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Artificial biomembrane morphology: a dissipative particle dynamics study

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Artificial membranes mimicking biological structures are rapidly breaking new ground in the areas of medicine and soft-matter physics. In this endeavor, we use dissipative particle dynamics simulation to investigate the morphology and behavior of lipid-based biomembranes under conditions of varied lipid density and self-interaction. Our results show that a less-than-normal initial lipid density does not create the traditional membrane; but instead results in the formation of a ‘net’, or at very low densities, a series of disparate ‘clumps’ similar to the micelles formed by lipids in nature. When the initial lipid density is high, a membrane forms, but due to the large number of lipids, the naturally formed membrane would be larger than the simulation box, leading to ‘rippling’ behavior as the excess repulsive force of the membrane interior overcomes the bending energy of the membrane. Once the density reaches a certain point however, ‘bubbles’ appear inside the membrane, reducing the rippling behavior and eventually generating a relatively flat, but thick, structure with micelles of water inside the membrane itself. Our simulations also demonstrate that the interaction parameter between individual lipids plays a significant role in the formation and behavior of lipid membrane assemblies, creating similar structures as the initial lipid density distribution. This work provides a comprehensive approach to the intricacies of lipid membranes, and offers a guideline to design biological or polymeric membranes through self-assembly processes as well as develop novel cellular manipulation and destruction techniques.

Keywords: biomembrane; lipid; dissipative particle dynamics; self-assembly

1. Introduction

Current techniques for the prediction and modeling of not only inorganics but also more complex biological materials have made possible the study of technologically relevant soft materials, such as recently developed artificial lipid-based biomembranes (Mashaghi et al., 2013; Whitesides & Lipomi, 2009). These structures are worth studying via simulation in order to build knowledge relevant to medical technology and industry while simultaneously lessening the need for expensive, uncontrollable, or dangerous physical experiments. The morphology of a lipid membrane is strongly dependent on the density of lipids and the interactions between the lipids, and thus these conditions are what we will be focusing on for this work. To begin with, the lipid membrane is a ubiquitous construction in the natural world, forming the structural support for living cells and able to keep the cellular structures inside while regulating the passage of molecules. The utility of the lipid membrane is the foundation of complex organisms and has received a large amount of attention and research, both for its chemical and mechanical properties (Essmann, Perera, & Berkwitz, 1995; Grunze, Fedyaev, & Persin, 2009; Israelachvili & Wennerstrom, 1992; Kranenburg & Smit, 2005; Long, Zhang, & Qian, 2006; Lyubartsev, 2005; Mao, Chen, Liang, Guo, & Yan, 2016; McIntosh & Simon, 1996; Peng et al., 2013; Persin, Platonov, & Grunze, 2007; Rangamani et al., 2014; Smit, Kranenburg, Sperotto, & Venturoli, 2006; Venturoli, Sperotto, Kranenburg, & Smit, 2006). Due to their usefulness and relative simplicity, designed nanoscopic assemblies of lipids in the form of membranes and micelles are used in various fields, from soft matter physics to actual synthetic biology, where lipids are used to generate systems mimicking biological structures (Mashaghi et al., 2013). Artificial membranes are a burgeoning technology allowing for an explosion of research into synthetic biology and medicine (Dankers et al., 2011; Lee et al., 2008; Malinova, Belegirinou, Ouboter, & Meier, 2010; Zhao et al., 2010). Designed membranes are able to accomplish sensitive tasks unsuited to natural structures, such as binding selected surfaces, serving as catalytic nanoreactors for controlled chemical reactions, dispersing CNTs into solution, and the carrying and delivering drugs or other payloads into cell interiors (Adeli, Kalantari, Parsamanesh, Sadeghi, & Mahmoudi, 2011; Angius, Murgia, Berti, Baglioni, & Monduzzi, 2006; Anraku, Kishimura, Oba, Yamasaki, & Kataoka, 2010; Baca et al., 2011; Beales & Vanderlick, 2009; Bombelli et al., 2009; Lee, Lee, Kim, Suh, &
Kawai, 2009; Mashaghi et al., 2013; Mayer, 2005; Schoonen & van Hest, 2016; Wang, Michielssens, Moors, & Ceulemans, 2009).

