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Time-domain R-PDLF NMR for molecular structure determination in complex lipid membranes

Anika Wurl[1], Kay Saalwächter[1], and Tiago Mendes Ferreira[1]

[1]NMR group, Institute for Physics, Martin Luther University Halle-Wittenberg

Correspondence: Tiago Mendes Ferreira (tiago.ferreira@physik.uni-halle.de)

Abstract. Proton-detected local field (PDLF) NMR spectroscopy, using magic-angle spinning and dipolar recoupling, is presently the most powerful experimental technique to obtain atomistic structural information from small molecules undergoing anisotropic motion such as peptides, drugs, or lipids in model membranes. The accuracy of the measurements on complex systems is however compromised by the number of transients required and by the difficulty of fitting experimental data due to the omnipresent RF spatial inhomogeneity in NMR probes. Here, we present a new methodology to analyse R-type PDLF NMR experiments that brings a significant improvement of accuracy and that enables to address more complex systems. The new methodology consists of fitting the time-domain data with NMR simulations accounting for RF spatial inhomogeneity, making it possible (1) to use shorter experiments which enables to measure samples with lower material content and prevents RF-heating, (2) to measure smaller C–H bond order parameter magnitudes, $|S_{\mathrm{CH}}|$, and smaller variations of $|S_{\mathrm{CH}}|$ upon perturbations of the system and (3) to determine $|S_{\mathrm{CH}}|$ values with small differences from distinct sites having the same chemical shift. The increase in accuracy is demonstrated by comparison with ^{2}H NMR quadrupolar echo experiments on mixtures of deuterated and non-deuterated dimyristoylphosphatidylcholine (DMPC). The methodology presented enables an unprecedented level of structural detail and will be highly useful for investigating complex membrane systems as illustrated with membranes composed of a brain lipid extract with many distinct lipid types.

1 Introduction

The methodology for characterizing the molecular structure in biological systems has been advancing rapidly over the last years (Cheng, 2018; Gauto et al., 2019; Wu and Lander, 2020). Among the various experimental techniques available, solid-state NMR spectroscopy provides the most powerful methods for investigating the molecular structure of smaller molecules (<30 kDa) undergoing anisotropic motion in membranes such as lipids, peptides and membrane proteins (Andersson et al., 2017; Löser et al., 2018; Bacle et al., 2021; Zerweck et al., 2017; Aisenbrey et al., 2019; Cady et al., 2007; Park et al., 2012; Mandala et al., 2020).

^{2}H NMR spectroscopy has been consistently used since the 1970s for molecular structural characterization of both lipids and peptides (Seelig, 1977; Davis, 1983; Strandberg and Ulrich, 2004; Leftin and Brown, 2011). This methodology is often used due to both the simplicity and high accuracy of the experiments, however, it requires specific ^{2}H isotopic labelling for site resolution which severely limits its application to investigate biological extracts or complex model membranes that mimic

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Open Access MAGNETIC RESONANCE Discussions

biological systems. An alternative to ^{2}H NMR are separated local field (SLF) 2D NMR experiments that make use of ^{1}H–^{13}C heteronuclear dipolar recoupling during the indirect time (Hester et al., 1976). This technique is highly advantageous over ^{2}H NMR since it delivers the same type of information with ^{13}C chemical shift selectivity and no requirement of isotopic labelling. SLF ^{1}H–^{13}C heteronuclear dipolar recoupling NMR techniques may be separated in two groups, carbon-detected local field (CDLF) and proton-detected local field (PDLF) experiments with the latter having enhanced resolution (Nakai and Terao, 1992; Schmidt-Rohr et al., 1994; Bärenwald et al., 2016). Here, we discuss only PDLF techniques which provide C–H bond site resolution and are therefore directly comparable to ^{2}H NMR.

