

NMRLipids IV: Headgroup & glycerol backbone structures, and cation binding in bilayers with PE and PG lipids

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Primarily measured but also simulated NMR order parameters will be collected also for other than phosphatidylcholine (these are discussed in NMRLipids I) headgroup. The information will be used to understand structural differences between different lipid molecules in bilayers.

INTRODUCTION

PE and PG lipids are most common lipids in bacteria [1]. Zwitterionic PE is the second most abundant glycerophospholipid in eukaryotic cells and has been related to the diseases [2–4]. Anionic PG lipids are less abundant, but is also proposed to be fundamental for terrestrial life [5]. PE and PG affect membrane protein functionality [6] and bind to various proteins [7]. PE headgroup is also prone for negative membrane curvature and causes membrane fusion [?]. Therefore, the PE and PG headgroup structures play probably essential roles in many biological processes.

Structural details of lipid headgroups are mainly studied using NMR experiments, which suggest that the glycerol backbone structures are largely similar irrespectively of the headgroup [8], glycerol backbone and headgroup structure and behaviour are similar in model membranes and in bacteria [8–10], and the headgroup structures are similar in PC, PE and PG lipids, while headgroup is more rigid in PS lipids [11, 12]. Some attempts to resolve conformational ensembles from NMR for PC lipids have been made, but lesser extend for other lipids [?]. Classical molecular dynamics simulations could potentially give such ensembles and therefore enable the detailed studies of lipid headgroup behaviour in complex biomolecular systems, but current force fields are not accurate enough to reproduce the correct conformational ensembles for PC and PS headgroups [13, 14]. Several MD simulations of PE and PG lipids have been published especially in the context of modeling inner membrane of Gram-negative bacteria [?], but glycerol backbone and headgroup structures have not been evaluated against experiments.

Besides the structure, also ion binding may regulate biophysical activity of especially negatively charged lipid headgroups [?]. Monovalent cation (except Lithium) binding to zwitterionic PC headgroups is very weak, while multivalent ion binding is stronger but still weak [?]. The ion binding affinity data for PE is more scarce [?], but large differences to PC would be surprising. Negatively charged lipids are suggested to bear same cation binding constants than zwitterionic lipids, but the amount of bound ions to negatively charged membranes would still be larger because the concentration of cations in the vicinity of membranes would be higher [10]. On the other hand, anionic PS lipids are proposed chelate with calcium ions [?]. In simulations, the cation binding affinity

to PC and PS membranes is typically overestimated [14, 15], which can be improved by applying the ECC to the partial charges of the force fields [16, 17].

Here, we use open collaboration and order parameters of glycerol backbone and headgroup to evaluate the accuracy of PE and PG headgroup structures, and the cation binding affinity to anionic membranes containing PG lipids in the current MD simulation force fields. The force field giving the best description for glycerol backbone and headgroup structures of PC, PS, PG and PE headgroups (CHARMM36) reproduces the essential differences in order parameters between these headgroups, and therefore enables the analysis of structural differences between the headgroups.

METHODS

Experimental C–H bond order parameters

The headgroup and glycerol backbone C–H bond order parameter magnitudes and signs of POPE and POPG were determined by measuring the chemical-shift resolved dipolar splittings with a R-type Proton Detected Local Field (R-PDLF) experiment [18] and S-DROSS experiments [19] using natural abundance ¹³C solid state NMR spectroscopy as described previously [20, 21]. POPE and POPG powder were purchased from Avanti polar lipids. The NMR experiments were identical to our previous work [14]. **1.Is this enough and correct, or should we repeat some methods from the NMRLipidsIVps paper?**

Molecular dynamics simulations

Molecular dynamics simulation data were collected using the Open Collaboration method [13], with the NMRLipids Project blog (nmrlipids.blogspot.fi) and GitHub repository (github.com/NMRLipids/NMRLipidsIVotherHGs) as the communication platforms. The simulated systems of pure PE and PG bilayers without additional ions are listed in Tables I and II, and lipid mixtures with additional ions in Table III. Further simulation details are given in the SI, and the simulation data are indexed in a searchable database available at

www.nmrlipids.fi, and in the NMRLipids/MATCH repository (github.com/NMRLipids/MATCH).

The C–H bond order parameters were calculated directly from the carbon and hydrogen positions using the definition

$$S_{\text{CH}} = \frac{1}{2} \langle 3 \cos^2 \theta - 1 \rangle, \quad (1)$$

where θ is the angle between the C–H bond and the membrane normal (taken to align with z , with bilayer periodicity in the xy -plane). Angular brackets denote average over all sampled configurations. The order parameters were first calculated averaging over time separately for each lipid in the system. The average and the standard error of the mean were then calculated over different lipids. Python programs that use the MDAnalysis library [22, 23] used for all atom simulations is available in Ref. 24 (`scripts/calcOrderParameters.py`). For united atom simulations, the trajectories with hydrogens having ideal geometry were constructed first using either `buildH` program [25] or (`scratch/opAAUA.prod.py`) in Ref. 24, and the order parameters were then calculated from these trajectories. This approach has been tested against trajectories with explicit hydrogens and the deviations in order parameters are small [25, 26].

2. `BuildH` program is now cited with a direct link to the GitHub repo. I think that a release to Zenodo would be nice in the final publication.

3. Maybe we should also shortly discuss here about the reasons for slight dependence of order parameter values on the method used to reconstruct hydrogens?

The ion number density profiles were calculated using the `gmx density` tool of the Gromacs software package [27].

TABLE I: List of MD simulations with PE lipids.

lipid/counter-ions	force field for lipids / ions	NaCl (M)	^a N _l	^b N _w	^c N _c	^d T (K)	^e t _{sim} (ns)	^f t _{anal} (ns)	^g files
POPE	CHARMM36 [?]]	0	144	5760	0	310	500	400	[28]
POPE	CHARMM36 [?]]	0	500	25000	0	310	500	100	[29]
POPE	CHARMM36 [?]]	0.11	500	25000	50	310	500	100	[30]
POPE	CHARMM36ua [?]]	0	336	15254	0	310	2×200	2×100	[31]
DPPE	Slipids [32]	0	288	9386	0	336	200	100	[33]
POPE	Slipids [32?]]	0	336	?	0	310	2×200	2×100	[34]
POPE	Slipids [?]]	0	500	25000	0	310	500	100	[35]
POPE	Slipids [?]] 4.	0.11	500	25000	50	310	500	100	[36]
DPPE	GROMOS-CKP [?]]	0	128	3655	0	342	2×500	2×400	[37]
POPE	GROMOS-CKP [?]]	0	128	3552	0	313	2×500	2×400	[38]
POPE	GROMOS-CKP [?]]	0	500	25000	0	310	500	100	[39]
POPE	GROMOS-CKP [?]]	0.11	500	25000	50	310	500	100	[40]
DOPE	GROMOS-CKP [?]]	0	128	4789	0	271	2×500	2×400	[41]
POPE	GROMOS 43A1-S3 [?]]	0	128	3552	0	313	2×200	2×100	[42]
POPE	OPLS-UA vdW on H [?]]	0	128	3328	0	303	2×200	2×100	[43]
POPE	OPLS-UA [?]]	0	128	3328	0	303	2×200	2×100	[44]
POPE	Berger-Vries [?]]	0	128	3552	0	303	2×200	2×100	[45]
POPE	Berger-largeH [?]]	0	128	3552	0	303	2×200	2×100	[46]
DOPE	Berger-Vries [?]]	0	128	4789	0	271	2×200	2×100	[47]
DOPE	Berger-largeH [?]]	0	128	4789	0	271	2×300	2×100	[48]
POPE	LIPID17 [?]]	0	500	25000	50	310	500	100	[49]
POPE	LIPID17 [?]]	0.11	500	25000	50	310	500	100	[50]

