c_{\text{wt}}(x')d\Omega'
\]  

(5.1)

where \( d\Omega' = dx'2\pi ds \). \( s \) is the integration variable in the radial direction (see Equation (8) and Figure 4 in [51] for details). This initially seemed to provide good results for the water-water electrostatic potential and the total concentration profile from the semi-classical framework and was described as the Empirical potential based quasi-continuum theory (EQT) in Raghunathan et al. [51].

However, a new student in the CMN group tried to implement the framework and reproduce the results and was unsuccessful. This led to trying to understand if I had made a mistake in the implementation of the framework. The following errors were found in the framework and the results I had published in [51]:

- Because the results were not reproducible by the new student, I found an error in the calculation and implementation of the integration given in Equation (10) in [51] by using the help of the online Mathematica integration tool. This led to an error in the results obtained for water-water electrostatic potential \( (U_{\text{water-water}}^{\text{Elec}}) \) and the water concentrations, \( c_{\text{water}} \), in comparison to what was reported in [51]. I attempted to correct the error in the implementation by using newer forms for the empirical water-water potential, \( u_{\text{elec}}^{\text{wt-wt}} \) and yet failed to capture the accurate water-water electrostatic potential.

- The coarse-grained MD (CGMD) results obtained in the paper were not reproducible by the new student. Using the same expression for the empirical water-water potential, \( u_{\text{elec}}^{\text{wt-wt}} \), he was not able to obtain the accurate concentration profiles that match explicit MD simulation calculations. The reason for this is there could be a mistake in the implementation of the CGMD simulations. This could also be related to the error in the implementation of the code in Gromacs.
• The LJ $R_{\text{crit}}$ and $R_{\text{min}}$ parameters used in the paper were different from those used in the earlier paper on LJ fluids by Raghunathan et al. [52]. The new parameters are not be easily explained using the existing multiscale framework.

Due to the above uncorrectable errors in the development of the empirical quasi-continuum theory framework (EQT) on extending the semi-classical framework to water, I take responsibility for the retraction of the paper [51] from literature.
Appendix A

Integration of the potential formulation for fluid-fluid LJ potential in the semi-classical framework

The LJ coarse-grained potential used in the semi-classical framework is given by:

\[ u_{LJ}^t(r) = \begin{cases} 
0 & r \leq R_{\text{crit}} \\
\left[2 - \left(\frac{r}{R_{\text{min}}}\right)^{2}\right]^4 u_{LJ}^{ff}(R_{\text{min}}) & R_{\text{crit}} < r \leq R_{\text{min}} \\
\left(\frac{C_{12}^{ff}}{r^{12}} - \frac{C_{6}^{ff}}{r^6}\right) & R_{\text{min}} \leq r \leq R_{\text{cut}}
\end{cases} \quad (A.1) \]

As discussed in Chapter 4, the fluid fluid LJ potential in the channel is calculated by using the equation:

\[ U_{\text{fluid-fluid}}(x) = \int_{x-R_{\text{cut}}}^{x+R_{\text{cut}}} \left[ \int_{0}^{\sqrt{R_{\text{cut}}^2-r^2}} u_{LJ}^t(r, s) c(x') (2\pi s) ds \right] dx' \quad (A.2) \]

To obtain the detailed fluid-fluid potential, we substitute \( u_{LJ}^t \) from Equation (A.1) into Equation (A.2) and ensure the appropriate limits for the integration when the point \( x \) is
close to the channel wall. Integrating out the inner integral, $U_{\text{fluid–fluid}}$ becomes:

$$
U_{\text{fluid–fluid}}(x) = \int_x^{x+R_{\text{crit}}} [f(R_{\text{crit}}) + g(R_{\text{min}})] c(x') dx' \\
+ \int_{x+R_{\text{crit}}}^{x+R_{\min}} [f(r) + g(R_{\min})] c(x') dx'
$$

(A.3)

Here, the functions $f$ and $g$ are defined as:

$$
f(p) = \frac{\pi R_{\min}^2 u_{LJ}^{ff}(R_{\min})}{5} \left\{ \left[ 2 - \left( \frac{p}{R_{\min}} \right)^2 \right]^5 - 1 \right\} ; \quad 0 \leq p < R_{\min}
$$

(A.4)

and,

$$
g(p) = \frac{\pi C_{12}^{ff}}{5} \left( \frac{1}{p^{10}} - \frac{1}{R_{\text{cut}}^{10}} \right) - \frac{\pi C_{6}^{ff}}{2} \left( \frac{1}{p^{4}} - \frac{1}{R_{\text{cut}}^{4}} \right) ; \quad R_{\min} \leq p \leq R_{\text{cut}}
$$

(A.5)

The notation in the above equations is the same as that given in Equations (4.19) and (4.21), in Chapter 4.
References


[64] G. Voth. Courtesy of the Voth research group.


Vita

Anjan Raghunathan was born in Chennai, Tamilnadu, India. He graduated from Birla Institute of Technology and Science, Pilani in 2002, with a Bachelors degree in Mechanical Engineering. He received a Master of Science degree from UIUC in 2005, under the supervision of Prof. Narayana R. Aluru, majoring in Mechanical Engineering. He then joined the PhD. program at UIUC under Prof. Alurus guidance in the department of Mechanical Science and Engineering. His research interests are in the areas of Atomistic simulations, Nanofluidics, Osmosis and Multiscale simulations. During the course of his graduate study, he has been involved with the NSF funded Center for Advanced Materials for Water Purification Systems (water-CAMPWS). Upon graduation, he would be moving to Portland, Oregon, to work as an RET engineer at Intel.