List of Figures

Figure	Title	Page
1.1	A schematic diagram showing amphiphilic surfactant molecules with a hydrophilic head-group and a hydrophobic tail. The surfactants are classified into four major categories based on the head-group charge.	2
1.2	A schematic diagram showing the amphiphile shape, the self-assembled structure and	
	the respective packing parameter which is denoted by $PP(=\frac{v_0}{a_h l_c})$. This figure has been taken from [Lombardo <i>et al.</i> , 2015].	4
1.3	Structure of protein α -helix, assisted by hydrogen bond formations between the oxygen atom of the carbonyl group and the hydrogen atom of the amino group. This image has been taken from [Georgiev and Glazebrook, 2019].	6
1.4	Schematic representation of different types of $\pi - \pi$ interactions in aromatic ring systems. M+ and X- denote the cation and anion respectively.	7
1.5	Flowchart of the steps performed in the molecular dynamics simulations.	9
1.6	A schematic representation of the hierarchy of the multiscale modelling based on the length and time scale of the system. AA, UA and CG stand for all-atom, united-atom amd coarse-grained models respectively.	9
1.7	A schematic diagram showing different phases of a bilayer (a) Liquid crystalline phase (L_c) , (b) Gel phase (L_{β}) , (c) Tilted gel phase $(L_{\beta'})$, (d) Ripple phase (P_{β}) and fluid	5
	phase (L_{α}) .	12
1.8	A schematic diagram showing the formation of a peptide by the linkage of amino acids and is facilitated by the elimination of water molecule.	13
2.1	Chemical structure of (a) BTMAC and (b) SA molecules in atomistic representation. Color codes: Blue, BTMAC head $(N+)$; Ice-blue, BTMAC chains; Red, SA chains; Yellow, SA head (O); White, Hydrogen.	20
2.2	Snapshots of systems S1 to S2 (reported in table 2.2) with decreasing water concentration and the BTMAC to SA ratio at 2:1. (a)-(g) show the random initial configurations and the final configurations after self-assembly of the all systems obtained after 20 ns. Color codes: Blue, BTMAC head (N+); Ice-blue, BTMAC chains; Red, SA chains; Yellow, SA head (O); White, Hydrogen; Orange, (Cl^{-1}) and green, water. In the final configurations, all of the water molecules are not shown for the sake of clarity. Micelles are transformed into bilayers where the shape slowly changes from sphere to ellipse to bilayers. The water concentrations below which it is a bilayer is 67.28 wt %.	23
2.3	Snapshot of (a) A1 with 84.56 wt% of water and (b) A2 with 62.35 wt% water. The color code is same as used in figure 2.2 Water molecules and chloride ions are omitted for the sake of clarity.	24
2.4	Time evolution of solvent accessible surface area (SASA) for A1 and A2. The SASA is converged for the last 120 ns for both A1 and A2.	24
2.5	g(r) of head of BTMAC and SA from the center of mass of the last bead of the tails for M1, M2, M3 are shown for A1 and BA11. The distribution function from simulations with larger system-size match well.	25
2.6	Density profiles of systems A2, BA21 and BA22 which have lower water content. These systems are simulated with different box-lengths to check the system size effect.	25 26