A number of PDLF pulse sequences have been implemented to investigate lipid membranes as well as other systems (Griffin, 1998; De Paëpe, 2012; Griffin, 1998; Molugu et al., 2017). The main difference between the distinct PDLF sequences reported are the heteronuclear dipolar recoupling blocks used to counteract the effect of magic angle spinning (MAS) on the anisotropic Hamiltonian terms during the indirect dimension. Several recoupling pulse sequences have been designed for this purpose such as in REDOR (Gullion), DROSS (Gross et al., 1997; Leftin et al., 2014), R-symmetry based pulse sequences (Levitt, 2007; Dvinskikh et al., 2004; Hou et al., 2011) and others (De Paëpe, 2012). The R-symmetry sequences are particularly advantageous since they enable to simultaneously recouple and decouple the heteronuclear and homonuclear dipolar interactions, respectively. Moreover, R-symmetry recoupling can be applied directly to an IS spin ensemble in thermal equilibrium with no need of generating transverse magnetization before the recoupling blocks and therefore avoiding potential T_2 losses during the recoupling period, i.e. increasing sensitivity. It is well known that, similarly to other dipolar recoupling pulse sequences, R-symmetry recoupling is rather sensitive to RF imperfections (Nishimura et al., 2001; Schanda et al., 2011) and therefore to the RF spatial inhomogeneity accross the sample investigated – one unavoidable and unique feature of the MAS probe used to perform experiments (Tošner et al., 2017). To minimise this problem, windowed R-symmetry sequences have been proposed that are not as sensitive to RF inhomogeneity as the original windowless R-symmetry sequences (Gansmüller et al., 2013; Lu et al., 2016). These windowed versions, however, require using higher RF radiofrequency fields which is a practical bottleneck due to hardware limitations.

In general, the strategy for developing better dipolar recoupling strategies has been to minimise the sensitivity to RF spatial inhomogeneity, by using/designing dipolar recoupling sequences that are less sensitive to RF imperfections and reducing the sample studied to a narrow volume, as well as using recoupling pulse sequences with a high scaling factor that enable to measure smaller dipolar couplings (Dvinskikh et al., 2005; Chevelkov et al., 2009; Schanda et al., 2011; Gansmüller et al., 2013; Lu et al., 2016; Asami and Reif, 2017). This last point is of significant importance, since higher scaling factors enable to achieve resolution in the indirect frequency domain with a lower number of indirect time-domain points.

Here, we present an alternative approach that enables to increase the accuracy and applicability of R-type PDLF NMR considerably through time-domain analysis (rather than frequency domain) of the dipolar modulation by taking into account the RF spatial inhomogeneity of the used probe explicitly, i.e., rather than trying to minimise the effect of RF spatial inhomogeneity we include it in the NMR simulations used to fit the experimental measurements. The novelty of the new methodology presented is therefore solely in the new experimental analysis procedure, no special hardware or different setup of the experiment is needed. The methodology is demonstrated on a DMPC/DMPCd sample enabling to compare the ^{1}H-^{13}C dipolar couplings determined

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with a $R18_1^7$-type PDLF sequence (R-PDLF (Dvinskikh et al., 2004, 2005)) with C–D bond order parameters determined from ^{2}H quadrupolar couplings. The proposed methodology is then implemented to investigate a system of complex lipid membranes composed of a brain lipid extract, enabling to measure several dipolar couplings from the membrane hydrophilic layer composed of a set of many types of distinct phospholipid headgroups. We believe that the new strategy presented will be a highly useful structural biology tool to study both model systems and complex membrane systems with a low signal to noise ratio such as biological lipid extracts, and potentially for in-cell molecular structural investigations.

2 Methodology

The typical approach for determining C–H bond order parameter magnitudes with PDLF dipolar recoupling NMR is by performing a Fourier transform,

$$I(\omega_1) = \int_0^{+\infty} s(t_1)\exp(-i\omega_1 t_1)dt_1 \tag{1}$$

of the time-domain recoupled dipolar modulation over the indirect dimension, $s(t_1)$, and measuring the splitting(s) of the resulting spectral dipolar line shape (Dvinskikh et al., 2004; Gross et al., 1997). If the scaling factor, κ, for the particular pulse sequence under use is known, determining the magnitude of a C–H bond order parameter from the observed splitting(s) is straightforward by using

$$|S_{\mathrm{CH}}| = \kappa^{-1}\frac{\Delta\nu}{d_{\mathrm{CH}}} = \left|\frac{1}{2}\left\langle 3\cos^2\theta - 1\right\rangle\right| \tag{2}$$

where d_{CH} is the magnitude of the rigid dipolar coupling for a static C–H bond equal to ≈22 kHz, the angle θ is between the C–H bond and the symmetry axis of its uniaxial motion (in case of lipid membranes this is the bilayer normal), and the angular brackets denote a time average over a time interval up to approximately the inverse of the splitting measured.