In accordance with this wide range of applications, in order to further the progression of science and technology focused on biomimetic structures it is imperative to not only to understand the structure of the normally seen lipid bilayer, but also investigate the properties and behaviors of lipid membrane behavior beyond the standard. Previous studies into the behaviors of lipid-based structures have dealt with the dynamics of lipid type, concentration, and structure, but have focused on vesicles or otherwise have not gone in-depth into the finer characteristics and limits of specifically membrane formation and morphology (Arai, Yasuoka, & Zeng, 2013; de Meyer, Benjamini, Rodgers, Misteli, & Smit, 2010; Kranenburg, Vlaar, & Smit, 2004; Lin, Li, Sheng, Wu, & Tsao, 2012; Murtola, Falck, Patra, Karttunen, & Vattulainen, 2004; Roszycki & Lipowsky, 2015; Tan, Shen, Li, Elson, & Ma, 2008; van Hoof, Markvoort, van Santen, & Hilbers, 2014; Yamamoto, Maruyama, & Hyodo, 2002). There are many conditions wherein cells display unusual or non-flat membranes, such as when exposed to chemoattractant, (Mckay, Kusel, & Wilkin-1991) irregularities during culture growth, (Power, Neylan, & Collum, 1993) exposure to magnetic fields, (Chionna et al., 2005; Dini & Abbro, 2005) and cell shape change (Kapustina et al., 2016). These experimental results show that the addition of chemoattractant and exposure to magnetic fields can create rippled or bubbled lamellar membranes, while growth irregularities and the movement of a cell can cause protrusions and bulging of the cell membrane. It is rare to see works which tackle these specific cases, and so there is a need to explore the tendencies of cell membrane morphology under the influence of these effects.

In order to accomplish the necessary tasks utilizing this cutting-edge soft material technology, it is valuable to understand more completely the variability exhibited by such biomembranes under different conditions. We aim to build on previous literature in order to come up with a more comprehensive set of common membrane modes, and to examine and explore the conditions and formation dynamics of these modalities. This work seeks to employ dissipative particle dynamics simulation in order to determine the effect of varying lipid density and interaction on the stability and morphology of a modeled biomembrane, in order to mimic the effects of irregularly formed biomembranes. First, we describe the details of the simulation methodologies. Next, we present and analyze the results obtained by varying the initial parameters of the lipid density and interaction parameter. Conclusions are drawn and discussed in Section 4.

2. Computational model and methodology

In what follows, molecular dynamics simulations based on the open source code LAMMPS [version 13 August 2016] (Plimpton, 1995) developed by Sandia National Laboratories are employed to perform the simulation based on dissipative particle dynamics (DPD), a mesoscopic coarse-grained simulation method suitable for soft matter and biomembrane systems (Espanol & Warren, 1995; Groot & Rabone, 2001; Groot & Warren, 1997; Hoogerbrugge & Koelman, 1992; Moeendarbary, Ng, & Zangeneh, 2010). In these coarse-grained simulations, a group of atoms is treated to be a single bead located at the center of mass of the group, with beads on the same molecule interacting via a harmonic bond potential; this is the classic bead-spring model for coarse-grained lipids (Venturoli et al., 2006). Beads $i$ and $j$ interact with each other via a pairwise force consisting of a conservative force $F_{ij}^C$ representing excluded volume effect, a dissipative force $F_{ij}^D$ representing viscous drag between moving beads and a random force $F_{ij}^R$ representing stochastic impulse. Both $F_{ij}^D$ and $F_{ij}^R$ act together as a thermostat for the beads. Similar to molecular dynamics simulation, time evolution is also governed by the Newton’s equation of motion. The total force on bead $i$ can be expressed as

$$ F_i = \sum_{i \neq j} (F_{ij}^C + F_{ij}^D + F_{ij}^R) $$

$$ = \sum_{i \neq j} (a_{ij}\omega(r_{ij}) \dot{r}_{ij} - \gamma\omega^2(r_{ij}) (\dot{r}_{ij} \cdot v_{ij}) \dot{r}_{ij} + \sigma\omega(r_{ij}) \zeta_{ij} \Delta t^{-1/2} \hat{r}_{ij} $$

where $a_{ij}$ is the maximum repulsive force, $r_{ij}$ the distance, $\dot{r}_{ij}$ the unit vector and $v_{ij}$ the relative velocity between beads $i$ and $j$. $\omega(r_{ij})$ denotes a random number with zero mean and unit variance, and

