Simulating Azeotropic Clusters at Vapor-Liquid Equilibrium Using MD Simulations

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by

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Certificate

This is to certify that this dissertation entitled Simulating Azeotropic Clusters at Vapor-Liquid Equilibrium Using MD Simulations towards the partial fulfilment of the BS-MS dual degree programme at the Indian Institute of Science Education and Research, Pune represents study/work carried out by Snehash kumar Behera at Indian Institute of Science Education and Research under the supervision of Arnab Mukherjee, Professor, Department of Chemistry , during the academic year 2022-2023.

Arnab Mukherjee

Committee:

Arnab Mukherjee

Anirban Hazra

I dedicate this thesis to my Lab

Declaration

I hereby declare that the matter embodied in the report entitled Simulating Azeotropic Clusters at Vapor-Liquid Equilibrium Using MD Simulations are the results of the work carried out by me at the Department of Chemistry, Indian Institute of Science Education and Research, Pune, under the supervision of Arnab Mukherjee and the same has not been submitted elsewhere for any other degree.

Snehash kumar Behera
Snehash kumar Behera

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I would also like to express my deepest gratitude to my parents for their unwavering love, encouragement, and support throughout my academic journey. Their guidance and sacrifices have been instrumental in helping me reach this point, and I am truly blessed to have them in my life.

Finally, I would like to express my gratitude to IISER Pune for providing me with the opportunity to pursue my master's degree in a vibrant environment and for offering every possible platform to help me grow both personally and professionally.

Abstract

Several research papers have predicted the existence of azeotropic clusters. Our motivation was to validate this prediction by simulating and observing azeotropic behaviour in vapour-liquid equilibrium. To achieve this, we employed three distinct techniques: cluster formation, free energy surface analysis, and vapour-liquid simulation. Our study was able to form clusters in the simulation, as well as analyze the free energy surface of the vapour-liquid phase. Furthermore, we were able to achieve vapour-liquid equilibrium during our experiments.

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Chapter 1

Introduction

A mixture refers to a combination of two or more substances that are physically mixed together but not chemically combined. They can be homogeneous or heterogeneous, depending on whether the components are evenly distributed or not. The properties of a mixture depend on the properties of its individual components and the nature of the interactions between them. One important concept in the study of mixtures is Raoult's law, which relates the vapor pressure of a component in a solution to its mole fraction .

1.1 Raoult's Law

Raoult's law is a fundamental concept in the field of thermodynamics that plays a crucial role in our understanding of solutions. This law states that the dependence of a component of vapour pressure of the solution is equal to the mole fraction of that component times the vapor pressure of that component in pure substance. In simpler terms Raoult's law allows us to predict how much a component of the solution will evaporate into air based on its concentration in the solution and its vapour pressure in pure form[2].

$$p_1 = x_1 p_1^* \tag{1.1}$$

$$p_2 = x_2 p_2^* \tag{1.2}$$

$$p_{total} = p_1 + p_2 \tag{1.3}$$

In these equations, p_1 and p_2 are the vapour pressures of components 1 and 2 while p_1^* and p_2^* are the vapour pressures of the component in pure form respectively.The mole fraction of the components in the solution are x_1 and x_2 and the total pressure of the system is p_{total}. The above equations represent raoult's law mathematically.

1.1.1 Deviations from Raoult's Law

Despite its utility in predicting the behavior of ideal solutions, Raoult's law, like any other scientific concept, is not without its limitations. For instance, when dealing with non-ideal solutions, Raoult's law may yield inaccurate results as it does not account for the interactions between different molecules in the mixture. This results in a significant deviation from raoult's law[3]. This phenomenon may lead to the formation of Azeotropic mixtures.

1.2 Azeotrope

When a liquid mixture enters the process of distillation the liquid with the lowest boiling point would vaporize first and condense into a separate container,leaving behind the component with higher boiling point. However, in the case of an azeotrope, the components in the mixture after reaching a particular ratio are inseparable because they have the same ratio in liquid as well as vapour form. This ratio is called an Azeotropic ratio and this is mixture can no longer be separated into its individual components. Azeotropes can be divided into two parts.[4]

1.2.1 Maximum boiling Azeotrope

A maximum boiling azeotrope is a type of azeotrope where the components in the mixture have lower boiling point than that of the mixture . This occurs when the components in the mixture have a strong affinity for each other, which results in a more stable, homogeneous mixture with a higher boiling point. The individual interactions within the components are overcome by the intermolecular forces between the components, leading to a higher boiling point of the mixture. Some examples of maximum boiling point azeotrope are Nitric acid and water , Hydrofluoric acid and water.

1.2.2 Minimum boiling Azeotrope

A minimum boiling azeotrope is a type of azeotrope where the components in the mixture have higher boiling point than that of the mixture . This occurs when the components in the mixture have a less affinity for each other,but still are able to form a homogeneous mixture with a lower boiling point. Benzene-methanol azeotrope falls under this category of mixtures.

1.3 Previous literature

Despite the long-known existence of azeotropes, their separation remains a challenging issue in the fields of chemistry and chemical engineering. The reason for this challenge is that the molecular dynamics of azeotropes is not yet fully understood, making it difficult to develop efficient separation methods. The theory mentioned in this paper[5], proposed by Qi Junjie et al., explains the existence of azeotropes by postulating the presence of molecular clusters. This theory proposes that azeotropic mixtures are created through self-association of molecules within the same species and cross-association between molecules from different species. This process leads to the formation of a large cluster structure where there are no un-clustered molecules present in either the liquid or vapour phases at the azeotropic point. Then , at the azeotropic point, the physical properties of a mixture are primarily determined by the intracluster interaction between the cluster rather than the intramolecular interaction within individual molecules. This leads to azeotropic mixtures. Gergely et. al[6] have performed DFT calculation to show the existence of Benzene methanol clusters .

This concept of azeotropic molecular clusters has been investigated through experimental studies utilizing spectral analysis. Jalilian et. al[7] have reported the effect of azeotrope formation on certain vibration modes in ^{1}H NMR signal, as well as on the FT-IR and FT-Raman spectra. Moreover, the unit structure of the azeotrope was determined by analyzing several factors, including the stociometric ratio of its components, the decrease in boiling point, changes in the fundamental frequency spectrum, and the chemical shift[5].

In recent years, many molecular simulations methods have been performed to study the azeotropic mixtures . One of the well known methods is GEMC (Gibbs ensemble Monte Carlo). This method simulates the exchange of particles between phases , to study the thermodynamic properties of the system in equilibrium. Dongyang Li et. al[8] and Hong Li et. al[9] have shown that this method almost reproduces the vapour -liquid equilibria from experimental data. Manjul[10] from our lab, also managed to get the azeotropic boiling point close to experimental results. However , such simulations are unable to depict the dynamics of the molecules and formation azeotropic clusters since the exchange of the particles happens randomly based on Boltzmann factor.

This leads to Molecular dynamic simulation . It is a widely-used simulation technique for studying the behaviour of atoms and molecules over time. By numerically solving the Newton's equations of motion, MD simulations can accurately simulate the motions of atoms and molecules . Brian Morrow et. al[11] , shows a method to perform vapour-liquid equilibrium using MD simulation to look at Interfacial tension (IFT) and critical properties of hydrocarbons. We would be using their method in one our simulations. One of the members in our lab, Anant, has conducted a structural analysis of the benzene-methanol azeotrope, as referenced in[12]

1.4 The Aim of the Project

To understand the molecular mechanism of cluster formation, we need to simulate the vapor-liquid equilibrum using MD simulation at the azeotropic point. Generally till now most of the liquid - vapour equilibrium in azeotropes was achieved using monte-carlo simulation. However, in order to determine the structure of the cluster, it is necessary to observe its time evolution and track the changes in the system over time. Thus, we will pursue the following objectives:

Cluster Formation Simulation

The aim of this system is to investigate the formation of the azeotropic cluster,from the gaseous phase to liquid phase. Then we look at the composition of the cluster with time.