^aNumber of lipid molecules with largest mole fraction^bNumber of water molecules^cNumber of additional cations^dSimulation temperature^eTotal simulation time^fTime used for analysis^gReference for simulation files**5. We need citations for the force fields.**

TABLE II: List of MD simulations with PG lipids.

lipid/counter-ions	force field for lipids / ions	NaCl (M)	^a N _l	^b N _w	^c N _c	^d T (K)	^e t _{sim} (ns)	^f t _{anal} (ns)	^g files
POPG/K ⁺	CHARMM36 [?]] 6.	0	118	4110	0	298	100	100	[51]
POPG	CHARMM36 [?]]	0.11	500	25000	49	310	500	100	[52]
POPG	CHARMM36 [?]]	0	500	25000	0	310	500	100	[53]
POPG/Na ⁺	Slipids [54]	0	288	10664	0	298	250	100	[55]
DPPG/Na ⁺	Slipids [54]	0	288	11232	0	314	200	100	[56]
DPPG/Na ⁺	Slipids [54]	0	288	11232	0	298	400	100	[57]
POPG	Slipids [?]] 7.	0	500	25000	0	310	500	100	[58]
POPG	Slipids [?]] 8.	0.11	500	25000	49	310	500	100	[59]
POPG	LIPID17 [?]]	0	500	25000	0	310	500	100	[60]
POPG	LIPID17 [?]]	0.11	500	25000	49	310	500	100	[61]
POPG	GROMOS-CKP [?]]	0	500	25000	0	310	500	100	[62]
POPG	GROMOS-CKP [?]]	0.11	500	25000	49	310	500	100	[63]

^aNumber of lipid molecules with largest mole fraction^bNumber of water molecules^cNumber of additional cations^dSimulation temperature^eTotal simulation time^fTime used for analysis^gReference for simulation files

9. We need citations for the force fields.

TABLE III: List of MD simulations with PE and PG lipids mixed with PC.

lipid/counter-ions	force field for lipids / ions	NaCl (M)	CaCl ₂ (M)	^a N _l	^b N _w	^c N _c	^d T (K)	^e t _{sim} (ns)	^f t _{anal} (ns)	^g files
POPC	CHARMM36 [?]]	0.11	0	500	25000	48	310	500	100	[64]
POPC:POPG (7:3)	CHARMM36 [?]]	0.11	0	350	?	?	310	500	100	[65]
POPC:POPG (1:1)/K ⁺	CHARMM36 [?]]	0	0	250:250	18158	0	298	200	200	[66]
POPC:POPG (1:1)	CHARMM36 [?]]	0	0.34 10.	250:250	20798	128	298	200	200	[67]
POPC:POPG (1:1)	CHARMM36 [?]]	0	1.36 11.	250:250	18114	445	298	200	200	[68]
POPC:POPG (4:1)/K ⁺	CHARMM36 [?]]	0	0	400:100	18664	0	298	200	200	[69]
POPC:POPG (4:1)/K ⁺	CHARMM36 [?]]	0	1.0 12.	400:100	18647	419	298	200	200	[70]
POPC	CHARMM36 [?]]	0	0	256	8704	0	300	300	250	[71]
POPC:POPE (1:1)	CHARMM36 [?]]	0	0	128	8704	0	300	300	250	[72]
POPC	Slipid [?]]	0.11	0	500	25000	48	310	500	100	[73]
POPC:POPG (7:3)	Slipid [?]]	?	0	?	?	?	310	500	100	[?]] 13.
POPC	Berger [?]] 14.	0	0	256	10240	0	300	300	200	[74]
POPC:POPE (1:1)	Berger [?]] 15.	0	0	128	11008	0	300	300	200	[75]
POPC:DOPE (1:1)	Berger [?]] 16.	0	0	128	10240	0	300	300	200	[76]
DOPC	Berger [?]] 17.	0	0	256	11008	0	300	300	200	[77]
DOPC:DOPE (1:1)	Berger [?]] 18.	0	0	128	11008	0	300	300	200	[78]

^aNumber of lipid molecules with largest mole fraction^bNumber of water molecules^cNumber of additional cations^dSimulation temperature^eTotal simulation time^fTime used for analysis^gReference for simulation files

19. Data for POPC:POPG mixtures by listed by Antonio Peon is missing from this table

20. We need citations for the force fields.

RESULTS AND DISCUSSION

Headgroup and glycerol backbone order parameters of POPE and POPG from ^{13}C NMR

Absolute values of the headgroup and glycerol backbone order parameters from PE and PG lipids are measured previously using ^2H NMR [8, 11, 79, 80]. Because also the order parameter signs bear essential information about the lipid structures [13, 81], we measured the magnitudes and signs of POPE and POPG C–H bond headgroup and glycerol backbone order parameter in liquid phase using the 2D-RPDLF and S-DROSS experiments, as described previously [14, 20, 21]. For POPE, the glycerol backbone and α -carbon peaks in INEPT spectra were assigned based on previously measured POPC spectra [20] and the β -carbon peak was assigned based on ^{13}C chemical shift table for amines available at <https://www.chem.wisc.edu/areas/reich/nmr/c13-data/cdata.htm> (Fig. S1). For POPG, the glycerol backbone peaks in INEPT spectra were assigned based on previously measured POPC spectra [20], while α and γ -carbon peaks **21.How were these assigned?** (Fig. S2). The numerical value of the β -carbon order parameter could not be determined, because its peak overlapped with the g_2 peak from glycerol backbone in POPG. However, the order parameter of β -carbon is expected to be clearly smaller than for g_2 based on previous ^2H NMR measurements [8, 11, 80]. Therefore, the beginning of the S-DROSS curve gives the sign for g_2 order parameter and end for β (Fig. S2 (E)). This is confirmed with SIMPSON calculations using negative value for g_2 and positive value for β order parameter (Fig. S3). The POPE experiments were recorded at 310 K and POPG experiments at 298 K, where the bilayers are in the liquid disordered phase [82]. **22.Details to be checked by Tiago.**

