

Coming Phase to Phase with Surfactants

Stuart Bartlett¹ and Seth Bullock¹

¹Institute for Complex Systems Simulation, University of Southampton, Southampton, SO17 1BJ
S.J.Bartlett@soton.ac.uk

Abstract

We introduce a fast cellular automata model for the simulation of surfactant dynamics based on a previous model by Ono and Ikegami (2001). Here, individual lipid-like particles undergo stochastic movement and rotation on a two-dimensional lattice in response to potential energy gradients. The particles are endowed with an internal structure that reflects their amphiphilic character. Their head groups are weakly repelled by water whereas their hydrophobic tails cannot be readily hydrated. This leads to the formation of a variety of structures when the particles are placed in solution. The model in its current form compels a myriad of potential self-organisation experiments. Heterogeneous boundary conditions, chemical interactions and an arbitrary diversity of particles can easily be modelled. Our main objective was to establish a computational platform for investigating how mechanisms of lipid homeostasis might evolve among populations of protocells.

Introduction

The debate concerning the containers within which the first biochemistries developed is hotly contested. One uncontroversial observation however, is that Nature has since fixed upon a single class of molecule to use as the barrier between cell contents and the external environment, be it the intercellular space or the outside world. These special molecules - lipids - possess the crucial property of being amphiphilic, they contain both hydrophilic and hydrophobic groups. Amphiphilic molecules are an example of a surfactant, a substance which reduces the interfacial tension between two fluids (we shall use the terms amphiphile, surfactant and lipid interchangeably). They are thus endowed with an ability to arrange themselves into meso-scale structures when placed in solution. The shapes of these structures reflect the systems' attempts to minimise contact between hydrophobic groups within the amphiphiles, and water molecules. One such structure, the vesicle, can be conveniently used to separate one aqueous environment from the surrounding water. It is this molecular device that organisms have adopted as a means of separating the inner cell space from its exterior. All nutrients and waste products must pass through this barrier in order to carry out their function within a cell. The

membrane must also grow, sever, re-connect and undergo various other transformations during the cell cycle. Other lipid membranes separating organelles from the intracellular space must also adopt various shapes and curvatures in order to maximise their function. Given the tremendous importance of membranes both during the early stages of the evolution of life and in contemporary organisms, it is easy to justify the pursuit of a complete understanding of amphiphile dynamics.

The electrostatic interactions between the constituents of lipid molecules are fairly well understood as are the equations of motion for the behaviour of such molecules in solution. Furthermore, the equilibrium properties of surfactant-water-oil systems have been analysed using a lattice model first introduced by Widom (1986). Having successfully reproduced some key features of surfactant phase diagrams, Widom's simple lattice model as well as other spin-based models (so-called due to their being isomorphic to a spin- $\frac{1}{2}$ Ising model), stimulated a profusion of investigations to be carried out both analytically and through Monte Carlo simulation (Larson et al., 1985). For a summary of the research performed during this period, see also the review of Kawakatsu et al. (1994). Despite these successes, there remain significant analytical obstacles to the complete understanding of more complex, biologically relevant lipid systems (for example, if we wish to include processes such as the synthesis and decay of lipids through metabolic pathways). Life is the antithesis of thermodynamic equilibrium, and exhibits highly non-linear dynamical behaviour to boot. These factors, among others, have presented what appear to be insurmountable barriers to a pure analytical understanding of the higher level systems of molecular biology. Instead we must, for the time being at least, look to computational methods. Even numerical integration of the equations of motion is a daunting task. Real systems of interest involve massive numbers of molecules, and interesting dynamic behaviour occurs over time scales which are much longer than typical numerical integration steps. Therefore models derived from first principles which solve the exact system of equations (molecular dynamics) are very expensive in terms

of computational resources. Multi-scale and hybrid models have been put forward by Ayton and Voth (2002) and Lyubartsev (2005) for example, but simulations over longer time scales and mesoscopic length scales with the potential for variable environments and boundary conditions are still relatively rare.