Density Metadynamics

Next, we try to predict the free energy barrier between vapour and liquid phases, and explore its temperature-dependent behaviour.

Vapour-Liquid equilibrium

Next, we focus on achieving a vapour-liquid equilibrium by utilizing molecular dynamics simulations and analyze the composition of phases during the simulation.

Chapter 2

Methods

2.1 Methodology

Before we begin the simulation, it is important for us to understand the techniques that will be employed throughout the simulation process. This will enable us to effectively and efficiently carry out the simulation and ensure that we obtain accurate and reliable results. By gaining an understanding of the techniques that will be used, we can also identify potential challenges or limitations that may arise during the simulation, and develop strategies to overcome them.

2.1.1 Molecular Dynamics

Since the advent of computers, chemists have been exploring ways to harness computational power to simulate the intricate movement and dynamic behaviour of molecules. The method developed to perform these kinds of tasks are called Molecular simulations.[13] Using this method, researchers can study the dynamics and interactions of atoms and molecules in a variety of conditions, including at different temperatures, pressures, and concentrations.Through these simulations, molecular dynamics can provide valuable insights into the behaviour of complex systems and help guide experimental research in fields such as chemistry, materials science, and biophysics.

2.1.2 Force Field

To perform a molecular dynamics simulation, it is necessary to represent the atoms and molecules of the system in a way that a computer can understand. This is typically done by creating a model of each atom as a point particle and then describing how the particles move over time using a potential energy surface. This potential surface describes the interactions between the particles in the system and is determined by forcefield parameters, which are chosen based on the specific properties of the atoms. We use a particular type of forcefield named OPLS-AA.[14]The most important properties are:

1. Atomic charges and masses: This contains the masses and charges of each atom.
2. Bonded parameters: These values describe the strength of bonds between the atoms, which atoms are bonded and at what angle.
3. Non bonded parameters: These values describe the forces that act between the atoms that are not bonded with each other like Lennard-Jones parameters and coulombic parameters.

$$E\left(r^N\right) = E_{\text{bonds}} + E_{\text{angles}} + E_{\text{dihedrals}} + E_{\text{nonbonded}} \tag{2.1}$$

$$E_{bonds} = \sum_{bonds} K_r (r - r_0)^2 \tag{2.2}$$

$$E_{\text{angles}} = \sum_{\text{angles}} k_\theta (\theta - \theta_0)^2 \tag{2.3}$$

$$E_{\text{dihedrals}} = \sum_{\text{dihedrals}} \left(\sum_{j=1}^{4} \frac{V_j}{2} \left[1 + \cos(\phi - \phi_j)\right] \right) \tag{2.4}$$

$$E_{\text{nonbonded}} = \sum_{i>j} f_{ij} \left(\frac{A_{ij}}{r_{ij}^{12}} - \frac{C_{ij}}{r_{ij}^{6}} + \frac{q_i q_j e^2}{4\pi\epsilon_0 r_{ij}} \right) \tag{2.5}$$

2.1.3 Thermostat

As we delve deeper into the intricacies of molecular interactions, it is of utmost importance to ensure that the forcefield of atoms is implemented with precision and accuracy. However, to truly mimic the behavior of real-world molecular systems, it is imperative to regulate the temperature of the model system. There are many methods to control the simulation temperature in which the one that we chose is V-rescale thermostat[15] to maintain the temperature. As its name suggests ,in its simplest form V-rescale or velocity -rescaling method rescales the velocity of each particle at certain intervals depending upon the predefined temperature.

$$\alpha = \sqrt{\bar{K}/K} \tag{2.6}$$

In the above equation $\bar{K}$ is the average kinetic energy of the target temperature while K is the total kinetic energy of the system . Here α is the rescaling parameter , which is multiplied with velocites of every atom.

To make the simulations more realistic , the improved version of vrescale uses a stochastic term that ensures a better kinetic energy distribution.

$$dK = (\bar{K} - K)\frac{dt}{\tau_T} + 2\sqrt{\frac{KK_o}{N_f}}\frac{dW}{\sqrt{\tau_T}} \tag{2.7}$$

where τ_T is the temperature coupling , N_f the number of degrees of freedom and W a Wiener process.

2.1.4 Barostat

Pressure is a critical thermodynamic parameter that profoundly affects the behaviour and properties of the simulated system. Therefore, it is crucial to regulate and control the pressure during a simulation, which can be achieved by utilizing a barostat. A barostat works by controlling the size of the simulation box, which indirectly affects the pressure within the simulated system. The algorithm modifies the dimensions of the simulation box to adjust the volume of the system and, in turn, regulate the pressure. There are various types of barostats, each with its own algorithm and approach. One such barostat that we use in our simulation is Parrinello-Rahman barostat[16][17]. For this barostat the box vectors b obey the equation, where V is the volume of the box and W is a matrix that determines the strength of the pressure coupling. P and P_{ref} current and reference pressure matrix

$$\frac{db^2}{dt^2} = VW^{-1}b'^{-1}(P - P_{ref}) \tag{2.8}$$

To keep the total energy of a system constant while changing the pressure of the box, terms corresponding to the barostat are added to the Hamiltonian.

$$H = E_{pot} + E_{kin} + \sum_i P_{ii}V + \sum_{i,j} \frac{1}{2} W_{ij} (\frac{db_{ij}}{dt})^2 \tag{2.9}$$

On solving the equations of the motion from the Hamiltonian, following equations come out

$$\frac{d^2r_i}{dt^2} = \frac{F_q}{m_i} - M\frac{dr_i}{dt} \tag{2.10}$$

$$M = b^{-1}[b\frac{db'}{dt} + \frac{db}{dt}b']b'^{-1} \tag{2.11}$$

By introducing the term $M\frac{dr_i}{dt}$, the Parrinello-Rahman Barostat exerts an influence on the dynamics of all particles within a system, allowing for control of the system's volume and pressure.

2.1.5 Metadynamics

During molecular dynamics simulations, it is not uncommon to encounter situations where the simulation fails to sample a particular state of the system. This is because the energy required to transition to that state is higher than the energy available to the system . This can result in a significant increase in the computational time required to reach the desired state, especially since the probability of transitioning to this state using traditional molecular dynamics is $e^{-E/k_b t}$.To overcome these limitations, a series of techniques are available to us called enhanced sampling. One such technique is metadynamics.

To use this technique, we choose a collective variable along which we will bias the evolution of the system. The collective variable $\vec{S}$ of the system can be described by simple descriptors, such as interatomic distances, angles, or a linear combination of multiple descriptors. The dimensionality of the descriptors is denoted by d.