2.7	Angle distribution of head-middle-end of BTMAC and SA chains for (a) systems A1 and BA11 which have higher water content (84.56 wt%), (b) systems A2, BA21 and BA22 having lower water content (62.35 wt%). The schematic representation of vectors considered to compute the angular distribution are shown in the inset of subfigure (a) where θ signifies the angle between the two vectors.	26
2.8	Time evolution of radius of gyration (R_g) of (a) M1, (b) M2, (c) M3, (d) average for system A1 after averaging over all aggregates. Error bars of R_g calculated from equation 2.4 are not shown for individual M1, M2 and M3 since their sizes are of the sizes of the	
2.9	symbols. Error bars of R_g calculated from R_h are shown. Deuterium order parameter (S_{CD}) of (a) BTMAC (b) SA after averaging over all aggregates. S_{CD} of systems A1 and BA11 having higher water content is close to zero	28
2.10	for both BTMAC and SA due to the spherical nature of the micelles. Number of aggregations present in A1 at (a) 283 K, (b) 300 K, (c) 323 K and (d) 330	29
2.11	K. Different aggregates get fused together or fragmented with different temperatures. Bilayer thickness (a-c) and interdigitation (d-f) superimposed on Voronoi area per head group at 283 K, 338 K and 345 K. The unit of all color bars is in nm. The plot shows	30
	the presence of rippling along y-axis till 338 K which disappears at 345 K.	31
3.1	Mapping of AA (a) BTMAC and (b) SA to CG degrees of freedom. cpk represents the AA model and the bigger spheres represent the respective CG model. VMD v1.9 [William <i>et al.</i> , 1996] is used for the snapshots.	34
3.2	Snapshot of BTMAC cylindrical micelle obtained from (a) AA simulation and (b) CG simulation of A1 using MARTINI (M), Water molecules and ions are ignored for the cause of clarity. Color codes: Purple; head, Green; tail	38
3.3	Comparison of distribution of BTMAC bonds, AA vs CG in system A1 for (a) bond-1, (b) bond-2, (c) bond-3, (d) bond-4 and (e) bond-5.	38
3.4	Comparison of distribution of BTMAC angles, AA vs CG in system A1 for (a) angle-1, (b) angle-2, (c) angle-3 and (d) angle-4.	39
3.5	g(r) of BTMAC head with respect to the centre of mass of all tails. The AA and CG $g(r)$ match well with each other confirming the shape of the micelle to be cylindrical.	40
3.6	AA vs CG bonded distributions in system B11 for bonds in (a) BTMAC, (b) SA and for angle distributions in (c) BTMAC and (d) SA. CG BTMAC and SA bonded distributions match well with the AA ones for all models. CG angle distributions match reasonably well with the AA ones.	41
3.7	g(r) of head beads from the centre of mass of end bead for B11, showing the micellar size distributions from all CG models. Model M_b results in the best match in to the AA ones.	41
3.8	Snapshot of self-assembled spherical micelle formed from CG simulation in system B11 using M_b . Color codes: Purple; BTMAC head, Green; BTMAC tail, Red; SA head,	
	Cyan; SA tail.	42
4.1	Area per surfactant (APS) and solvent accessible surface area (SASA) for all systems at AA and CG resolutions. The AA simulation of S8 has longer run than other systems since its per chain configurational entropy of the surfactants did not converge well until 400 ns. Similarly, the CG S8 system is simulated for 6 μ s so that the SASA and APS of the system are well converged.	49
4.2	Final configurations of all asymmetric bilayers obtained from CG simulations. (a), (e), (f) and (g) correspond to bilayers S1, S5, S6 and S8 respectively obtained from biased configurations. Bilayers S2, S3, S4 and S7 obtained after self-assembly from random initial configurations are shown in (b), (c), (d) and (h) respectively. Similar	54
4.3	configurations are observed from AA simulations. AA and CG bonded distributions of BTMAC and SA in maximum asymmetry bilayer S1. (a)-(e): BTMAC bonds, (f)-(i): BTMAC angles, (k)-(n): SA bonds and (o)-(q):	54
	SA angles. AA and CG bonded distributions are in good agreement with each other.	55