For a dipolar modulation corresponding to a single C−H bond order parameter and acquired under optimal experimental conditions, the use of equation 2 enables to obtain accurate values provided that the digitised signal, $s(t_1)$, extends to a time longer than the reciprocal of the scaled dipolar coupling frequency (e.g. 4 times the reciprocal gives approximately 10% error). If $s(t_1)$ is instead a superposition of two distinct contributions with different S_{CH}, for resolving the two components in the spectrum, the signal acquisition must be, at least, longer than half of a beat period defined by the frequencies of the crystallite orientations responsible for the two splittings (Lindon and Ferrige, 1980). This is illustrated in Figure 1 for a superposition of two Pake patterns. Therefore, both for single-component dipolar modulations with low order parameters and for two-component dipolar modulations with a small frequency difference between the two components, a high number of indirect dimension points is needed in 2D dipolar recoupling experiments which severely increases the experimental time, specially for samples requiring the acquisition of a high number of transients in the direct dimension. Moreover, there is a maximum limit to the number of indirect dimension points acquired both due to RF heating of samples and to maintain the integrity of the NMR probe.

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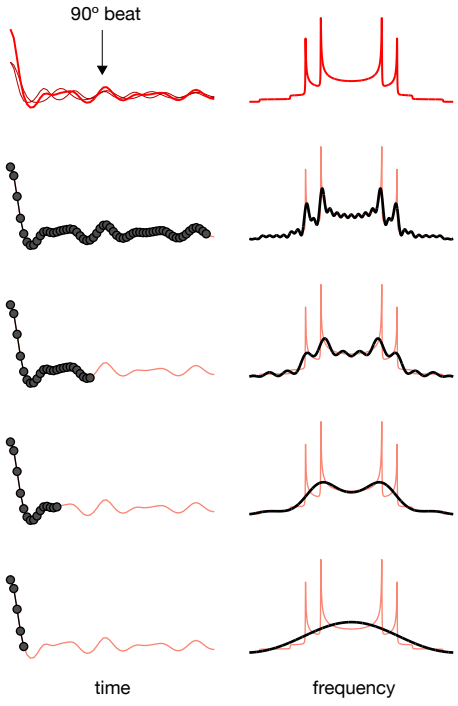

Figure 1. The effect of using a limited number of time-domain points to describe a superposition of two Pake patterns with distinct splittings.

Time-domain analysis can be used to circumvent the limitations outlined above entirely. The practical bottleneck for time-domain analysis is the RF inhomogeneity across the sample, intrinsic to the majority of experimental setups (Tošner et al., 2017), combined with the sensitivity of recoupling pulse sequences to RF strength accuracy and the effect of chemical shift offsets (Schanda et al., 2011; Lu et al., 2016). Figure 2 illustrates such dependencies for the R-PDLF pulse sequence (Dvinskikh et al., 2004), showing a non-linear dependence of the dipolar modulation on the RF pulse power level deviation from the ideal value and on the ^{1}H chemical shift offset. The effect of RF miscalibration becomes rather pronounced at RF frequencies higher or lower than 6% of the ideal frequency. This means that in typical experiments, for which the RF spatial inhomogeneity profile may reach 80% of the maximum value in the outer parts of the sample (Tošner et al., 2017), one should expect deviations from the ideal dipolar lineshape. The effect of the ^{1}H chemical shift offset is almost negligible up to 4 ppm above which large deviations from the ideal behavior occur. For achieving optimal resolution in an R-PDLF experiment the chemical shift offset should therefore be no more than 4 ppm.

The outcome of an experiment is always the sum over all the spatially distributed sample volumes detectable. Therefore the experimental data measured with an R-PDLF experiment is a sum over dipolar modulations, each modulation with a characteristic lineshape that depends on the local RF field. To simulate realistic R-PDLF experiments accounting for RF inhomogeneity, we first measured the RF inhomogeneity in the probe used in this work by the method suggested by Odedra