As discussed previously for PC and PS headgroups [14, 81], also the headgroup and glycerol backbone order parameters of PE and PG are essentially independent of acyl chain composition, and therefore manifest mainly headgroup chemistry (Fig. 1). The glycerol backbone order parameters are similar for all the lipids, although they move slightly toward positive values (closer to zero) in the order $\text{PC} < \text{PE} < \text{PS} < \text{PG}$. Also the headgroup order parameters of PC lipids are close PE, although the latter gives systematically slightly more positive values (Fig. 1). The α -carbon order parameter of PG is similar to PE and PG, while the positive value of β -carbon is distinct from the other lipids. Notably, this difference was not observed in previous ^2H NMR experiments, because absolute value of β -carbon order parameter is similar in PG, PE and PC lipids and the order parameter signs were not measured [8, 11, 80].

In conclusion, the order parameter experiments suggest that the glycerol backbone conformations in all lipids and the headgroup conformations in PC and PE lipids are relatively similar, while PS and PG headgroups exhibit distinct conformational sampling. The details of sampled conformation are difficult to deduce from order parameters only, but the distinct

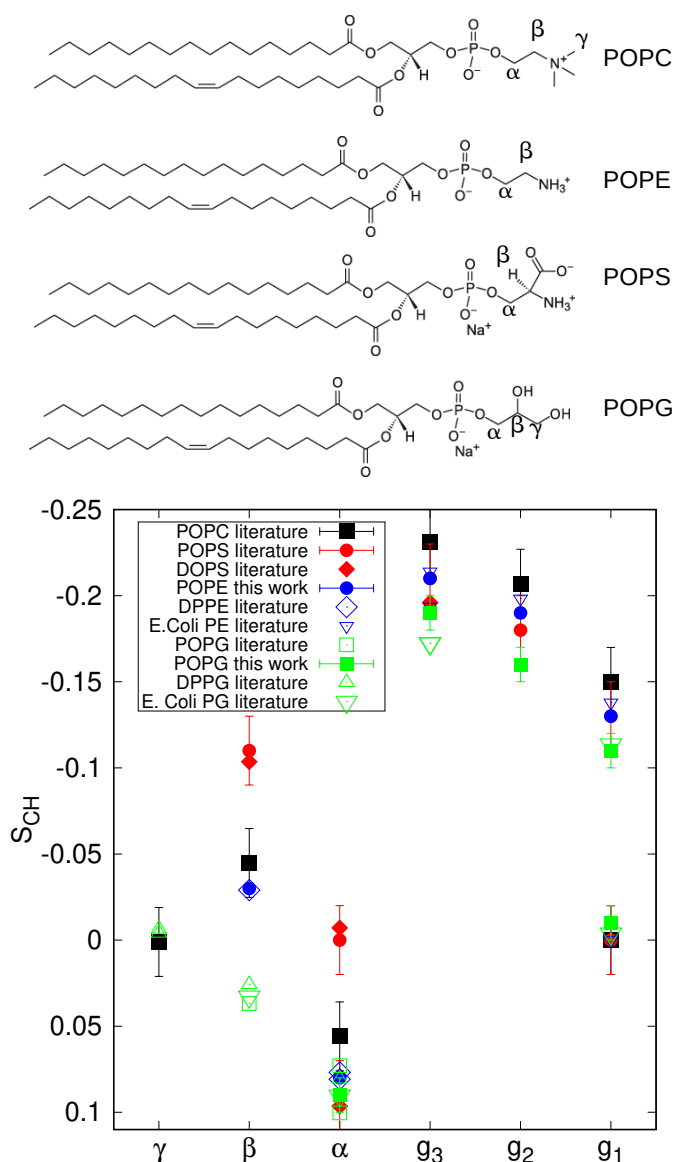


FIG. 1: (top) Chemical structure of different lipids. (bottom) Headgroup and glycerol backbone order parameters from different experiments in lamellar liquid disordered phase. The values and signs for POPE (310 K) and POPG (298 K) measured in this work, and for POPS (298 K) [14] and POPC (300 K) [20, 21] previously using ^{13}C NMR. The literature values for DOPS with 0.1M of NaCl (303 K) [83], POPG with 10nM PIPES (298 K) [80], DPPG with 10mM PIPES and 100mM NaCl (314 K) [11], DPPE (341 K) [79], E.coliPE and E.coliPG (310 K) [8] are measured using ^2H NMR. The signs from ^{13}C NMR are used also for the literature values.

23.The bottom figure could be clarified as Fig. 2 in the NMRlipids IVps paper.

headgroup order parameters of PS lipids are previously related to the more rigid structure of the headgroup [12, 14, 83].

Headgroup and glycerol backbone of POPE and POPG in MD simulations

Headgroup and glycerol backbone order parameters of PE and PG lipids show wide variation between different force fields and none of the force fields reproduce all values within experimental error bars. (Figs. 2 and 3), as observed previously also for PC and PS lipids [13, 14]. The poor performance of headgroup order parameters in Berger model can be probably explained by ring like structures seen in Fig. 6 in Ref. 84, which is a typical feature for Berger based lipid force fields containing explicit hydrogen atoms in the headgroup [85–87]. The poor performance of glycerol backbone of Slipids simulations is systemically observed also for other lipids in previous studies [13, 14]. **24. Should we comment more the relative quality of different force fields and/or make the subjective force field ranking figures?**

Without further discussion about poorly performing force fields, we focus on more detailed analysis of CHARMM36 simulations, which give the best overall agreement with experiments for the headgroup and glycerol backbone order parameters of all PC, PS, PG and PE lipids in this and our previous studies [13, 14]. Even though many order parameters in CHARMM36 simulations are not within the experimental error bars, it seems to capture the essential differences between different headgroups. In previous study, CHARMM36 predicted the more negative β -carbon order parameter and larger forking of the α -carbon in PS headgroup than in PC [14]. In this work, the PE headgroup order parameters are similar to the PC [13] and β -carbon order parameters is positive in PG headgroup, while negative values observed in other lipids. Therefore, we use CHARMM36 simulations to analyze the structural differences between headgroups (Fig. 4).