$$ \omega(r_{ij}) = \begin{cases} 1 - \frac{r_{ij}}{r_c}, & r_{ij} < r_c \\ 0, & r_{ij} > r_c \end{cases} $$

is a normalized distribution function, $r_c$ being the cut-off radius; $\gamma$ and $\sigma$ are parameters related to each other as $\sigma^2 = 2\gamma k_B T$, $k_B T$ being the unit of energy. The standard values $\sigma = 3.0$ and $\gamma = 4.5$ are used in our study (Zhang, Becton, & Wang, 2015; Zhang & Wang, 2015a, 2015b). The mass, length, and time scales are all normalized in the DPD simulations, with the unit of length taken to be the cut-off radius $r_c$, the unit of mass to be that of the solvent beads, and the unit of energy to be $k_B T$. All other quantities are expressed in terms of these basic units. The reduced DPD units can be converted to SI units by examining the membrane thickness and the lipid diffusion coefficient. The simulated value of bilayer thickness is 10$r_c$ and the effective time scale of
simulation can be determined from the simulated lateral diffusion constants of lipid bilayer (Zhang et al., 2015). The typical phospholipid bilayer has a thickness of about 4 nm with a diffusion coefficient around 5 μm²s⁻¹, (Murray, Rog, & Pasenkiewicz-Gierula, 2005; Shillcock & Lipowsky, 2005) by comparison with typical experimental values, it can be shown that one DPD length unit corresponds to approximately 0.8 nm in physical units and the time unit to τ = 24.32 ps. The time step is taken as Δt = 0.01τ. All simulations are performed using LAMMPS.

The phospholipid phosphatidylcholine (PC) is chosen as the base for this DPD model, as it is a common component of biological membranes. To simulate the molecule here, three types of beads are used: hydrophobic, hydrophilic, and water-like. The lipid model is constructed by connecting hydrophilic ‘head’ beads with hydrophobic ‘tail’ beads via harmonic springs, with bond angle constraints controlling the chain bending stiffness. The dimensions of the periodic simulation box are 120rₑ × 120rₑ × 100rₑ, with the lipids being inserted into a 120rₑ × 120rₑ × 10rₑ sized volume before the system is equilibrated. Water is inserted into the volume outside the lipid bilayer such that the system is maintained at a particle density of approximately 3 particles per unit volume (hereafter, density is taken to be unitless) (Nielsen, Ensing, Ortiz, Moore, & Klein, 2005). The initial simulation system consists of the biomembrane made of lipid molecules and solvent particles. Solvent beads are not shown for clarity. The lipid molecule is represented by the coarse-grained model proposed by Groot and Rabone (2001) as shown in Figure 1(a); it consists of 3 lipid hydrophilic head beads and 10 lipid hydrophobic tail beads (in two tail chains of 5 beads each). The repulsive interaction parameters between lipid beads of the same type are typically taken as aᵢⱼ = 25, and those for beads of different types are set as aᵢⱼ = 100. Hydrophobic bead interactions with water are set as aᵢⱼ = 100, while hydrophilic bead-water interactions have the parameter aᵢⱼ = 25 (Y. F. Li, X. J. Li, Z. H. Li, & H. J. Gao, 2012). Within a lipid molecule, an elastic harmonic force,

\[ F^e = k_s \left( 1 - \frac{r_{ij}}{r_s} \right) r_{ij} \]

is used to connect two consecutive beads, where kₛ and rₛ are the spring constant and equilibrium bond length, respectively. Here we use kₛ = 100.0 and rₛ = 0.7rₑ for lipid molecules (Venturoli, Smit, & Sperotto, 2005). The bending resistance of the lipid chain is represented as an additional force due to a harmonic constraint on two consecutive bonds

\[ F^b = -\nabla V_{bend} = -\nabla \left[ k_0(\theta - \theta_0)^2 \right] \]

where k₀, θ and θ₀ are the bending constant, inclination angle and equilibrium angle, respectively. As shown in Figure 1(a), for three consecutive lipid tail beads or three consecutive lipid head beads in a lipid molecule, we take k₁ = 6 and θ = 180°; for the last head-bead and the top tail-beads k₂ = 3 and θ = 120°; for the bottom two consecutive head beads and the first bead in each tail k₃ = 4.5 and θ = 120° (Y. Li, X. Li, Z. Li, & H. Gao, 2012). A sample structure of lipids congregated into a biomembrane is shown in Figure 1(b) and (c). Where mentioned, a biomembrane’s amplitude refers to the time-averaged equilibrium value of the distance between the lowest and highest (along the z-axis) lipid bead in the membrane or structure; however, it is assigned a negative value when the membrane incompletely separates the simulation box (incomplete or perforated membrane). All simulations are treated as NVE and run for 1,000,000 time steps to ensure that a representative structure is taken, with time-averaged equilibrium data taken from time steps 500,000 – 1,000,000 (~122 – 243 ns) as all structures reach their final state before 300,000 time steps (~73 ns). We now turn our focus on characterizing the biomembrane itself.