The popularisation of cellular automata (CA) models has given birth to a family of simulation techniques which have shown considerable promise for modelling complex systems such as amphiphile solutions (Kier et al., 1999; Nilsson and Rasmussen, 2003; Rothman and Zaleski, 2004). CAs are discrete time and space models in which all interactions occur on a local scale. These properties allow CAs to be much less computationally demanding than traditional numerical schemes. The lattice and discretisation constraints of CAs can cause problems with respect to invariance under geometric transformations but there is one class which has been shown to mimic reality with surprising effectiveness. So-called lattice gas models simulate hydrodynamics by allowing a set of particles to move and collide on a lattice. The rules of interaction are defined such that mass and momentum are conserved and one can derive the Navier-Stokes equations from the microdynamical rules of the CA (Frisch et al., 1986). The basic lattice gas has been extended for a variety of applications including the fluid dynamics of water-oil-surfactant mixtures (Boghosian et al., 1996, 2000; Mayer et al., 1997). Both of these models were successful in re-creating some key lipid phases and were later applied to more specific systems including, in the case of the model of Boghosian et al. (1996), self-reproducing micelles (Coveney et al., 1996), which showed impressive agreement with the experimental results of Bachmann et al. (1992).

In this investigation, we explored the abilities of a new CA for the simulation of amphiphile solution systems based upon the artificial chemistry model of Ono and Ikegami (2001). This model differs from the lattice gases mentioned above. Particles move in pursuit of potential energy minima, but they do not collide and exchange momentum. We perform this simplification of neglecting the individual particle momenta because we wish to focus on the self-assembly process and the meso-level dynamics of more complex systems with variable boundary conditions. By ignoring the explicit hydrodynamics of the system, the formulation of the model is greatly simplified as are the computational demands. We believe that the key dynamics of the self-assembly process are nevertheless retained.

An important feature of our simulations is the way in which surfactants are defined. Rather than a generic ‘membrane’ particle, we have applied a more explicit representation of the internal structure of amphiphiles. In addition, we introduced three different lipid species, each with its own geometry. Real cell membranes consist of many different lipid types. Some of them naturally form bilayers but there are also non-bilayer forming lipids present. The exact func-

tion of these non-bilayer lipids has been debated for many years and it is likely that they play several roles in the cellular performance (Lindblom et al., 1986). The stability, robustness and versatility of cell membranes derives in part from the homeostatic balance of the distribution of these varied lipid species (Beard et al., 2008). Therefore we aimed to endow our model with the additional freedom of having lipids with a range of membrane-forming properties. Our objective was to construct a platform which we could use to investigate the spontaneous evolution of lipid homeostatic mechanisms. Ono and Ikegami (2001) have already shown that simple cell-like entities arise spontaneously within their model framework. We aim to extend that model framework such that we can simulate not only the formation of protocells, but also the evolution by those protocells of mechanisms for balancing the lipid composition of their membranes. In our model, the geometry of vesicles (or protocell membranes) resulting from the spontaneous organisation process depends not only on environmental factors but also on the distribution of the different lipid species, since each species has its own preferred membrane curvature.

In this paper we wish to present the model in its current form as a tool for simulating an interesting and important class of complex system. As well as simulating the emergence of lipid homeostasis, the model could easily be modified to simulate complex reaction-diffusion or self-reproducing micellar systems, among others. We shall first give a brief description of the workings of the model, before describing the main results of our investigations so far. These will include simple phase separation of water and hydrophobic monomers, micelle formation, bilayer formation, ternary mixtures leading to monolayer formation and finally a set of hysteresis experiments. We shall then conclude with a discussion of the significance of these results before suggesting some relevant systems which will be simulated by our model in the future. Due to space restrictions, we shall not present a strong focus on the technical details of the model, instead we shall describe the most important features and highlight its phenomenological successes.

Model Description

The mechanics of our model are essentially the same as those of Ono and Ikegami (2001); Ono (2005). The simulation domain is a 2-dimensional triangular lattice over which particles move and interact. An arbitrary number of particles can reside on each lattice site, and the boundaries of the lattice are periodic. The model proceeds via a standard metropolis algorithm (relaxation towards a global potential energy minimum). All interactions between possible particle pairs across all relative orientations are defined *a priori* in the form of a lookup table. Same site interactions consist of a strong excluded volume repulsion which is the same for all particle types and acts between all particle types. The nearest-neighbour interactions take several different forms.