Then we can write V_{bias} as

$$V_{bias}(\vec{S}) \equiv V_{bias}(S_1(\vec{r}), ...S_d(\vec{r})) \tag{2.12}$$

To begin the simulation, we continuously add small amounts of a bias potential energy along this collective variable over time. As the simulation progresses, the potential energy of the most visited states keeps increasing, making it less likely for the simulation to revisit those states. This encourages the simulation to explore new and unexplored states, ultimately leading to a more comprehensive sampling of the system's free energy surface.

$$H = T + V + V_{bias}(\vec{S}, t) \tag{2.13}$$

In the given equation (2.12), H represents the Hamiltonian of the system, which encompasses both the kinetic energy (T) and the potential energy (V). The bias potential (V_{bias}) of the system is continuously updated based on the collective variable ($\vec{S}$) and the time t. If small packets of potential are gaussian, then bias potential V_{bias} at a time t is

$$V_{bias}(\vec{S}, t) = \int_0^t dt' \omega \exp(-\sum_{i=1}^{d} \frac{S_i(r) - S_i(r(t'))}{2\sigma_i^2}) \tag{2.14}$$

where ω is the rate at which the bias potential gets updated and σ_i is the width of the gaussian of the ith descriptor. After all the states of collective variable gets explored, V_{bias} becomes the unbiased free energy curve of the collective variable as shown in equation(2.14).

$$V_{bias}(S, t \longrightarrow \infty) = -F(S) + C \tag{2.15}$$

where F is the unbiased free energy function of the collective variable and C is just a additive constant.

This is how free energy is calculated, using metadynamics.[18]

2.2 Setting up the simulation

The first step before performing simulation was to prepare the system, which involved constructing a simulation box with the desired dimensions and adding the necessary molecules.The equilibration of the simulation box plays a crucial role , as it serves as the initial state for subsequent simulation processes. Therefore, ensuring that the box is properly equilibrated is of paramount importance for obtaining accurate and reliable results in the subsequent simulations.

2.2.1 Preparing an azeotropic mixture box

The molecules were created using Avogadro[19] software, and the LigParGen[20] topology generator was used to generate the parameter files required for the OPLS-AA forcefield. The gmx insert molecules tool was used to generate a box containing a 3:2 azeotropic ratio of benzene and methanol with 250 molecules . The simulation was run using the GROMACS[21] simulation software. Next, the steepest descent algorithm was used to reduce the potential energy of the box to make it stable. Once the box was stable with negative potential energy, a 10ns NVT (constant volume) simulation was performed at a temperature of 300K using a V-rescale thermostat. The thermal coupling constant was set to 0.1 ps. Finally, a 100ns NPT (constant pressure) simulation was carried out to stabilize the system at 1 bar pressure with Parrinello Rahman Barostat and a temperature of 300K using V-rescale thermostat . The Pressure coupling constant was set to 2.0 ps . For all the subsequent simulations V-rescale thermostat , and Parrinello Rahman Barostat is used with same coupling constants.

2.2.2 Cluster Formation

The purpose of this simulation is to determine if gas molecules undergo aggregation at an azeotropic ratio. As the gas molecules experience a gradual decrease in temperature in the gas phase, they tend to aggregate together due to the attractive forces between them. This phenomenon is driven by the intramolecular forces that exist between the molecules. As a result, it is possible to observe the azeotropic behavior in this process, as the formation of azeotropic clusters is also driven by intramolecular forces.

The system was subjected to an extreme temperature of 450K, while maintaining a constant pressure of 1 bar. The temperature was maintained for 20ns using the same thermostat.During the simulation, the volume of the box was observed.After the volume of the box stabilized, the system was allowed to equilibrate at the extreme temperature for a sufficient period of time. This forces the system to reach gaseous phase. The temperature of the box was then lowered by 5K, and the system was allowed to equilibrate at constant pressure and temperature (NPT) for 10ns .After the equilibration period, the density of the box was checked to see if it had returned to normal.If the density of the box had not returned to its normal value, the above steps were repeated until the volume of the box returned to its original value.

2.2.3 Density Metadynamics

In vapour-liquid simulations, a free energy barrier must exist to prevent the molecules to transition from the liquid phase to the gaseous phase. To accurately determine this barrier, we use metadynamics, which involves the use of the density collective variable. By performing metadynamics along this variable, we can effectively explore the free energy landscape and obtain information about the transition pathway from the liquid to gaseous phase. This approach allows for a more comprehensive understanding of the vapour-liquid transition.

The metadynamics simulation was performed using the PLUMED[22] software package, which adds a bias potential to the system to explore the free energy landscape of the collective variable. To perform a metadynamics simulation, we first set the height of the Gaussian bias potential to 0.3 kJ/mol. The width of the Gaussian bias potential is then determined based on one-third of the standard deviation of the density at gas phase, which is found to be 0.06 kg/m^3. We then verified that the standard deviation of gas at different temperatures is very close to 0.06 kg/m^3 and thus decided to use the same width of the Gaussian bias potential at all temperatures.

2.2.4 Vapour-Liquid equilibrium

To simulate a vapour-liquid system accurately, it is crucial to ensure that both phases are present inside the simulation box. One way to achieve this is by elongating the box along one direction and performing a constant volume molecular dynamics simulation. As the simulation progresses, the liquid molecules in the middle of the box will gradually evaporate and diffuse into the empty space as a gas, creating a vapour phase.The pressure exerted by the vapour phase in the simulation box can be used to estimate the vapor pressure of the system. So we perform this simulation at different temperatures until the vapour pressure of the system is close to atmospheric pressure. This simulation method has been used previously, but to perform an IFT (interfacial tension) study.[11]

Again we start with the 300K constant pressure equilibrated box. The shape of the box was edited with the help of GROMACS tool editconf. One dimension of the box was extended to 40nm . Multiple constant volume simulations were carried out at different temperatures to study the behaviour of the system under different conditions.The simulation with the pressure closest to the atmospheric pressure was selected for further analysis.

2.3 Clustering

When one needs to partition a set of data points into groups based on similarities and dissimilarities of certain parameter , then the clustering[23] method comes to the rescue. This technique uses machine learning and data analysis to cluster the data without any knowledge of underlying data structure. There exists many clustering algorithms like K-Means,Hierarchical clustering, DBSCAN which has their own strengths and weaknesses . For our purposes, we need to cluster the positions of particles based on distance in between the particles . We found that DBSCAN is a highly effective method for clustering particles when the number of clusters is not known.

2.3.1 DBSCAN

DBSCAN[1] (Density-Based Spatial Clustering of Applications with Noise) is a clustering algorithm widely used in machine learning and data analysis to group together similar data points based on their proximity to one another. Unlike other clustering algorithms, DBSCAN can determine the number of clusters automatically based on the density of the data points, rather than relying on a specified number of clusters in advance.

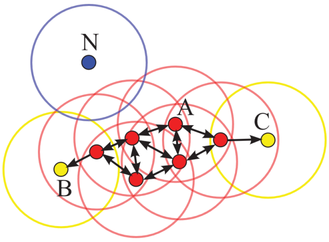


Figure 2.1: *An image explaining minimum density level. Apart from N , A,B,C belong to the cluster*[1]

The way DBSCAN works is by defining a neighborhood around each data point using a specified radius, and then grouping together data points that are within that neighborhood. The algorithm then expands the clusters iteratively by including additional nearby points until no more points can be added. Any data points that do not belong to any cluster are classified as outliers.