3. Results and discussion

3.1. Classification of biomembrane morphology

To characterize the various types of biomembrane morphology, we turn to the physical behaviors of lipid biomembranes. It has been shown that the lipid bilayer structure exhibits a number of suitable characteristics for its ubiquity in biological structures, including flexibility and adaptivity. Here, we observe that at the density and parameters described in the Methods section, the typical
behavior of the lipid bilayer membrane is to form a flat sheet with minimal ‘ripples’ or ‘waves’. Figure 2 gives the typical lipid agglomeration modes that form during our runs with different initial conditions. Here the modes are labeled and described. Figure 2(a) shows the formation of ‘clumps’, which happens when the lipids do not form a singular contiguous membrane but rather congregate into small micelle structures. Figure 2(b) illustrates ‘net’-like behavior wherein the membrane is stretched too tight to form a solid membrane, or has sustained irreparable damage. Figure 2(c) is the typically seen ‘flat sheet’ bilayer, and what is typically referenced as the textbook membrane. Figure 2(d) is a ‘wavy’ or ‘rippled’ membrane, which occurs when the membrane is not in tension but rather experiences compressive forces. Figure 2(e) conveys what happens when the compressive force on the membrane becomes large enough that the membrane ripples self-adhere and fuse together, forming inner ‘pockets’ or ‘bubbles’; this phenomenon can be considered a smaller scaled, incomplete version of the bilayer-vesicle transition observed previously (Wu & Guo, 2008). Finally, Figure 2(f) displays the outcome of further formation of bubbles beyond a single membrane layer, labeled here as ‘stacked’. These are the major morphologies noted in this work; both the ‘clumps’ and the ‘stacked’ modes extend to their respective ends: with fewer lipids the ‘clumps’ become smaller until they are singular lipids in water, and at the other end of the spectrum the ‘stacked’ formation becomes larger and larger until it fills the system. Due to these reasons, we consider these six modes to be the major ones that we will explore.

3.2. Effect of lipid density

There is a certain range of lipid density wherein the membrane model most accurately depicts typical membrane structures. However, it is important to examine cases near this specific density to investigate the behavior and mechanical properties of membranes that may have a
deficit or overabundance of lipids in them, such as when a cell changes shape and ends up with an excess or lack of membrane for the cell volume (Kapustina et al., 2016). Here, we will explore the cell membrane morphology for cases where the membrane lipid density is above or below that which is normally observed in cellular biomembranes. To study this, we create the membrane as mentioned in the Methods Section, putting the lipids into a plane of $120r_c \times 120r_c \times 10r_c$ sized volume. The original density of 3 beads per unit volume is then varied to insert more or fewer lipids into this volume, and the system is then allowed to evolve to equilibrium. The morphological changes that the membrane undergoes as the lipid density is increased from 0.78 to 45 are shown in Figure 3, as snapshots along with the evolution of the measured amplitude of the bilayer membrane, with ‘incomplete’ membranes such as ‘clumps’ or ‘nets’ being assigned negative values for clarity. An incomplete membrane is one that does not create separate sections of the simulation box, and thus would not hinder the flow of water or small molecules across it. The amplitude is plotted as a way to visualize the morphology changes stemming from the increasing density. Figure 3 plots the initially set density of the lipid layer vs. the measured amplitude of the layer at equilibrium. From the insets, it can clearly be observed how the amplitude can be used to track the evolution of the morphological mode as a function of the initial density.