4.4	Density distributions of all BTMAC and SA along the bilayer normal in system with (a, b) maximum asymmetry, (c) intermediate asymmetry (d, e) minimum asymmetry. Solid lines: AA, dashed lines: CG. red and green: two monolayers including head to tail in a chain. Black: tails excluding the head groups. Dark green : CG molecules with high entropies.	56
4.5	Bilayer thickness superimposed on the Voronoi area per head group in AA (a-c) and CG (d-f) resolutions for bilayers prepared from biased configurations. The unit of color-bar is in nm.	57
4.6	Interdigitation superimposed on the Voronoi area per head group in AA (a-c) and CG (d-f) resolutions for bilayers prepared from biased configurations. The unit of color-bar is in nm.	58
4.7	Thickness (a) and interdigitation (b) superimposed on the Voronoi cells in CG resolution for larger bilayer (S6) with intermediate asymmetry. The unit of color-bar is in nm.	58
4.8	Bilayer thickness superimposed on the Voronoi area per head group for bilayers resulting from random initial configurations with maximum and minimum asymmetries. (a), (b): AA; (c), (d): CG. The unit of color-bar is in nm.	59
4.9	Interdigitation superimposed on the Voronoi area head per group for bilayers resulting from random initial configurations with maximum and minimum asymmetries. (a), (b): AA; (c), (d): CG. The unit of color-bar is in nm.	59
4.10	Interdigitation superimposed on the Voronoi cells at AA level for bilayers with maximum asymmetry (S1), intermediate asymmetry (S5) and minimum asymmetry (S8) at 283 K (a-c), after heating to 308 K (d-f) and after cooling back to 283 K (g-i). The unit of color-bar is in nm.	61
4.11	Time evolution of per chain configurational entropy of S1 and S2 with maximum asymmetry averaged over all molecules, (a)-(d) AA, (e)-(h) CG. Molecules with higher and lower entropies are referred to as disordered and ordered molecules. The error bars represent the standard deviations in per chain configurational entropies obtained from averaging over all the molecules.	63
4.12	Time evolution of per chain configurational entropy of S5 and S6 with intermediate asymmetry, (a)-(d) AA, (e)-(h) CG. The error bars represent the standard deviation in per chain configurational entropy arising from averaging over all molecules in two classes.	63
4.13	Time evolution of per chain configurational entropy of S8 and S7 with minimum asymmetry, (a)-(d) AA, (e)-(h) CG. The error bars represent the standard deviation in per chain configurational entropy arising from averaging over all molecules in two classes.	64
4.14	Tilt vectors (\vec{t}) of BTMAC and SA for less and more populated leaflets for the final configurations of bilayers created using Packmol. Blue arrows: ordered molecules, green arrows: disordered molecules. (a), (b): maximum asymmetry, (c), (d): intermediate asymmetry and (e), (f) minimum asymmetry at AA resolution. Similarly tilt vector in the CG resolution is shown in (g), (h): maximum asymmetry, (i), (j): intermediate asymmetry and (k), (l).	65
4.15	Tilt vectors (\vec{t}) of BTMAC and SA for less and more populated leaflets for the final configurations of bilayers with random initial configuration. Bilayer S2 has maximum asymmetry whereas S7 has minimum asymmetry. Blue arrows: ordered molecules, green arrows: disordered molecules. (a), (b): maximum asymmetry, (c), (d): minimum asymmetry at AA resolution. (e), (f): maximum asymmetry; (g), (h): minimum asymmetry at CG resolution.	66
4.16	Time averaged tilt vectors ($\langle \vec{t} \rangle$) of BTMAC and SA for more populated leaflets for the bilayers with (a) Maximum asymmetry, 1D ripple (system S2), (b) Intermediate asymmetry, 2D ripple (system S5) and (c) Minimum asymmetry, Gel phase (system S8).	
	The tilt vectors are superimposed on the bilayer thicknesses. The unit of colorbar is in nm.	67