Chapter 3

Results and Discussions

3.1 Preparing an azeotropic mixture box

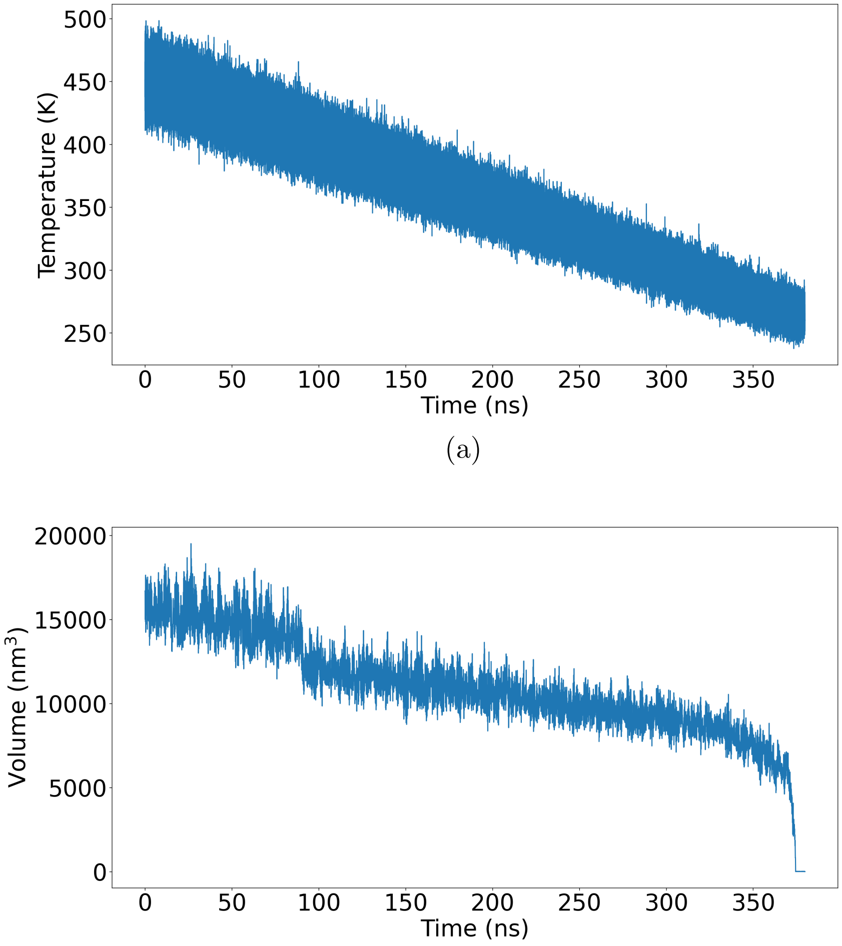
On performing the simulation based on the method 2.2.1, the average density of the system came out to be 831.66 kg/m^3 at 300K. This is close to the experimental value 841.0 kg/m^3[24].

3.2 Cluster Formation Simulation

The box underwent a series of simulations to study its behaviour under different conditions. First, it was exposed to a high temperature of 450K in a constant volume simulation for 10ns. Next, a constant pressure simulation was performed at the same temperature, which caused the box to expand significantly and its density to decrease. The density of the gas after the simulation came out to be 1.2kg/m^3 , which is clearly the density of a gas.

To further investigate the box's behavior, it was slowly cooled down by reducing the temperature in increments of 5K and performing another 10ns constant pressure simulation. The temperature profile is shown in *figure 3.1(a)*. This process gradually lowered the temperature of the box to 265K, at which point the volume of the box returns to normal as shown in *figure 3.1(b)*.

Upon analyzing the trajectory of this simulation, using DBSCAN it was observed that



(a)

(b)

Figure 3.1: *Figure (a) shows the decrease of temperature with time. (b) shows the decrease of volume with time. The sharp dip in the end is due to the condensation to liquid phase*

clusters had formed during the transition from gas to liquid phase as shown in *figures 3.2* and *3.3*. We utilized PYMOL, a visualization software, to aid in our identification of molecular clusters. In order to accurately identify these clusters, we carefully selected the appropriate epsilon value for the DBscan clustering algorithm. Additionally, we set the minimum number of molecules in each cluster to 5.

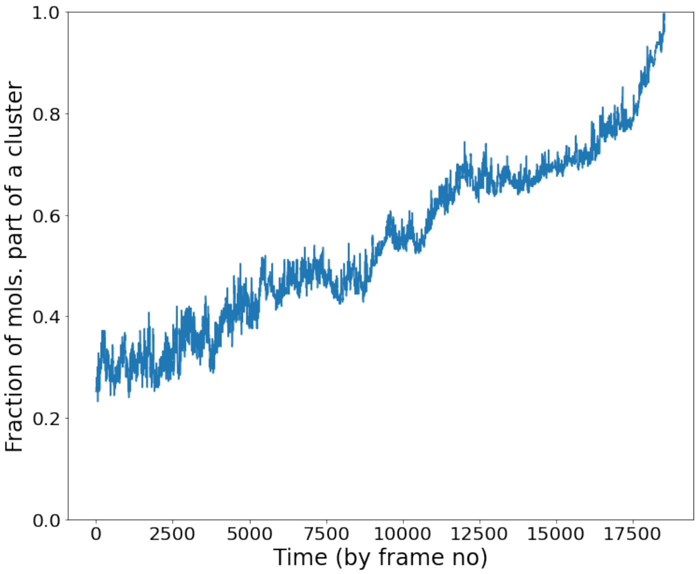


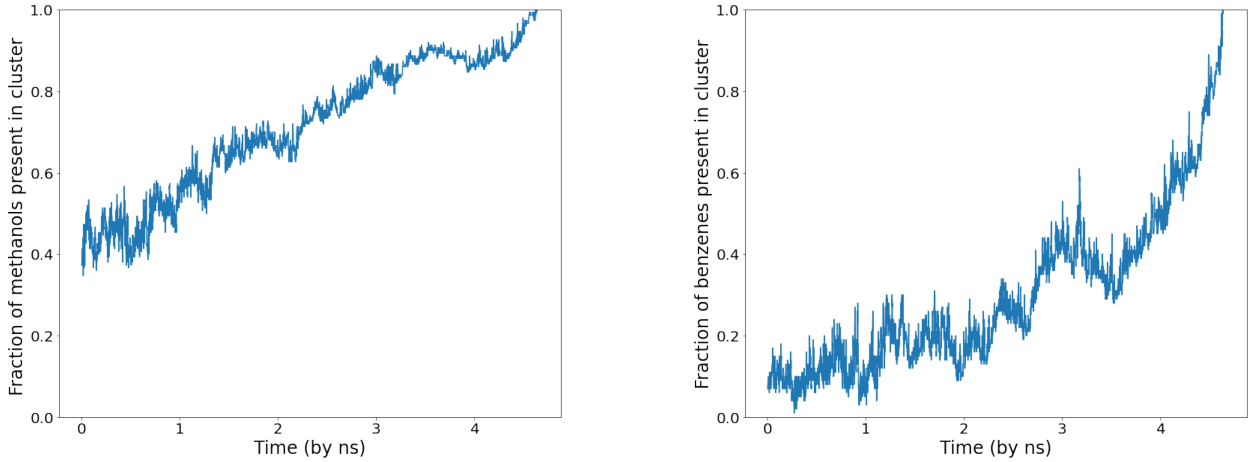
Figure 3.2: *A plot showing the slow formation of clusters.*

After completing the initial simulation, we conducted 100ns trajectory simulations at temperatures higher than 265 K. The purpose was to identify the critical temperature at which the molecules are unable to form clusters and instead remain in the gaseous phase.

When the gas particles coalesce, they are drawn together by intermolecular forces. These same forces should be responsible for the formation of azeotropes. Therefore, when the gas particles form clusters, we should expect to find the same azeotropic ratio as in the original azeotropic mixture . In other words, the relative amounts of each gas component in the cluster should be the same as in the original gas mixture, due to the intermolecular forces that govern their behaviour.