All forces are repulsive but the strength depends on the physical properties of the two particles involved in the interaction. In order to approximate the effect of hydrogen bonding, water particles repel one another with almost negligible force. Hydrophobic monomers also repel each other weakly. There is a strong repulsion felt between water particles and hydrophobic monomers. This is due to the frustration of the surrounding water molecules, which are unable to satisfy all of their potential hydrogen bonds. Interactions involving surfactants are slightly more complicated.

The crucial differences between our version of the model and that of Ono and Ikegami (2001), are the structure and interactions of the surfactants. We make use of a more explicit representation of lipid particle geometry. Although the surfactants have internal structure, we do not model the harmonic motion of the individual molecular components. Each surfactant is represented as a rigid particle free only to rotate in discrete increments (reflecting the discrete nature and underlying symmetry of the lattice). The pairwise interactions between these particles are computed using the sum of a set of Lennard-Jones functions. These calculate Van der Waals forces for the four interactions between the hydrophilic heads and hydrophobic tails of all pairs of surfactants which are nearest neighbours. Physically, these four terms represent the dipole-dipole interaction between the polar head regions, the dipole-induced dipole interactions between the heads and hydrocarbon tails, and the induced dipole-induced dipole interaction between the two tail regions.

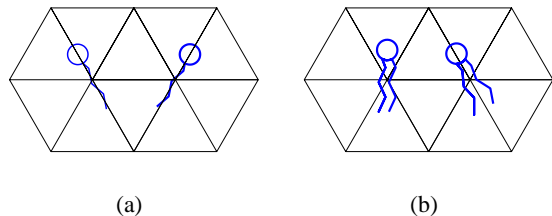


Figure 1: Equilibrium orientations of pairs of surfactant particles. a) M_1 particles at adjacent lattice sites align with their tails closer than their heads due to their cone-like geometry. b) an M_2 particle and an M_3 particle prefer to align with an angle of $\pi/6$ between their axes. This is due to the wider splay of the tails of M_3 particles.

M_1 particles are modelled on detergent particles with single alkyl chains. This gives them a cone-like shape with a broader head region. Figure 1(a) shows a schematic illustration of their pairwise equilibrium configuration. The two M_1 particles align with an angle of $\frac{\pi}{3}$ between their vertical axes. M_2 particles are based on lipids with double hydrocarbon chains giving them a cylindrical geometry. As a result

they prefer to align parallel with one another. M_3 particles have broader tail regions, wider than their head groups. A second example of the equilibrium configuration of a pair of particles is shown in figure 1(b), which illustrates how the cylindrical M_2 particle and the broad-tailed M_3 particle prefer to align with one another. Since the M_2 particle has a cylindrical geometry but the M_3 particle has a broader tail region, these two particles prefer to align with an angle of $\frac{\pi}{6}$. The other equilibrium configurations are defined in a similar way, e.g. an angle of $\frac{\pi}{3}$ for pairs of M_3 particles (with head groups closer than tails) and an angle of 0 for pairs consisting of an M_1 and an M_3 particle.

We now turn to defining the interactions between surfactants and water. Clearly the head groups of M_1 particles will be attracted to water over a broader range of angles than those of M_2 and M_3 . The repulsion between the tails of M_3 particles and water will also extend over a wider range of angles than the other two particles. These varying affinities for water are summarised in figure 2, which shows the variation of the pairwise potential ϕ for an amphiphile neighbouring a water particle over a range of orientation angles θ . The M_2 particle with its cylindrical geometry, feels an anti-symmetric repulsion as a function of θ . Conversely, the M_3 particles feel a broad ranged repulsion when their tails face water and only over a narrow range do they experience an attraction to water.