25. The structures are already in Fig. 4, but we need also the dihedral distributions to finish the discussion.

26. Maybe we should analyze also some other structural features, at least P-N angles.

PC headgroup interactions with PE and PG

According to the electrometer concept, the PC headgroup order parameters increase with the addition of negatively charged PG or PS lipids, but are not affected by the addition of zwitterionic PE and SM lipids or cholesterol (Fig. 5) [9, 89, 90]. The different responses of PC headgroup order parameters to PE and PG are roughly reproduced in CHARMM36 simulations, although the changes are slightly overestimated upon addition of PE and underestimated upon addition of PG (Fig. 5). Interestingly, the response of POPC headgroup order parameters to POPE is close to experiments also in Berger-OPLS simulations, even though the response of Berger force field to cholesterol was significantly overestimated in our previous work [13]. In all force fields except Slipids, the α -carbon order parameters of different hydrogens are responding differently when mixed with PE or PG lipids

29. Maybe we should figure out what is the reason for this. 30. Maybe we should

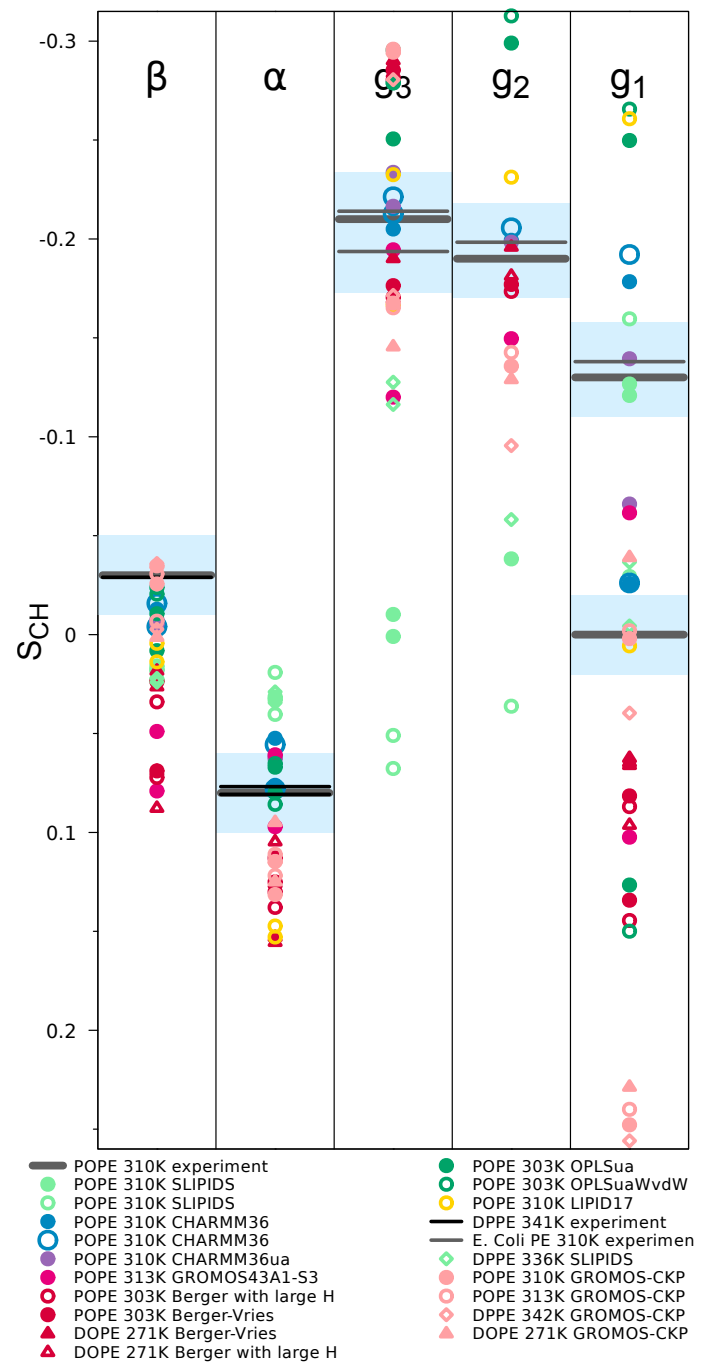


FIG. 2: The headgroup and glycerol backbone order parameters of PE lipids from experiments (POPE and signs this work, DPPE from Ref. 79 and E.coliPE from Ref. 8) and simulations with different force fields.

27. This should be clarified as in NMRlipidsI and error bars should be added. Probably larger error bars for united atom models based on the report by Fuchs et al.