- 4.17 Time averaged tilt angles superimposed on the Voronoi cells of less and more populated leaflets in AA resolution for the bilayers with lamellar phase as the configuration (a), (b): maximum asymmetry; (c), (d): intermediate asymmetry and (e), (f) minimum asymmetry in AA resolution. Similarly (g), (h): maximum asymmetry; (i), (j): intermediate asymmetry and (k), (I) minimum asymmetry in CG resolution. The unit of colorbar is in degree(°).
- 4.18 Time averaged tilt angles superimposed on the Voronoi cells of less and more populated leaflets for the bilayers with random initial configurations. (a)-(d) AA, (e)-(h) CG. The unit of colorbar is in degree(°).
- 4.19 Time averaged tilt angles superimposed on the Voronoi cells of (a)-(b) AA and (c)-(d) CG bilayer S4. The unit of colorbar is in degree($^{\circ}$).
- 4.20 Order parameters, P_2 , for two monolayers for all the systems in (a) AA and (b) CG resolution. P_2 across two layers are shown in same location to describe the difference in P_2 between the two leaflets. (c) and (d) show the differences in order parameters (ΔP_2 with respect to asymmetry percentage at AA and CG levels respectively.
- 4.21 Variation of per chain configurational entropy with asymmetry at AA resolution: (a) BTMAC, (b) SA and CG resolution: (c) BTMAC, (d) SA. The data point shown in star: S6 bilayer with larger system size. S^{per-chain}_{conf} increases with increasing asymmetry percentage. The error bar represents the standard deviation around time-frames over which S^{per-chain}_{conf} converged and over all molecules.
- 4.22 Variation of per chain configurational entropy with bilayer thickness (a)-(b) and interdigitation (c)-(d). Black: AA, red: CG. The data point shown in star: S6 bilayer with larger system size. $S_{conf}^{per-chain}$ increases with bilayer thickness and decreases with interdigitation. The error bar represents the standard deviation around time-frames over which $S_{conf}^{per-chain}$ converged and over all molecules.
- 4.23 Variation of per chain configurational entropy with $(1 P_2^2)$ at AA resolution: (a) BTMAC, (b) SA and CG resolution: (c) BTMAC, (d) SA. The data point shown in star: S6 bilayer with larger system size. The error bar represents the standard deviation around time-frames over which $S_{conf}^{per-chain}$ converged and over all molecules.
- 5.1 Snapshots of P-1 (a) monomer and (b) parallel slipped stacked dimer. Color codes: Red, oxygen; Green, carbon; Blue, nitrogen and White, hydrogen. For clarity, two monomers are shown in green and yellow and P-1 nitrogens are shown in blue.
- 5.2 A schematic representation of (a) right handed helix (anticlockwise rotation) and (b) left handed helix (clockwise rotation). The orientations of the helices are similar as discussed in [Xu *et al.*, 2017].
- 5.3 Initial snapshots of dimers with (a) positive inter-planar angle, (b) negative inter-planar angle. The inter-planar angle is the angle between the two vectors formed by joining the nitrogen atoms of the PDI cores. (c) RH and (d) LH (referred in figure 2) showing different stackings (CC/ π or CH/ π or T type π -interactions) with shortest distances.
- 5.4 Stacking energies of P-1 dimers upon changing the inter-planar angle without and with dispersion corrections. (RH) and (LH) dimers correspond to anticlock-wise and clockwise inter-monomer rotations respectively.
- 5.5 Snapshot of initial configurations of P-1 dimers with (a) positive inter-planar angle (RH) and (b) positive inter-planar angle (LH) solvated in water. Water molecules are shown in green color.
- 5.6 Normalized UV-vis absorption spectra obtained for 3% (7.5 μ M) THF-Water solvent. The absorption peak at 500 nm corresponds to $\pi - \pi$ stacking interactions between the P-1 monomers in the self-assembled super-structure.

68

69

70

71

72

72

73

79

79

80

80

81

83

5.7	Snapshots of dimers with (a) positive inter-planar angle (RH) and (b) negative inter-planar angle (LH) from molecular dynamics simulations. Green dots: water. Side aromatic Phe rings in the P-1 molecule are labeled from 1-8. Snapshots of dimers with (c) positive and (d) negative inter-planar angle showing hydrogen bonding in P-1 dimers. Dotted black and blue lines represent π -stacking and hydrogen bonding respectively.	
5.8	Water are not shown for the sake of clarity. Radial distribution function, g(r), of the center of mass of PDI core and side rings (Phe motif) of dimers with (a) positive inter-planar angle, RH and (b) negative inter-planar	85
5.9	angle, LH. Black dashed line denotes the distance for π -stacking interactions. Distribution of inter-molecular angle for (a) positive inter-planar angle, RH and (b) negative inter-planar angle, LH dimers. Rings only within π -stackings are considered. The cartoon diagrams (1), (2) and (3) schematically show orientations of Phe motifs	86
	for π -stacking	87
5.10	Distribution of hydrogen bonds formed in P-1 obtained from MD simulations for LH	
0.20	(negative) and RH (positive) interplanar angle dimer.	87
5.11	Distributions of non-bonded energies of dimer with positive (RH) and negative (LH)	01
0.11	inter-planar angle. (a) Coulombic energy, (b) Lennard-Jones interaction energy and (c)	
	total non-bonded potential energy.	88
5.12	The overlapping histograms for (a) LH dimer and (b) RH dimer each obtained after 10	00
J.12	ns of umbrella sampling simulations in the presence of 10%THF-water and THF solvents	
		20
F 12	respectively.	89
5.13	Potential of mean force (PMF) of dimer with negative (LH) and positive (RH) inter places angle in THE and 10% THE water respectively. The inset shows the minima	
	inter-planar angle in THF and 10% THF-water respectively. The inset shows the minima	00
F 14	for them.	90
5.14	Snapshots of (a) negative (LH) and (b) positive (RH) dimer corresponding to the configurations with minimum potential of mean force obtained from umbrella sampling	
	simulations in the presence of 10% THF-water and THF respectively (figure 5.13 inset).	
	Dotted black and blue lines represent π -stacking and hydrogen bonding respectively.	
	Solvent molecules are omitted for the sake of clarity.	91
5.15	Radial distribution function $(g(r))$ of PDI rings and side aromatic rings in (a) positive	51
5.15	(RH) dimer in pure THF and (b) negative (LH) dimer in presence of 10% THF-water.	91
5.16	Hydrogen bond distribution in LH and RH dimers in the presence of 10% THF-water	91
5.10		02
E 17	and pure THF solvents.	92
5.17	Radial distribution function of water and THF near (a) PDI rings and (b) side rings for	02
	the negative (LH) and positive (RH) dimers.	93
6.1	(a) Open and (b) Folded PyKC dimer conformers drawn using ChemDraw. These two	
	structures are the initial configurations for the geometry optimization.	97
6.2	The initial stacked configurations of (a) open PyKC dimer and (b) folded PyKC	
-	dimer, configurations of stacked PyKC dimers obtained after geometry optimization	
	using dispersion corrections for (c) open and (d) folded chains, (e) geometry optimized	
	structure of folded PyKC dimer with dispersion correction. The pyrene rings stack in a	
	parallel fashion and contribute towards $\pi - \pi$ stacking (H-type). (f) Snapshot of two	
	stacked folded PyKC dimers obtained after the geometry optimization. For clarity, the	
	pyrene rings are shown in magenta color. The rings participate in both H-type and	
	T-type of $\pi - \pi$ stacking and thus have strong stacking energy.	99
6.3	Time evolution of (a) potential energy and (b) solvent accessible surface area (SASA)	00
0.5	to examine the equilibration for the system.	100
6.4	Snapshot of PyKC folded dimers in presence of water (green color) obtained from	100
0.4	the MD simulation. Well-defined interfaces of water and PyKC can be seen which	
	-	
	manifest the compartmentalization of PyKC and water. The inset in figure shows	