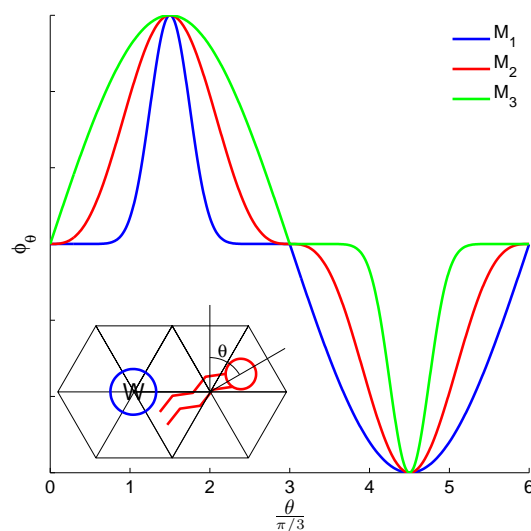


Figure 2: Pairwise potential ϕ for a water and surfactant particle at neighbouring lattice sites. The potential varies as a function of the surfactant orientation θ and takes on a different functional form for each of the three surfactant species. Note that in the model, the possible values of θ are discretised, the continuous curves are indicative only.

At each time step, the potential energy field for each particle type is calculated using the interactions described above.

Particles then undergo stochastic transitions in pursuit of local energy minima. These transitions consist of translation by one lattice spacing and rotation (in the case of the anisotropic surfactant particles). Particle states are updated synchronously. As the particles relax into local minima the system as a whole tries to reach a state of global energy minimum analogous to the process of simulated annealing. The probability of a particle undergoing a transition is proportional to the value of the energy response function, evaluated for that transition (Ono and Ikegami, 2001):

$$f(\Delta\Phi) = \frac{\Delta\Phi}{e^{\beta\Delta\Phi} - 1} \quad (1)$$

$\Delta\Phi$ is the potential energy change of the transition and $\beta = 1/T$ is the inverse temperature (we take Boltzmann's constant equal to unity). This function is designed to implement the basic character of a Boltzmann factor without the risk of the value diverging for large negative $\Delta\Phi$ (transitions which are energy-reducing are not guaranteed to be accepted, as in a standard Monte Carlo algorithm). Simulations proceed by making use of this function to calculate transition probabilities. Particle states are then updated synchronously and randomly, biased by these probabilities.

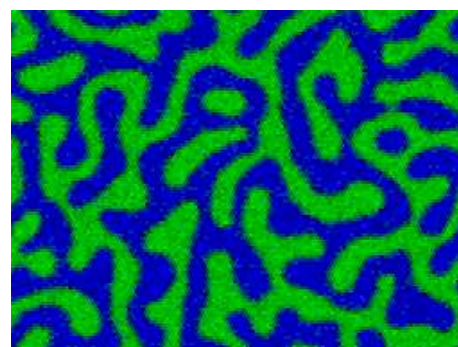
Results

We shall now examine the most important results from testing the model over a range of conditions. Note that all images shown here are sections taken from larger systems therefore the boundaries in the images do not wrap around in the periodic way that they do in the simulation. In all figures, depth of green corresponds to the concentration of oil particles, depth of blue corresponds to water concentration and depth of red to surfactant concentration.

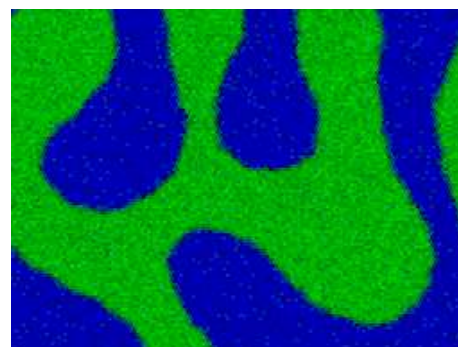
Phase Separation

We begin with a simple, characteristic situation: a 50:50 water-oil mixture. Since polar and organic solvents do not mix due to their differing capabilities for hydrogen bond formation, we would expect such a system to relax to a state of phase separation in which the surface tension (interfacial area or contour in 2D) between the two substances tends to a minimum. Figure 3 shows two snapshots from a simulation containing average densities of $\rho_w = \rho_o = 7.5$ particles per lattice site, at a temperature of $T = 0.8$. We can see in figure 3(a) that the system separates into regions of almost pure water and oil in the early stages. Over time the average curvature of the interface between the two regions is persistently reduced. Close observation reveals the propagation of capillary waves across this interface (see animation at: <http://tinyurl.com/lipid-CAs>), a characteristic surface tension effect. Given sufficient time, the system will reach a state of a single straight interface separating the two phase regions. Since the relaxation time scales approximately exponentially with system size, one would have to

run the simulation for an extremely long time to reach this state. However we can already see this minimum energy configuration at smaller length scales within the system.