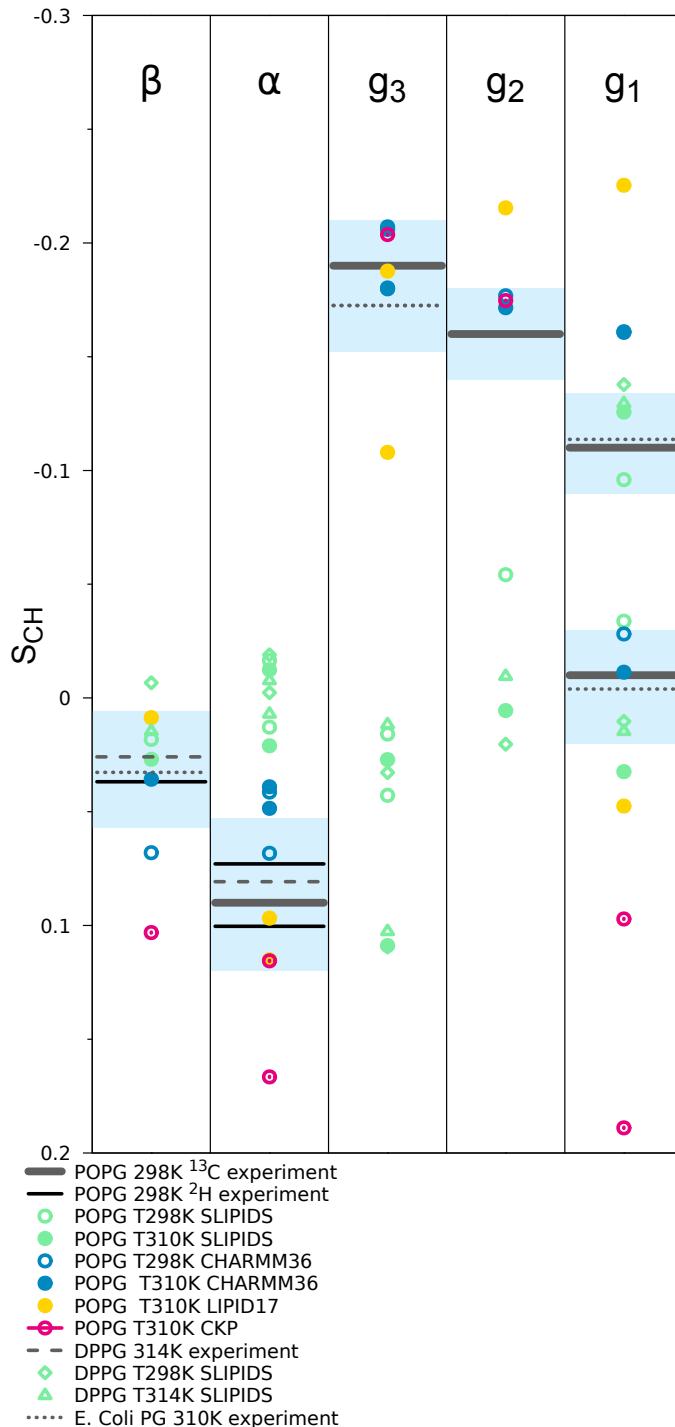


FIG. 3: The headgroup and glycerol backbone order parameters of PG lipids from experiments (POP and signs from this work and from Ref. 80, DPPG with 100mM NaCl from Ref. 11, and E. Coli PG results from Ref. 8), and simulations with different force fields.

analyze the P-N vector angle from different simulations.

For β -carbon order parameter in PG headgroup, experiments report mild increase [88] or no change [80] upon addition of PC lipids (Fig. 6). Simulations with all the tested force

fields give only very small changes also for the α -carbon order parameter (Figs. S4 and 6). Therefore, the simulations are generally in line with experiments, suggesting that the interactions with PC do not essentially effect the PG headgroup structure. This is in contrast with previous results for PS headgroup [90], where all the force fields significantly overestimated the structural response of PS headgroup to the interactions with PC lipids.

31. This is text by P. Fuchs, copied from the blog.

Area results in nm^2 , the error is $\leq 0.003 \text{ nm}^2$

- pure POPC

CHARMM36: 0.624

Berger : 0.649

- POPC/POPE 50:50

CHARMM36 : POPC 0.609, POPE 0.557

Berger-hacked: POPC 0.637, POPE 0.632

One can see that CHARMM 36 predicts a drop in the area on going from pure POPC to POPC/POPE 50:50. This means that POPC pack tightly to POPE. In contrast, the values for Berger are not that changed. The POPE value predicted by CHARMM 36 (in the mixture POPC/POPE 50:50) is much smaller than that predicted by Berger.

The experimental acyl chain order parameters for POPE [91] seem larger than reported for POPC [20], which supports the more condensed PE bilayer. This is interesting, but to avoid the overexpansion of the manuscript, it is probably better to keep the focus in headgroups and ion binding also in this manuscript.

Sodium binding to PE and PG lipid bilayers

In our previous study about PS lipids [90], the underestimated increase of PC headgroup order parameters upon addition of negatively charged lipids was related to the overestimated counterion binding affinity, which would overcompensates the effect of negative charge. Similar correlation is observed here in Lipid 17 simulations, which exhibits stronger counter-ion binding affinity to pure POPG bilayer (Fig. 7) and larger decrease in POPC β carbon order parameter upon addition of POPG than other simulations. Together with the lower area per molecule (59.5 \AA^2) than in experiments (66.1 \AA^2), the results suggest that the counterions bind too strongly and shield the electrostatic repulsion between PG headgroups in bilayers simulated with Lipid17 parameters. In GROMOS-CKP simulations, however, the β -carbon order parameter of POPC increases upon addition of POPG more than in CHARMM36 and Slipids simulations even though the binding affinities in these simulations are similar. On the other hand, the responses of different hydrogens attached in α -carbons are different in all simulations except in Slipids, most severe in Lipid17 and GROMOS-CKP where other increases and other decreases 32. Can we figure out the reason for this?. In conclusion, the counter-ion binding seems to be overestimated in Lipid17 with the strongest affinity among the tested models, while with this data we cannot fully evaluate binding affinity in the other models.

Similarly to POPG, the Lipid17 exhibits stronger sodium binding affinity to POPE bilayers than Slipids, CHARMM36 and GROMOS-CKP (Fig. 8). In Lipid17 the sodium binding affinity to POPE is approximately similar as to POPC, while in other models exhibit weaker binding to POPE (Fig. S5). The difference is small in Slipids and CHARMM36, while GROMOS-CKP predicts substantially stronger binding to POPC. Experimental data for sodium binding to PE lipids is not available, while simulations in agreement with electrometer data from NMR suggests that sodium binding to POPC is weaker than in any of the simulations here (Fig. S5) [15, 16]. Assuming that the binding to POPE would be similar than to POPC, the sodium binding affinity to POPE is potentially realistic in CHARMM36, Slipids, and GROMOS-CKP simulations here, but substantially overestimated in Lipid17 simulation. **33.The potential differences in the used ion models should be checked.**

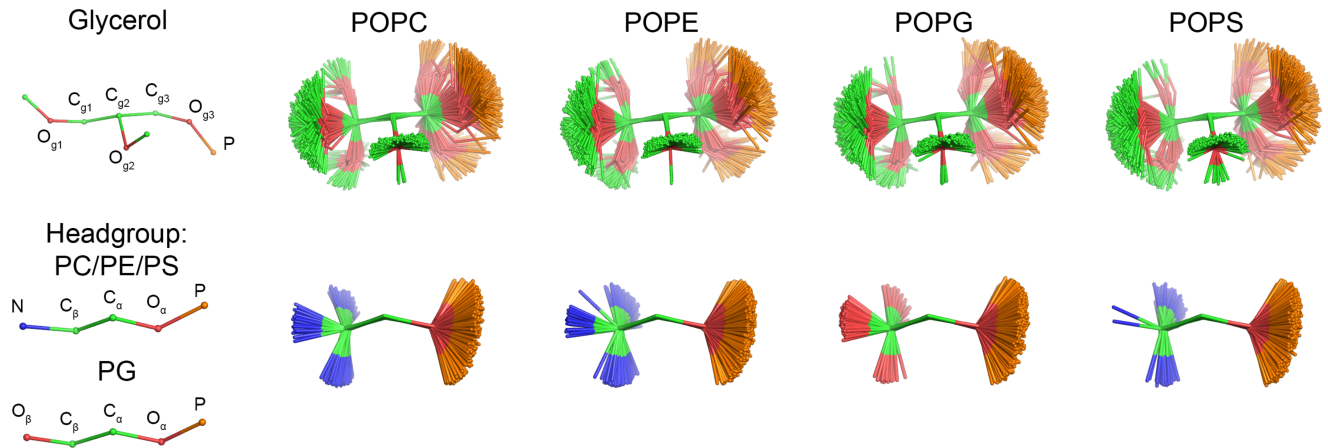


FIG. 4: Overlaid snapshots from CHARMM36 simulations of different lipids which give the best agreement with experiments.