At low densities the membrane cannot form at all; instead the attractive force between similar lipid beads and the repulsive force between water and lipid tail beads cause nearby lipids to cluster together and form micelles or ‘clumps’, as is evidenced by the lowest-density subfigure of Figure 3; at this stage, there is a relatively large negative amplitude, as the clumps float around with little effect on each other, creating a large distance between the highest and lowest lipids. When the initial lipid density is increased, the lipids form an incomplete membrane, referred here as ‘net’ form. This evolution occurs due to the strong surface tension and self-adhesion of the lipid membrane. When there are enough lipids to prevent the separation of the lipids into individual micelles, yet few enough that a flat bilayer membrane is not energetically favorable, the lipid structure forms a ‘net’-like assembly, where many small holes initiate and converge to form large, circular holes in the typical membrane structure. The ‘net’ mode has a small negative value, as the surface tension felt by the net keeps it very flat and taut. The process of net formation from the initial layer structure is detailed in Figure 4, including periodic images to more clearly demonstrate the net-like structure. It can be perceived from the progression seen in Figure 4 that the number of lipids is insufficient to keep a stable flat membrane, as holes spontaneously form. At first, the system changes rapidly, with holes forming and then merging repeatedly. After formation, these holes then congregate together to form large, stable holes, giving the incomplete membrane the appearance of a ‘net’ as shown in Figure 2(b). The configuration in Figure 4(h) was formed after approximately

![Figure 3](image-url)

Figure 3. Height difference between upper and lower edges of the membrane as the initial lipid density increases, with associated images (log scaling for x-axis). A negative value denotes that the membrane is incomplete (does not completely separate the top and bottom sections of the simulation box).
300,000 timesteps (~73 ns). The simulation was continued until 1,000,000 timesteps (~243 ns), and no further evolution or change in structure was detected; thus the simulation was judged to have reached equilibrium status. At a normal density of 3, there is a small region where there are enough lipids to form a stable, complete membrane as seen in Figure 2(c), yet not so many that out-of-plane deformation occurs. It can be said that in this window, the interior and exterior force of the lipid bilayer are balanced.

At initial lipid densities higher than the normal, a membrane will form, but due to the increased number of lipids the bilayer formed repulses itself as it tries to form a membrane that is larger than the simulation box. This leads to ‘rippling’ behavior as the excess repulsive force of the membrane interior overcomes the bending energy of the membrane. This ‘rippling’ behavior is seen in Figure 2(d). Once the density reaches a certain point however, ‘bubbles’ appear inside the membrane, reducing the rippling behavior and eventually generating a relatively flat, but thick, structure with micelles of water inside the membrane itself. The formation process of the intra-membrane bubbles seen in Figure 2(e) is illustrated in Figure 5. It can be seen that at high densities, the repulsive interactions between the lipids drive them outwards, creating a disordered membrane that cannot form stable long-wavelength ripples before the lipids shunted to the exterior of the membrane self-contact and fold over, forming bubble structures around small amounts of water. These bubbles in the interior of the membrane stabilize the repulsion forces between lipids by balancing the surface area and volume of the membrane. Beyond

Figure 4  Evolution process of the ‘net’ membrane mode. Note the formation of multiple small holes joining together to form large, stable holes. The wire box in subfigure (a) represents the unit cell of the simulation.
the membrane mode with a single layer of bubbles, the membrane starts forming stacked layers of bubbles, as displayed in Figure 2(f). Additional increases to the initial lipid density merely increase the eventual thickness of this layer; as such a mode keeps stable even at extremely large densities. In fact, rippled lamellar and bubble-like formations have been observed in cell membranes exposed to magnetic fields for long durations (Chionna et al., 2005; Dini & Abbro, 2005). Similar unusual or non-flat membrane structures have also been found in human neutrophils exposed to chemoattractant, as shown in Figure 6 (Mckay et al., 1991). Figure 6(a) shows normal cell membranes, with the corresponding simulating membrane morphology shown in Figure 6(b). Figure 6(c) shows the abnormal, bulging, and rippled cell membranes of neutrophils exposed to chemoattractant, with
the corresponding simulational morphology shown in Figure 6(d). Although we have seen the mechanisms of formation for these several types of extraordinary membranes, merely noting the effect of the initial density of the lipid bilayer cannot help us get a true grasp of the formation and stability of the different biomembrane modes.