(a)



(b)

Figure 3: System configuration after a) $t = 1 \times 10^4$ and b) $t = 1 \times 10^6$ time steps for a binary mixture of water and oil particles.

Surfactant-Water Mixtures

We now turn our focus to the behaviour of the surfactant particles in the presence of water. Experimental results from studies of real lipid systems lead us to expect structures such as micelles, bilayers and vesicles among others (Tresset, 2009). We also know that the appearance of such structures should depend on certain parameters such as the temperature and surfactant concentration.

Micelles M_1 particles were designed to emulate detergent molecules with single alkyl chains. We represented this in the model by endowing them with a cone-like structure: a narrow tail region and broad head section. We would expect such particles to coalesce into micelles in the presence of water. In a micellar configuration, the contact between hydrocarbon tails and water is minimised whilst the energetic aspirations of the amphiphiles are also reasonably satisfied. We can see from figure 4 that the equilibrium structure exhibited by M_1 particles is the micelle. The configuration

shown contains average densities of $\rho_w = 12$ and $\rho_{M_1} = 3$ particles per lattice site and had a temperature of $T = 0.3$. Increasing the surfactant concentration does not alter the micellar configuration, it simply causes a greater number and hence closer packing of micelles. Likewise decreasing the M_1 concentration simply results in a smaller number of micelles as the surfactants have a lower probability of encountering one another as they perform random walks over the lattice. Given time they do begin to aggregate but the process is slow. Furthermore, if the temperature is high, the micelles cannot form because they require a certain threshold number of constituents before they can remain robust to thermal fluctuations. Micelles containing only a small number of particles are not robust to these perturbations and thus do not persist. Hence at low surfactant concentrations, micelles can only form at low temperatures where fluctuations are less frequent. Below the critical micelle concentration (CMC), micelles would be unable to form at any temperature. In our model the CMC is very low ($\rho_{M_1C} < 1$ particle per lattice site) and we have not yet explored such low surfactant concentrations.

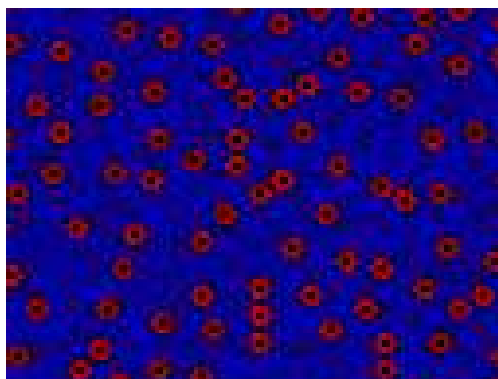


Figure 4: System configuration after $t_f = 2 \times 10^5$ time steps for a binary mixture of water and M_1 surfactant particles.

Bilayers We defined M_2 particles as being similar to lipids with a cylindrical geometry. Their energetic requirements are satisfied if they align parallel with one another forming a straight bilayer. As was the case for M_1 particles, this arrangement minimises the interfacial contact between hydrophobic tails and water while also satisfying the energetic preferences of the surfactants. Figure 5 shows a typical steady state of a water- M_2 mixture. It is clear that the self-assembly properties of this surfactant species are quite different from those of the M_1 particle. Under identical conditions and concentrations, M_2 particles assemble into bilayers, in contrast to the micelles formed by the M_1 particle. If the concentration of M_2 particles is very low, i.e., $\rho_{M_2} < 1$ particle per lattice site, below the critical bilayer concentration (CBC), micelles are formed rather than bilay-

ers. However they do not possess the central voids of the M_1 micelles so they could also be described as small clusters. At these low concentrations, tuning the temperature to a critical value of $T \approx 0.3$ allows a small number of bilayer sections to form but they are rapidly destroyed once the temperature reaches $T = 0.4$. This critical structure formation is analogous to the formation of micelles at low concentrations described in the previous section. Further investigations will reveal the nature of this transition region, within which well-defined structures form, but outside of which no such structures persist. As the concentration of M_2 particles is increased above the CBC, the system becomes more densely packed with bilayers and the interconnectivity of the bilayers increases concomitantly.