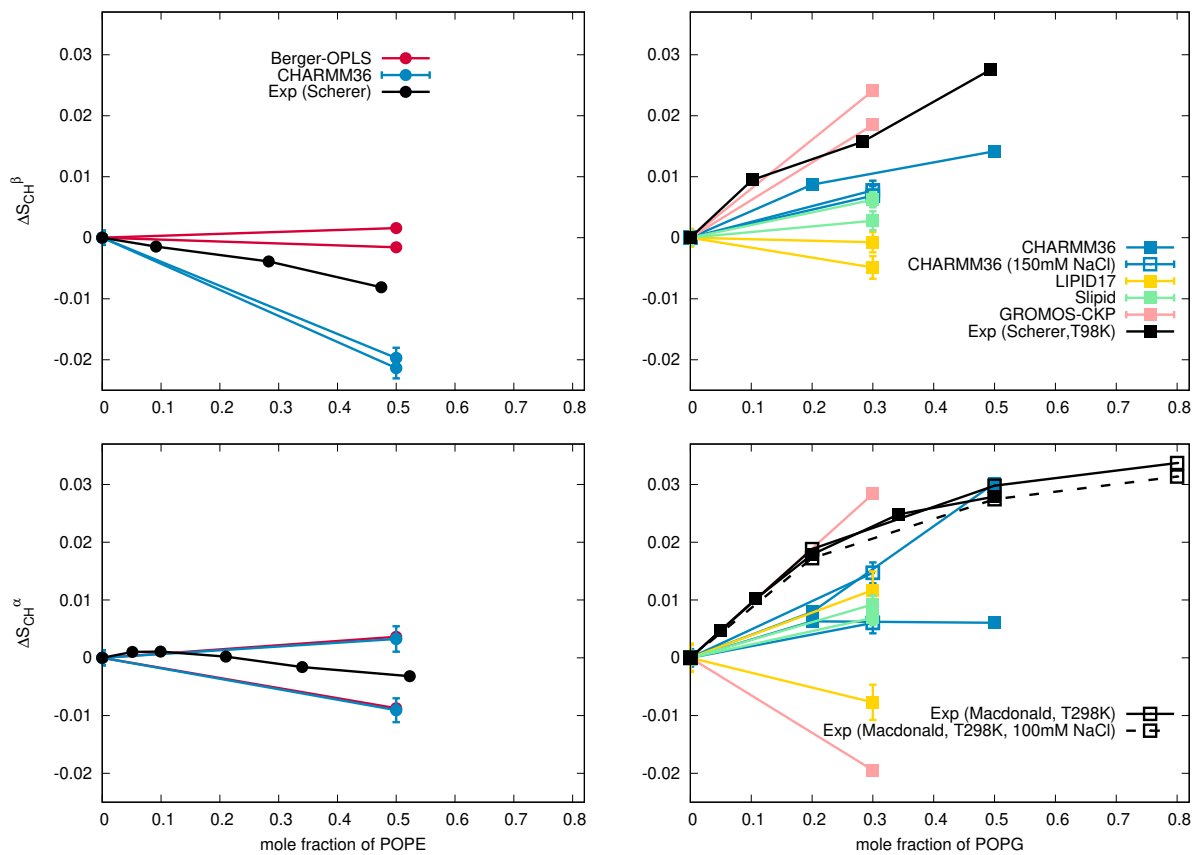


FIG. 5: Modulation of POPC headgroup order parameters with increasing amount of POPE (left) and POPG (right) in bilayer from experiments [9, 88] and simulations with different force fields. Signs are determined as discussed in [13, 81].

28.Data for CHARMM without ions to be added once this issue is solved: <https://github.com/NMRLipids/MATCH/issues/83>

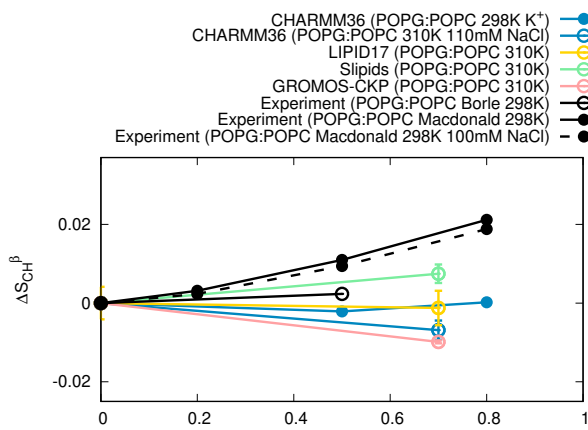


FIG. 6: Modulation of PG lipid headgroup order parameters with the increasing amount of PC in lipid bilayer from experiments [80, 88] and simulations with different force fields.

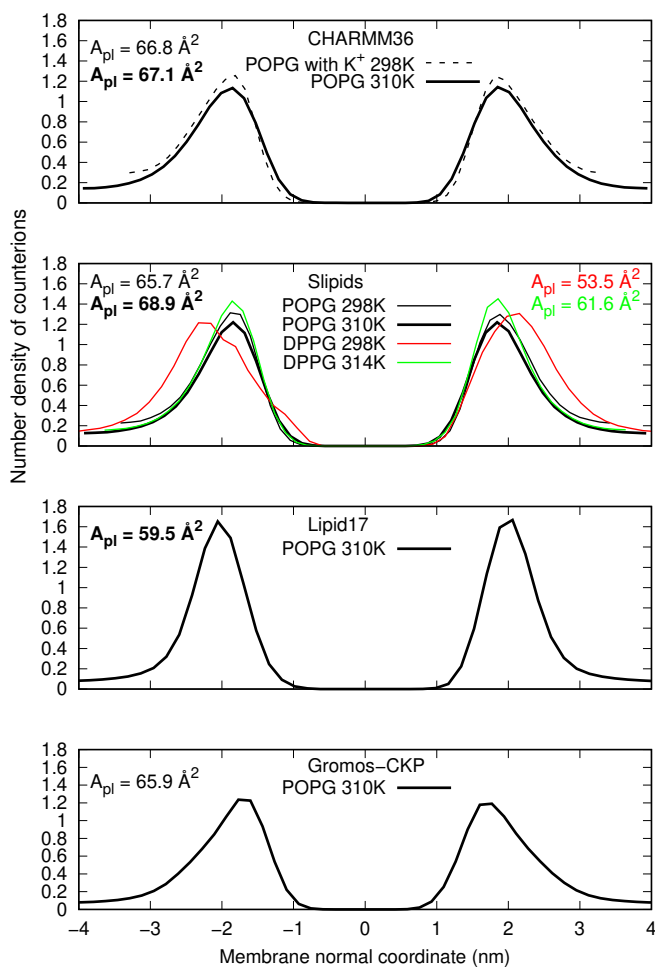


FIG. 7: Counterion densities and area per lipids from simulations with PG lipids. Experimental area for POPG at 303 K is 66.1 Å² and 67 Å² for DPPC at 323 K [92].