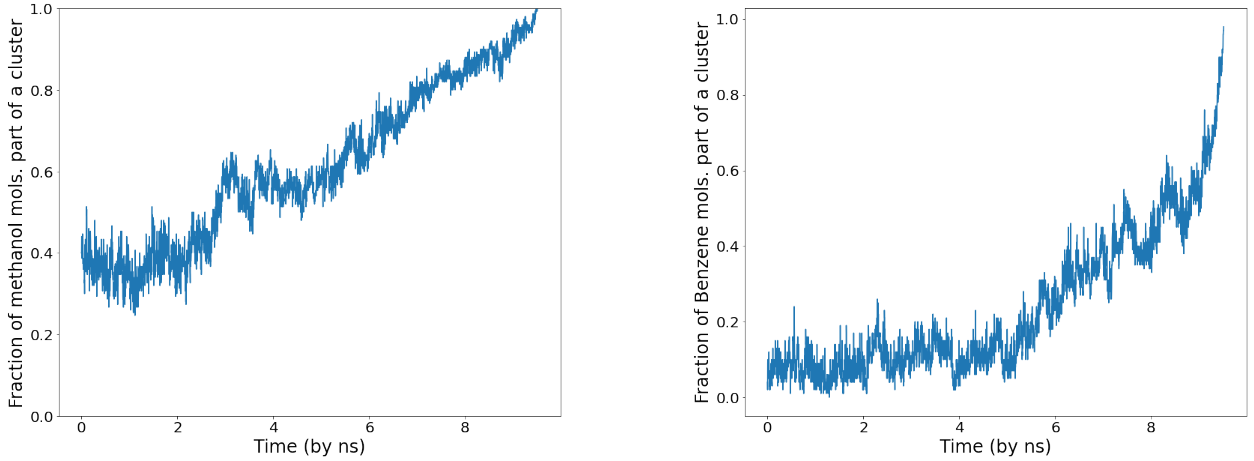
As we can see from the *figure 3.3*, in the early stages of the simulation , methanol has already more prevalent in clusters than benzene . This suggests that benzene self interaction is less than the methanol.

When we look at the formation of azeotropic clusters, the fraction of benzene molecules present in the clusters lags behind methanol by a significant margin as shown in *figures 3.3* . Only when the clusters grow in size to develop strong enough forces , they can attract and retain benzene molecules, thus enabling the formation of the liquid phase. These observations suggest that the interaction between methanol and benzene is not strong enough to facilitate the formation of clusters at an earlier stage of the simulation.



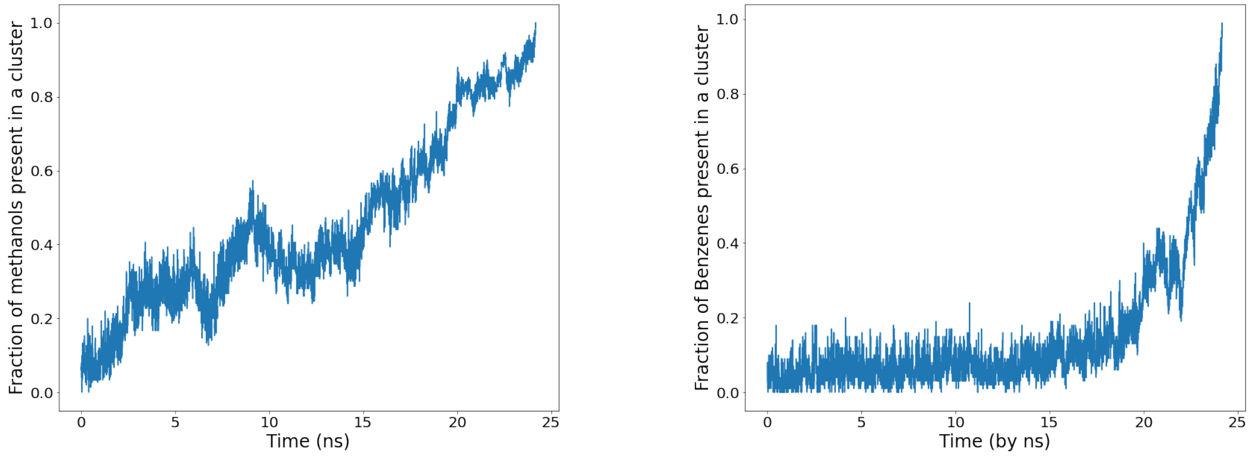
(a) T = 265K

(b) T = 265K

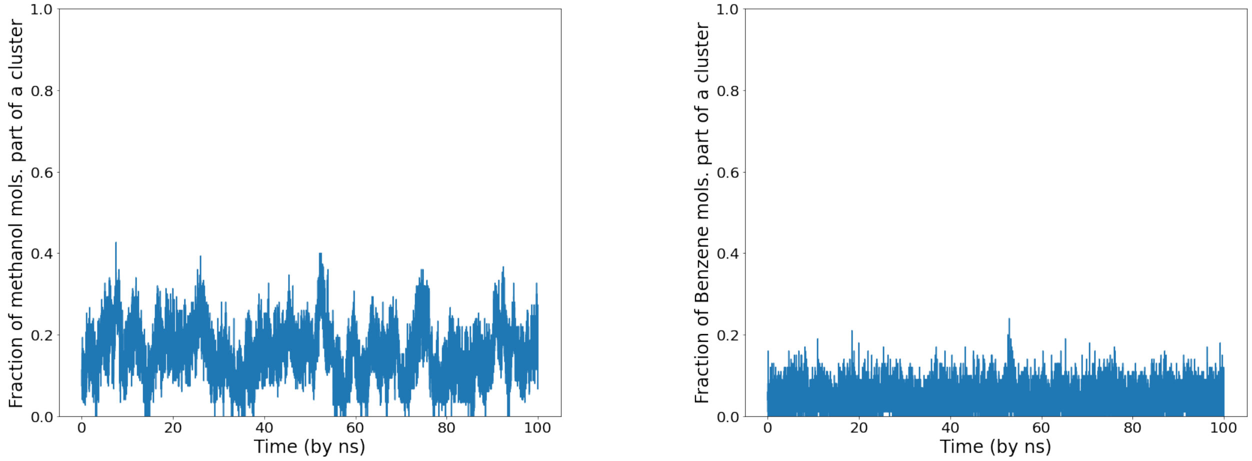


(c) T = 270K

(d) T = 270K



(e) T = 275K (f) T = 275K



(g) T = 280K (h) T=280K

Figure 3.3: *Figures on the right shows plots of ratio of Benzene molecules in cluster at different temperatures. Figures on the left shows plots of ratios of Methanol molecules in cluster at different temperatures*

However, as depicted in *Figure 3.3 (f) (g)*, cluster formation ceases to occur beyond 280K. This may be attributed to the increased thermal energy of the system, leading to weakened non-bonded interactions between benzene and methanol. Further analysis is required to fully understand the underlying mechanisms responsible for the observed behaviour.

To assess the probability of cluster formation at various sizes, we generated a plot that shows the likelihood of occurrence for each cluster size observed in the frames against the number of molecules within the cluster as shown in *figure 3.4*. We observed that the formation of 5 particles cluster was most likely among all other sizes of cluster. The second maxima was observed at a cluster size of 34 molecules. This means that the formation of clusters of any size may not be energetically equivalent. However, to gain a deeper and more comprehensive understanding of these processes, further analysis is necessary.