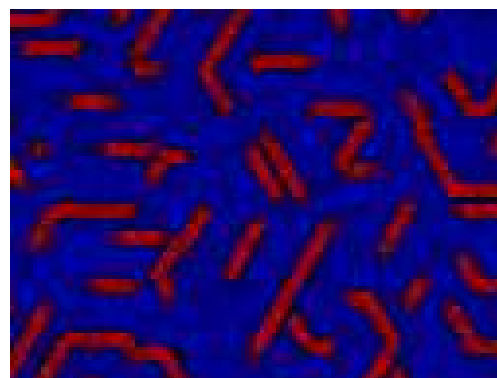
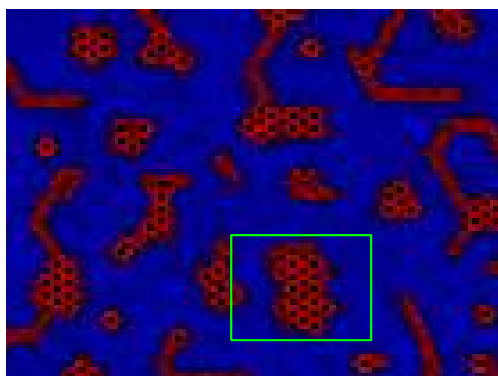


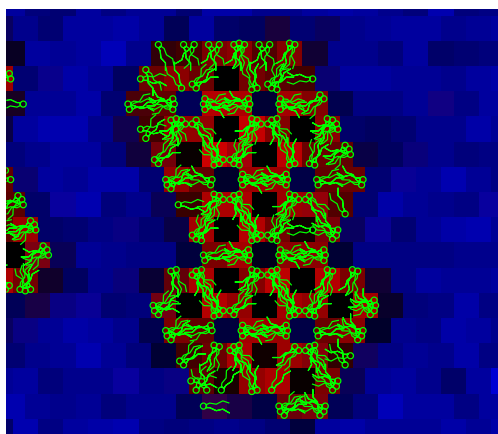
Figure 5: System configuration after $t_f = 2 \times 10^5$ time steps for a binary mixture of water and M_2 surfactant particles.

Bilayers and Reverse Micelles The M_3 surfactant possesses a broad tail region so it should be averse to micelle formation. Bilayers are also not the ideal structure since pairs of M_3 particles would prefer to align with an angle of $\frac{\pi}{3}$ between their long axes. In an organic solvent these particles would form reverse micelles, but it is not obvious what structures they would form in a polar solvent. Because M_3 particles prefer not to form micelles or bilayers, they actually attempt to create an environment in which reverse micelle formation is possible. Figure 6 shows the equilibrium configuration of a mixture of water and M_3 surfactants at the same concentration and temperature as the systems shown in figures 4 and 5. We can see that the system adopts a mixture of bilayers and clusters. On closer inspection, one finds that the clusters consist of amphiphiles forming a hexagonal phase. There are water particles at the centres of the reverse micelles due to the surfactant head groups being water soluble. In contrast the inter-micellar voids are just that, they are devoid of particles since they are apolar environments.

Monolayers Having evaluated the behaviour of water-oil and water-surfactant mixtures, we can now explore the equi-



(a)



(b)

Figure 6: a) System configuration after $t_f = 2 \times 10^5$ time steps for a binary mixture of water and M_3 surfactant particles. b) A closer view of the highlighted region from the upper figure showing a cluster of M_3 particles which have assembled into a honeycomb structure allowing the formation of reverse micelles. Particles are drawn where there are 2 or more surfactants present in that position and orientation.