the intramolecular hydrogen bonding within the peptide conjugate and the $\pi-\pi$ stacking operating across the pyrene moities which are responsible for the stability and

101

self-assembly of PyKC in water.

6.5	Density profile across the normal of PyKC layers obtained from MD simulation. Interfaces of PyKC and water layers are evident which show the presence of compartments of PyKC hydrogel and water. The hydrophilic atoms (N/O) of PyKC	
	stay buried inside the layer and drive few water molecules into the core. The water molecules which continuously stay near the inner core of PyKC layer are referred to as	
	trapped water (TW) and shown within the area designated as (a).	102
6.6	(a) Time evolution of the intramolecular hydrogen bonds between N and O atoms of	102
0.0	PyKC are calculated for the production run which are responsible for the stability of the	
	molecular arrangement of the hydrogel. (b) The time evolution of the intermolecular	
	hydrogen bonds between trapped water molecules (TW-TW), and among the amphiphilic	
	moities of PyKC and trapped water molecules (TW-NH and TW-O). The intermolecular	
	hydrogen bonds are computed for the time regime for which the TW molecules remain	
	confined inside the PyKC core.	103
6.7	g(r) of pyrene-pyrene determines the most probable location at ~0.42 nm which	
	corresponds to the distance of $\pi - \pi$ interactions.	103
6.8	Comparison of mean square displacements of bulk water (BW) and trapped water (BW).	
	BW obeys diffusive behavior whereas TW shows a sub-diffusive behavior which regards	
	to the slow dynamics of trapped water molecules.	104
6.9	Hydrogen bond auto-correlation function $(C_{HB}(t))$ of trapped and bulk water molecules.	
	Slow relaxation of TW is evident from the time variation of $C_{HB}(t)$. Longer relation	
	time (au_{HB}) and high activation energy for breaking of a hydrogen bond $(\Delta G^{\#}_{break})$ for	
	TW lead towards a slow transport of water molecules across the supra-molecular hydrogel.	105
A1	Density distributions of chloride ions and BTMAC head-groups obtained from AA	
	simulation for equilibration and production runs. The ions reside near the BTMAC	
	heads via electrostatic interactions and thus the location of ions do not change for both	
	the run-lengths.	108
A2	Density distributions of chloride ions and BTMAC head-groups obtained from CG	
	simulation for equilibration and production runs. The ions stay closer to the BTMAC	
	heads via electrostatic interactions and thus the location of ions do not change for both	
	the run-lengths.	108
A3	(a) Initial and (b) final snapshot of two open PyKC dimers. The open chain dimers	
	adopt a folded conformation after simulation in an NPT ensemble.	109