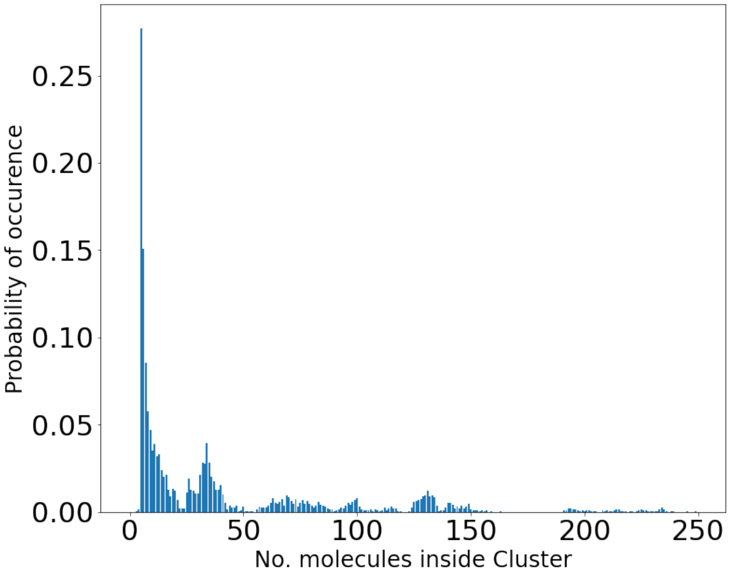
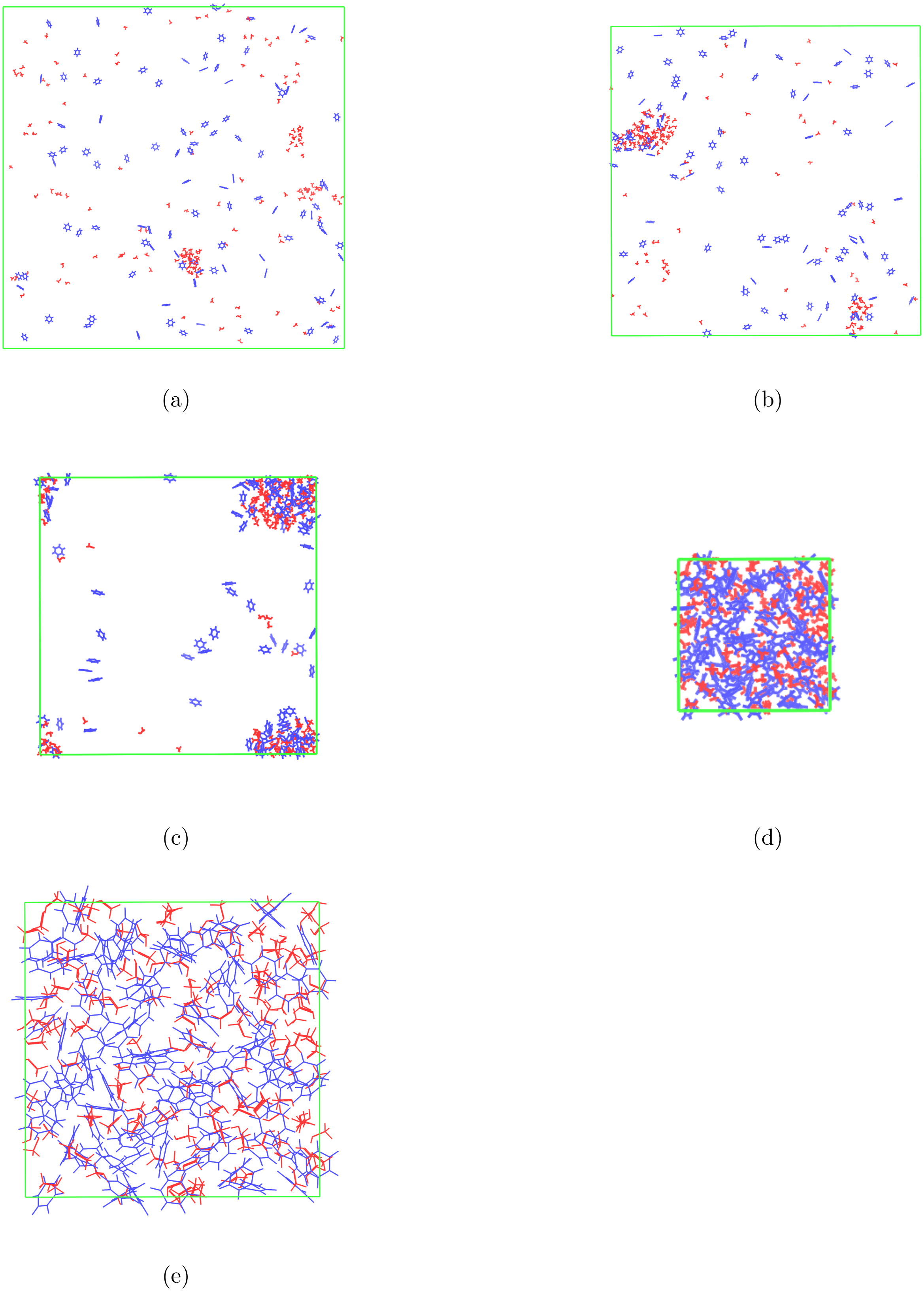


Figure 3.4: *A plot showing probability to find a cluster of a particular size in a random frame*



(a) (b) (c) (d) (e)

Figure 3.5: *Theses images are snapshots from 265 K clustering simulation.Figure(a) shows the snap shot at the start of the simulation. Figure(b) is a snapshot where most of the methanol has become the cluster. Figure (c) is the snapshot right before the collapse box . Figure (d) is a snapshot at the final phase of the simulation. Figure (e) is the zoomed in image of the liquid box*

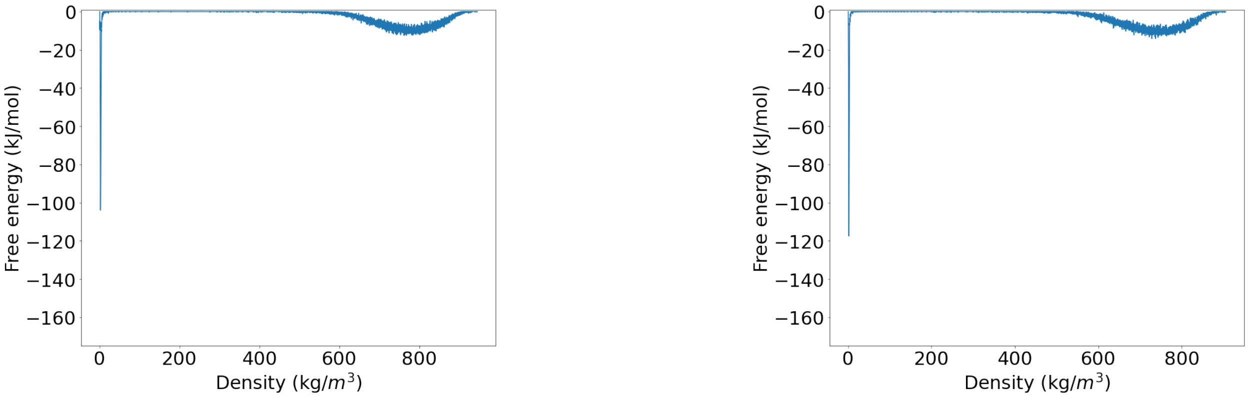
3.3 Density Metadynamics

A well-tempered metadynamics simulation was performed at different temperatures to study the vapor-liquid equilibrium of a fluid. By using density as the collective variable and systematically increasing the temperature of the simulation, the simulation can explore different regions of the phase space and determine the critical temperature and pressure at which the liquid and vapour phases coexist in equilibrium. The height of the gaussian was set to 0.3 kJ/mol and the width of the gaussian was taken to be 0.06 which was taken as one third of the standard deviation of the density at gas phase. Since the standard deviation of gas at different temperature turned out to be very close to 0.06, thats why the width of the gaussian was taken to be same at all temperatures. All of the simulations started from a constant pressure equilibrated box at their respective temperatures.