librium configurations of ternary solutions. The polar and organic solvents should again separate but now the surfactants can take up positions along the phase boundary in order to further minimise the total surface free energy. The surfactants should align themselves such that their polar heads are hydrated and their lyophilic tails mingle with the oil regions. Figure 7 displays such behaviour when we initialise a simulation with average densities of $\rho_w = \rho_o = 7$ and $\rho_{M_2} = 1$ and allow it to relax for $t_f = 2 \times 10^5$ time steps at a temperature of $T = 0.1$. The surfactants rapidly line the oil-water interface and at low temperatures the system reaches a steady state where the oil islands become stationary and almost completely cease to merge or divide. At higher temperatures the system adopts a configuration identical in geometric character to that in figure 8(a). At this temperature, $T = 0.4$ the system has more freedom to explore its mi-

crostates and hence over time the oil regions merge, grow in size and change shape in an effort to minimise their average curvature, analogous to the situation for the binary oil-water case. Fluctuations present in the initial conditions are gradually damped out. At these high temperatures, the process of potential energy minimisation struggles since the energy response function makes less of a distinction between transitions which are energy-reducing and those which incur an energy cost. So although there is phase separation and the surfactants assemble on the phase boundary, there are also surfactants spread thinly across the entire lattice. The bulk phase separation effects dominate here due to the large numbers of water and oil particles present and the high temperature. In contrast, at lower temperatures, the presence of the surfactants is more influential. This is visible in figure 7. Since M_2 particles prefer to align parallel to one another, the oil-water interface takes on a slightly different appearance. It is composed of straight sections punctuated by sharp corners, typically turning through angles of $\frac{\pi}{3}$. Because the surfactant monolayer is rather inflexible at this low temperature, the system does not undergo any significant geometric changes once settled into the bicontinuous state shown in figure 7. We also explored situations in which the average oil densities were lower than the water densities. In these cases, the so-called microemulsion phase is exhibited, in which droplets of oil form, surrounded by surfactant boundaries. These droplets were seen to merge when they encountered one another.

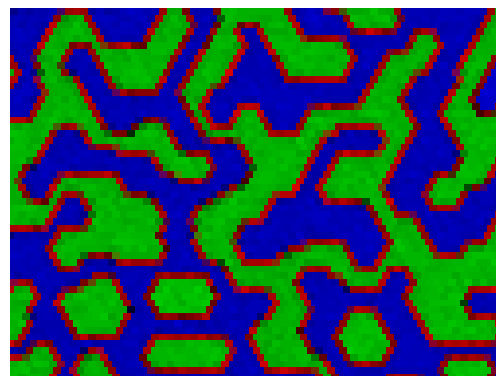
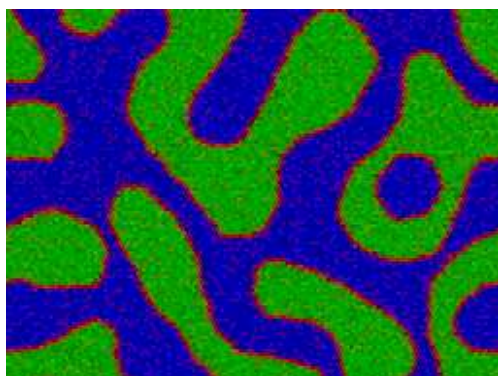


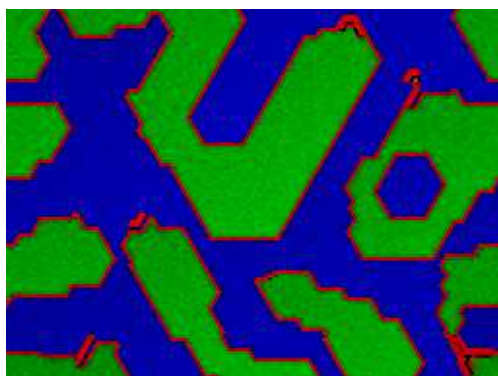
Figure 7: System configuration after $t_f = 2 \times 10^5$ time steps for a ternary mixture of water, oil and M_2 surfactant particles.