3.3. Effect of interaction parameter

Similar to the density of the lipids in the biomembrane, the interaction parameter between the lipid heads, lipid tails, and water beads can be tuned in order to more widely examine the different behaviors exhibited by biomembranes, which can be representative of certain factors indicating problems with a cell or similar artificial structure. The interaction parameter designates the repulsion effects which each lipid experiences from lipids nearby, and changing it mimics the tuning of biomembranes by inserting different types of lipid, or by electric or magnetic fields (Krishnan, Mojarad, Kukura, & Sandoghdar, 2010; Le Meins, Sandre, & Lecommandoux, 2011; Mashaghi et al., 2013; Woods, Li, Rosenblatt, Yager, & Schoen, 1989). To simulate this, we varied the interaction parameter between lipid beads mentioned in the Methods section. For the previous section, the repulsive interaction parameters between lipid beads of the same type are set as $a_{ii} = 25$, and those for two beads of different types are set as $a_{ij} = 100$. To study the effects of the interaction parameter, we modulated the self-interaction parameter between lipid beads of the same type by a set amount $P$; that is, $a_{ii} = 25 \times P$ for lipid beads only (not water beads) such that $P = 1$ is the normal value. The self-interaction of water beads is unchanged, as are the interactions between water beads and lipids and those between lipid beads of different type. It has been shown that there is a certain range of parameters which allows for the formation of lipid bilayers, but that range is fairly flexible (Kranenburg, Nicolas, & Smit, 2004). Due to this, we investigated the way the interaction parameter influences different behaviors that may occur irrespective of density.

Figure 7 demonstrates the effect of changing the parameter $P$ from 0.25 to 4 while keeping the initial lipid density at 3. This Figure reveals that, while keeping density at 3 and thus for the same number of lipids, lowering the interaction parameter causes the membrane to form holes and create a ‘net’ structure, while raising the interaction parameter forces the membrane to adopt the ‘rippled’ mode. This can be explained due to the fact that at an interaction parameter below unit, lipids cluster more compactly under pressure from the water, causing the membrane to shrink and upsetting the balance of interior repulsion and exterior surface tension, so that the membrane must form holes in order to stabilize. At an interaction parameter greater than unit, the repulsive force between lipids increase, pushing the balance between repulsion and surface tension in the opposite direction, such that the membrane bulges and forms ripples in order to maintain stability. However, observing the effect of $P$ for a single density does not help us get a comprehensive sense of the overall effect of the
interaction parameter. Thus, after running many cases, we formed a ‘phase diagram’-style graph as seen in Figure 8. From this, we can observe that the interaction parameter and the density are two sides of a coin; that is, increasing $P$ is similar to increasing the initial density in the effect it has on the morphology of the biomembrane. The result that these two seemingly disparate variables have similar effects lies in the fact that increasing either one results in an increased repulsion effect within the membrane itself, creating similar changes to the morphological mode. From this overview, we can use these results to gather an overview of the many different

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**Figure 7.** Height difference between upper and lower edges of the membrane at normal density as the interaction parameter changes, with associated images (log scaling for x-axis). A negative value denotes that the membrane is incomplete (does not completely separate the top and bottom sections of the simulation box).

**Figure 8.** Map of the different morphologies as a function of both density and interaction parameter (log scaling).
morphologies which a biomembrane structure can evolve into, dependent on the density and chemical makeup of the lipids composing it.

4. Concluding remarks
In summary, we have utilized DPD simulations to investigate the effects of various factors such as lipid density and interaction parameter value on the construction and characteristics of the typical lipid biomembrane. Our findings show that a smaller-than-normal initial lipid density does not create the traditional biomembrane; instead letting the system run to equilibrium results in the formation of a ‘net’, or at very low densities, a series of disparate ‘clumps’. As expected, a normal density and normal parameter result in a flat, stable biomembrane. When the initial lipid density is higher than normal, the membrane forms, but due to the increased number of lipids, the membrane formed is larger than the simulation box, leading to ‘rippling’ behavior as the excess repulsive force of the membrane interior overcomes the bending energy of the membrane. Once the density reaches a certain point however, ‘bubbles’ appear inside the membrane, reducing the rippling behavior and eventually generating a relatively flat, but thick, structure with micelles of water inside the membrane itself. Our simulations also demonstrate that the forces between lipids in a membrane, here represented by the interaction parameter of the DPD force field, play a significant role in the formation and behavior of lipid biomembrane assemblies, creating similar structures as the initial lipid density distribution. This work provides a comprehensive approach to the intricacies of lipid bilayer membranes, and can be used to develop novel cellular manipulation and destruction techniques.

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