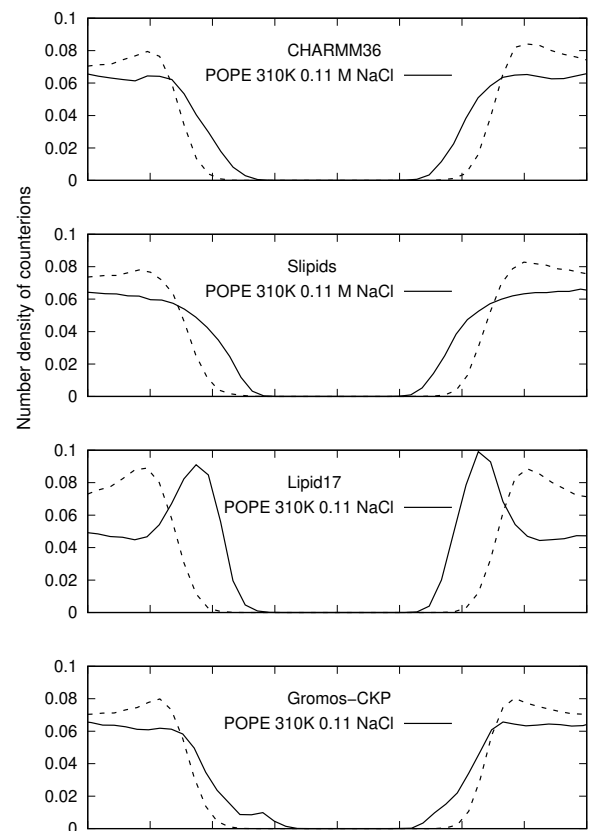


FIG. 8: Sodium (solid line) and chloride ion density profiles along membrane normal from different simulations with PE lipids.

The headgroup order parameters of PC lipids can be used to measure ion binding affinity to lipid bilayers, because their magnitude is linearly proportional to the amount of bound charge in bilayer according to the molecular electrometer concept [15, 89]. The molecular electrometer concept can be used also for bilayers containing PC lipids mixed with charged lipids [14, 80, 88, 93]. The electrometer concept has been very useful in evaluating ion binding affinity in simulations against experiments, because the headgroup order parameter changes as a function of ion concentration can be directly compared with experiments [14–16].

Calcium binding affinity to PC and PS lipid bilayers was not correctly described by any of the standard MD simulation force fields [14, 15], while recently introduced force field with electronic continuum correction (ECC) performed better [16]. The decrease of α -carbon order parameter of PC lipids in PC:PG mixtures as a function of calcium concentration is close to experiments CHARMM36 simulations (Fig. 9), but the decrease of β -carbon order parameter seems to be overestimated. However, the β -carbon order parameter was not actually measured from these samples, but they are calculated from empirical relation $\Delta S_\beta = 0.43\Delta S_\alpha$ [94]. The result is similar to the ~ 200 ns simulations with PC lipids in previous work [15]. However, when simulation was continued for μ s, the binding affinity substantially increased and interpretation was that calcium overbinds to PC lipid in CHARMM36. Therefore, the conclusion seems to be similar here, although the new NBfix parameters may complicate the situation 34. **The status of NBfix parameters in these simulations should be checked..**

The β -carbon order parameter of PG exhibits a rapid decrease with small CaCl_2 concentrations and a more modest decrease with larger concentrations in experiments [80] (Fig. ??). The rapid decrease with CaCl_2 is observed but overestimated in CHARMM36 simulation with POPC:POPG 1:1 mixture, but not in 4:1 mixture 35. **This is little bit weird, should be checked..**

36. We need PC:PG simulations with CaCl_2 from different force fields to finish the discussion.

CONCLUSIONS

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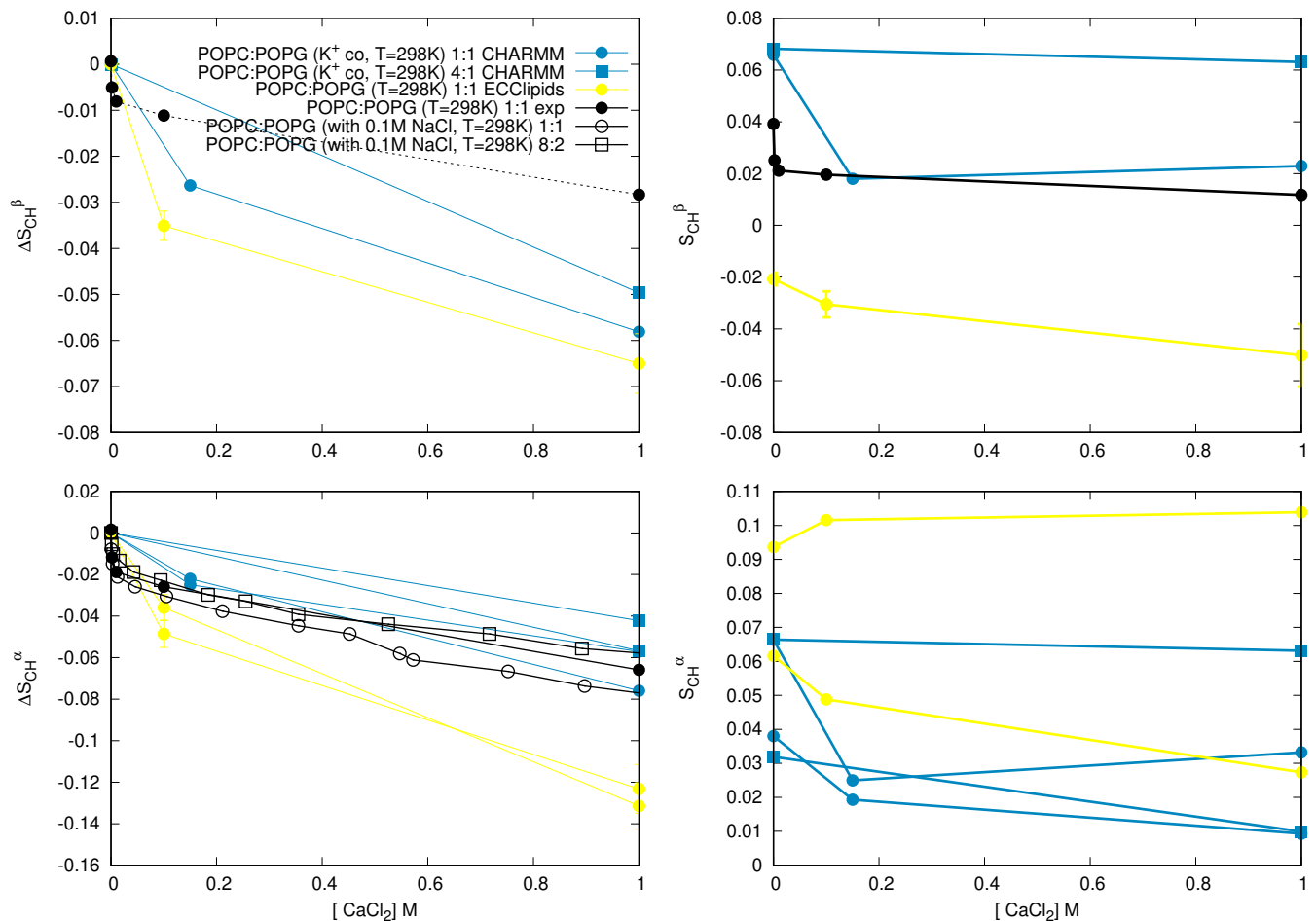