Melting and Re-freezing: Temperature-driven Hysteresis

In this section we shall present an example of a hysteretic effect in a ternary mixture. Comparison of figures 7 and 8(a), show that the temperature has a strong influence on the properties of the steady state structure. Higher temperatures allow a broader range of microscopic configurations



(a)



(b)

Figure 8: System configuration from a temperature-driven hysteresis experiment after a) $t = 6 \times 10^5$ and b) $t = 10 \times 10^5$ time steps, for a ternary mixture of water, oil and M_2 surfactant particles. An animation of this experiment can be found at: <http://tinyurl.com/lipid-CAs>

to be explored per unit time. However these structures are much less stable than those which emerge at low temperatures. At high temperatures, what we see at large scales is an average of a large number of possible configurations which are being adopted and then eradicated again in rapid succession. Alas the randomising effects of thermal energy reign. Since the absence of these effects allows the system to maintain its configuration over longer periods, we would expect that cooling a warm system should freeze in the approximate configuration which prevailed before the cooling began. So if we were to take a stationary cool system, heat it, allow it to relax and then cool it again, the final steady state will be different from that which results from leaving the system at a constant low temperature. It is this effect that gives glasses their amorphous structure. The relaxation time required for the molecular constituents of glasses to settle into their equilibrium positions is so long that they have the appearance of a liquid which has had its molecular motion suspended. We expect that we can create a similar effect

with our model system. We performed just such an experiment in which we initialised a simulation with identical parameters to those of the system shown in figure 7. It was allowed to relax for 2×10^5 time steps before the temperature was linearly raised from $T = 0.1 \rightarrow 0.4$ over a period of 2×10^5 time steps. The system was then left for another 2×10^5 time steps. The configuration at this point is shown in figure 8(a). The temperature was then returned to $T = 0.1$ linearly over 2×10^5 time steps and the system was allowed to relax once more. The final state of the system at the end of this process is shown in figure 8(b). The most prominent feature of figure 8 is that the high temperature state has indeed been ‘frozen in’ or quenched. However the alignment preferences of the surfactants have caused the monolayer to become much more rigid. Furthermore, because the total interface length has been reduced by the heating process, there are now more than enough surfactants to line it. As the temperature was lowered and potential minimisation became a stronger imperative, free drifting surfactants were forced out of the water regions and were adsorbed onto the monolayer. Some surfactants then started to form bilayer sections since joining the monolayer incurred a greater energy cost than extending a bilayer into the water region. This experiment showed that the geometric features of the configuration are not a simple function of state. They depend not only on the current conditions, but also on the system’s history. When the system is initialised at a low temperature and remains at that temperature, it retains remnants of its initial configuration. If the same system is heated and then cooled again, the final configuration reflects the state of the system at previous times when the environment was different. Not all details are retained but the differences between figures 7 and 8(b) highlight the fact that current environmental conditions alone are not sufficient to define the configuration of the system.

Conclusions

We have presented a model of amphiphile structure formation which is both simple and shows qualitative agreement with experiment. As a foundation we adopted the framework of the artificial chemistry model of Ono and Ikegami (2001). By re-formulating the way that surfactants are represented in the model, we have given it the ability to successfully simulate some of the most common phases of amphiphilic systems. We have shown its ability to reproduce micelles, bilayers, reverse micelles and monolayers. Other phases including microemulsions have also been simulated.

Armed with the knowledge that protocells spontaneously formed in the original model of Ono and Ikegami (2001), and having established the basic lipid phenomenology of this new model version, our future work will involve simulating protocellular chemical systems in which the cells can adopt different membrane curvatures depending on the distribution of lipids in their membranes. This lipid distribution will directly impact their robustness and hence their ‘fitness’

with respect to other cells within the system. For example, possessing a small number of M_1 and M_3 particles would enable a cell to have a membrane composed of straight sections (primarily M_2 particles) punctuated by high curvature corners (M_1 particles on the inner side of the bilayer and M_3 particles on the outer side). Such a membrane would have a significantly lower surface tension than one constructed purely from M_2 particles. The ability to exchange resources and wastes involved in the synthesis of new lipid particles controls how efficiently a protocell can repair damage to its membrane and also how easily it can grow and divide to form a pair of daughter cells. Therefore this 'full' version of the model might give clues as to how mechanisms for cellular lipid homeostasis might emerge spontaneously. Further selection pressure could be placed upon the protocells by relaxing the assumption of a uniform, stationary environment. We should also be able to simulate self-reproducing micelles (Bachmann et al., 1992), and complex reaction-diffusion systems (Szymanski et al., 2011).

Acknowledgements

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