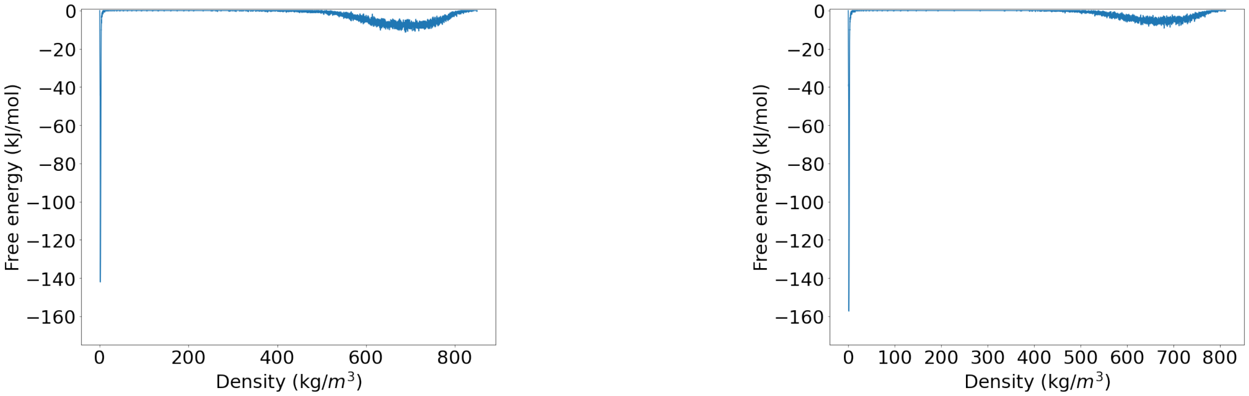
Looking at the free energy surfaces (*see figure 3.6*), we can notice there are two free energy minimas at all temperatures. One the minimas lies near 2kg/m^3 which represents gas. While other minima lies around 700kg/m^3 representing liquid phase. If we look at the zoomed in free energy surfaces of liquid and gaseous phase in *figure 3.7* we can clearly notice a trend. As the temperature of the system increases, the free energy of the gas decreases while the free energy of the liquid increases. This is in line with our expectations and supports the notion that temperature has a significant impact on the free energy of a system.

However we notice another property, the free energy minima of the vapour phase is always lower than the liquid phase at any temperature . Even in the Cluster formation simulation at 265K the gaseous phase condenses into the liquid phase. One of the explanation to this phenomenon is the non-bonded interaction cutoff. Often in Molecular Dynamics simulations , there is cutoff distance after which non-bonded interactions are considered negligible and ignored. This cutoff reduces the computational cost of the simulation. The cutoff is generally set before the simulation starts . If the cutoff is too short, important non-bonded interactions may be missed, leading to inaccurate results. If the cutoff is too long, the simulation becomes computationally expensive, as interactions between distant atoms must be calculated , or it can interact with itself under periodic boundary condition.

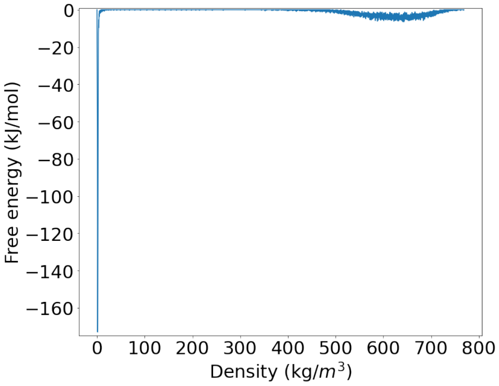
In our simulation system, when starting from the liquid phase, we set a cutoff for the intermolecular distance of liquid molecules. As the system goes to the gas state the cutoff becomes too small , and important non bonded interactions are missed. This leads to much



(a) T=265K (b) T=300K



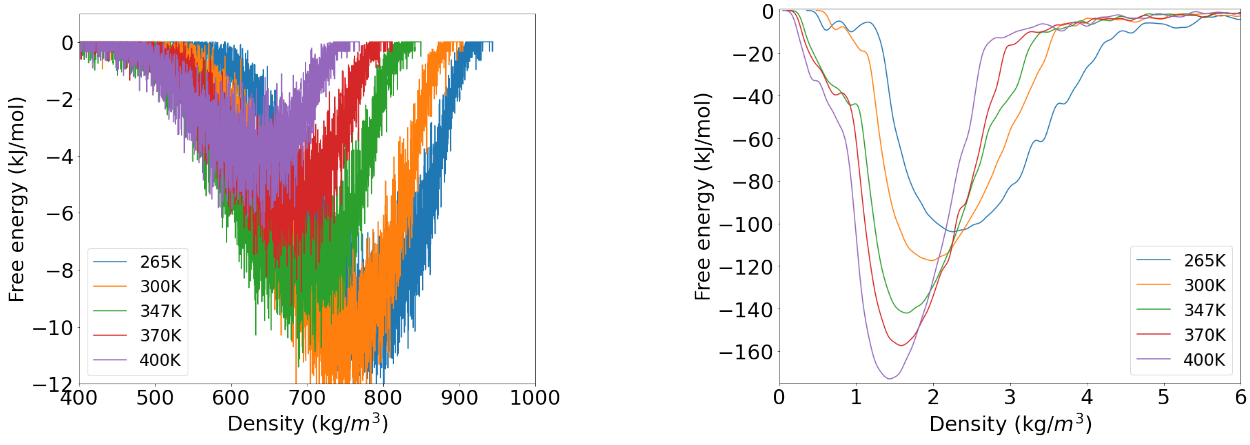
(c) T=347K (d) T=370K



(e) T=400K

Figure 3.6: *Free Energy Plot at different temperatures.*

lower free energy of the gas than expected.



(a)

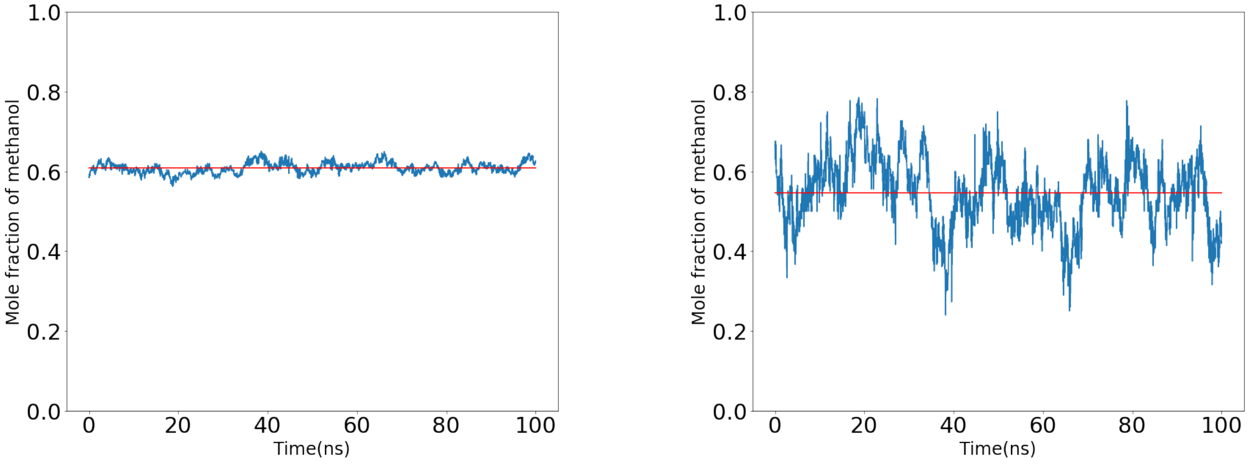
(b)