FIG. 9: (left) The headgroup order parameters of PC from PC:PG mixtures as a function CaCl_2 concentration from experiments [80, 88] and CHARMM36 simulations. Note that beta order parameter is calculated from empirical relation $\Delta S_{\beta} = 0.43\Delta S_{\alpha}$ [94], not actually measured. (right) The headgroup order parameters of PG from PC:PG mixtures as a function CaCl_2 concentration from experiments [80] and CHARMM36 simulations.

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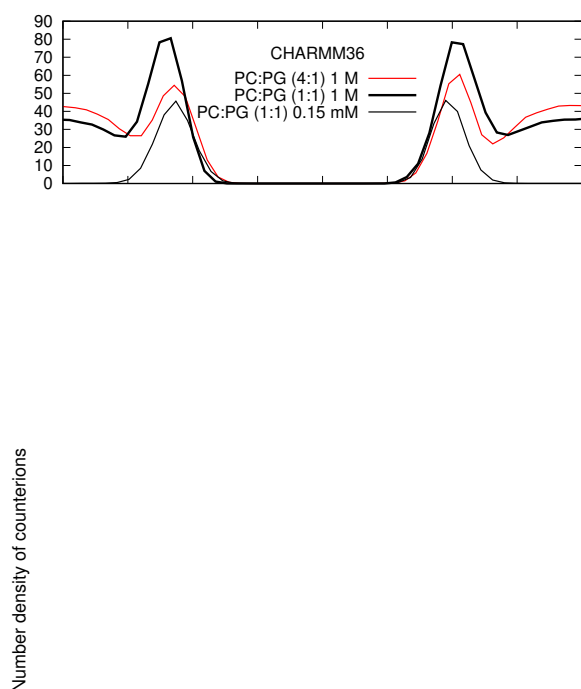


FIG. 10: Calcium ion density profiles along membrane normal from different simulations with PG lipids.

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ToDo

- | | P. |
|---|-----------|
| 1. Is this enough and correct, or should we repeat some methods from the NMRlipidsIVps paper? | 1 |
| 2. BuildH program is now cited with a direct link to the GitHub repo. I think that a release to Zenodo would be nice in the final publication. | 2 |
| 3. Maybe we should also shortly discuss here about the reasons for slight dependence of order parameter values on the method used to reconstruct hydrogens? | 2 |
| 4. Ion parameters? | 3 |
| 5. We need citations for the force fields. | 3 |
| 6. Correct citation for CHARMM POPG | 4 |
| 7. Ion parameters? | 4 |
| 8. Ion parameters? | 4 |
| 9. We need citations for the force fields. | 4 |
| 10. Concentration calculated based in total amount of calcium ions. This may not be reasonable due to the lack of counterions. | 4 |
| 11. Concentration calculated based in total amount of calcium ions. This may not be reasonable due to the lack of counterions. | 4 |
| 12. Concentration calculated based in total amount of calcium ions. This may not be reasonable due to the lack of counterions. | 4 |
| 13. Zenodo entry unclear. | 4 |
| 14. This is probable not plain berger, correct force filed should be described. | 4 |
| 15. This is probable not plain berger, correct force filed should be described. | 4 |
| 16. This is probable not plain berger, correct force filed should be described. | 4 |
| 17. This is probable not plain berger, correct force filed should be described. | 4 |

18. This is probable not plain berger, correct force filed should be described.	4	Berger-hacked: POPC 0.637, POPE 0.632	
19. Data for POPC:POPG mixtures by listed by Antonio Peon is missing from this table	4	—	
20. We need citations for the force fields.	4	One can see that CHARMM 36 predicts a drop in the area on going from pure POPC to POPC/POPE 50:50. This means that POPC pack tightly to POPE. In contrast, the values for Berger are not that changed. The POPE value predicted by CHARMM 36 (in the mixture POPC/POPE 50:50) is much smaller than that predicted by Berger.	
21. How were these assigned?	5	—	
22. Details to be checked by Tiago	5	The experimental acyl chain order parameters for POPE [91] seem larger than reported for POPC [20], which supports the more condensed PE bilayer. This is interesting, but to avoid the overexpansion of the manuscript, it is probably better to keep the focus in headgroups and ion binding also in this manuscript. . .	7
23. The bottom figure could be clarified as Fig. 2 in the NMRLipids IVps paper.	5	31. Can we figure out the reason for this?	7
24. Should we comment more the relative quality of different force fields and/or make the subjective force field ranking figures?	6	32. The potential differences in the used ion models should be checked	8
25. The structures are already in Fig. 4, but we need also the dihedral distributions to finish the discussion .	6	27. Data for CHARMM without ions to be added once this issue is solved: https://github.com/NMRLipids/MATCH/issues/83 . . .	9
28. Maybe we should figure out what is the reason for this	6	33. The status of NBfix parameters in these simulations should be checked.	11
29. Maybe we should analyze the P-N vector angle from different simulations	6	34. This is little bit weird, should be checked.	11
26. This should be clarified as in NMRLipidsI and error bars should be added. Probably larger error bars for united atom models based on the report by Fuchs et al.	6	35. We need PC:PG simulations with CaCl ₂ from different force fields to finish the discussion.	11
30. This is text by P. Fuchs, copied from the blog. Area results in nm ² , the error is <= 0.003 nm ²			
- pure	POPC		
CHARMM36:	0.624		
Berger :	0.649		
- POPC/POPE	50:50		
CHARMM36 : POPC 0.609, POPE	0.557		