Figure 3.7: *Figure (a) is a plot showing the free energy at the liquid region. Figure (b)is a plot showing free energy at the gas region*

3.4 Vapor Liquid Equilibrium

The 100 ns constant volume simulation was performed at different temperatures. The average pressure of each simulation was recorded and tabulated. The box pressure at 347 K was found to be closest to the atomspheric pressure. Since the vapor pressure of the box is equal to atmospheric pressure at the boiling point, we can argue that this is the boiling point of the Azeotrope. The experimental boiling point for benzene methanol azeotrope cluster is 328.7K which is close to our simulation result.

Simulation temperature (K)	Pressure of the box (bar)
300	-5.95358
330	-2.19209
345	0.60686
347	1.05722
350	1.70163
400	24.5342



(a)

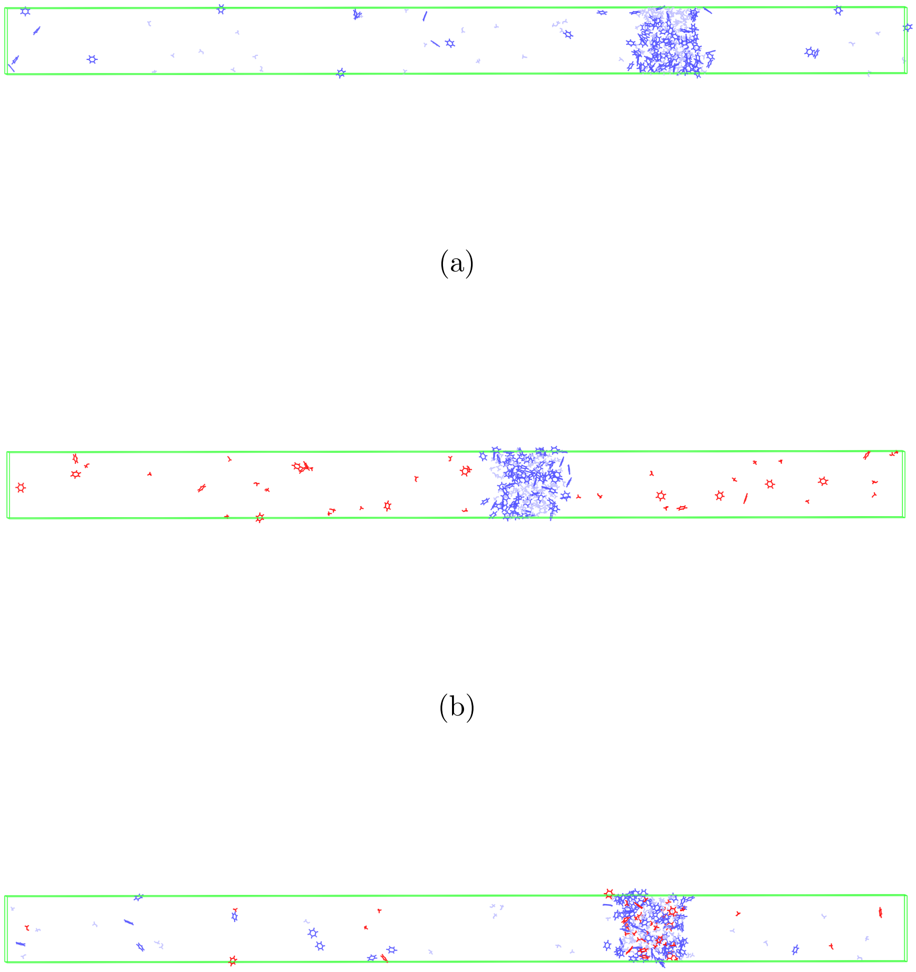
(b)

Figure 3.8: *Figure (a) is a plot showing mole fraction of Methanol molecules in Liquid phase. Figure (b)is a plot showing mole fraction of Methanol molecules in Vapour phase*

To differentiate between the liquid and gas phases in our simulation data, we employed a clustering algorithm to separate the two. We began by visually identifying the liquid phase from the gas phase using PYMOL. Next, we optimized the parameters of the clustering algorithm by selecting the appropriate epsilon value that effectively distinguished the two phases. We then entered this optimized epsilon value, along with a minimum sample size of 5, into the DBSCAN clustering program to cluster the data into separate liquid and gas phases.

Upon observing the trajectory (*see Figure 3.9(a)*), we can determine that the large cluster of molecules represents the liquid phase, while the widely-spaced molecules correspond to the gas phase. In order to illustrate the vapor-liquid equilibrium, we color the gas particles in one frame (*see Figure 3.9(b)*). Over time, we can observe that some gas particles transition into the liquid phase, while some liquid particles move into the gas phase.(*see Figure 3.9(c)*)

Next , we plot the mole fraction of the Methanol vs time as shown in *Figure (3.8)* . The mole fractions of methanol in both the gaseous and liquid phases have been determined to be 0.54 and 0.61, respectively. It's worth noting that these values are very close to the azeotropic composition, which is the point at which a liquid mixture boils at a constant temperature, without changing composition. Furthermore, the fact that the mole fraction of methanol is the same in both phases, suggests that this mixture behaves like an azeotropic mixture.



(a)

(b)

(c)

Figure 3.9: *Figure (a) is a snapshot of the VLE simulation at 347 K .Light blue colour represents methanol molecules while dark blue are benzene molecules. Figure (a) shows the red molecules which are in gas phase ,c shows the fraction of red molecules in liq phase signifying VLE*

Chapter 4

Conclusion

The main objective of this project was to study the dynamics of azeotropic clusters at vapour-liquid equilibrium using pure molecular dynamics (MD) simulations.

We were able to capture the formation of clusters in the transition from the gaseous phase to the liquid phase. Although the cluster composition did not conform to the azeotropic composition, an interesting finding emerged from the probabilistic analysis: the formation of certain cluster sizes was unstable. This could potentially explain why the cluster composition did not follow azeotropic behaviour. Further simulation is needed to better understand this phenomenon and its potential application in azeotropic cluster formation.

Our simulation results have led to successful identification of the free energy minima for both liquid and gas phases, which corresponded well with the expected densities. Our analysis shows the behaviour of free energy barrier for vapour and liquid across various temperatures. However, during our observations, we observed a deep free energy minimum in the gas phase due to particle distances exceeding the non-bonded interactions cutoff. The solution to this issue , would allows us to explore the unique characteristics of the gas phase in more detail.

From vapour -liquid simulations, we have successfully identified a temperature at which the vapour pressure approaches 1 atm, which is 347K. This means that boiling point is 347K. Additionally, both the vapour and liquid phases exhibit the same azeotropic ratio at the boiling point. This means that this method was able to simulate azeotropic mixture and achieve vapour liquid equilibrium .

Overall, the methods used in this study provide some insights into the complexities of azeotropic clusters. However, it is important to note that further investigation is needed to fully explain the observed features and behaviours of these clusters, which can in turn be used to develop efficient separation of azeotropic mixtures.

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