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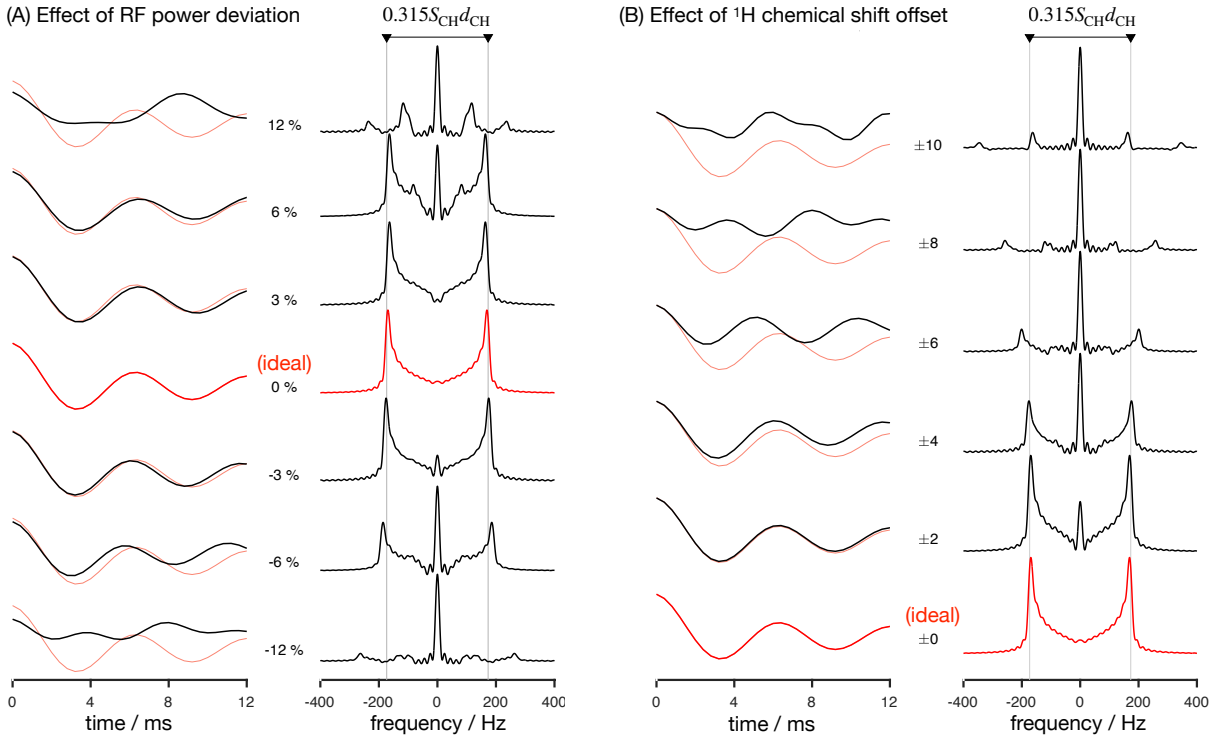

Figure 2. Numerical simulations of the R-PDLF pulse sequence for a fixed dipolar coupling displaying the effects of RF nutation frequency deviation from ideal settings (left) and ^{1}H chemical shift offset (right). The solid red and fainted red curves correspond to the dipolar modulation with ideal settings which yield a dipolar splitting equal to $0.315S_{CH}d_{CH}$. Negative and positive chemical offset shifts with the same magnitude have exactly the same effect.

and Wimperis (Odedra and Wimperis, 2013) (details given as SI). The simulation data was then generated by integrating over R-PDLF NMR simulations that covered the measured RF spatial inhomogeneity profile. This was done by composing a MATLAB script with SIMPSON call-outs enabling to build an R-PDLF simulation database with realistic modulations for a range of S_{CH} values. The generated database included the effect of chemical shift offsets and RF miscalibration with or without a built in RF spatial inhomogeneity profile. The MATLAB/SIMPSON files and the NMR database generated are available as open data (https://github.com/tfmFerreira/inhomogeneous-rf-nmr.git).

The result of accounting for RF inhomogeneity in the R-PDLF simulations is shown in Figure 3 for a two-component dipolar modulation, consisting of two distinct C–H bond order parameters of 0.03 and 0.04. The main effect of including RF spatial inhomogeneity in the simulation is the dampening of the signal and the non-zero long time average of the modulation which gives rise to a middle peak in the dipolar spectrum as also reported previously by Polenova and coworkers (Lu et al., 2016). Due to the limited number of points used, the distinct dipolar couplings are not visible in either dipolar spectrum of the two simulations. Figure 3D shows the result of adding random noise to the simulated data in Figure 3C and fitting the data either

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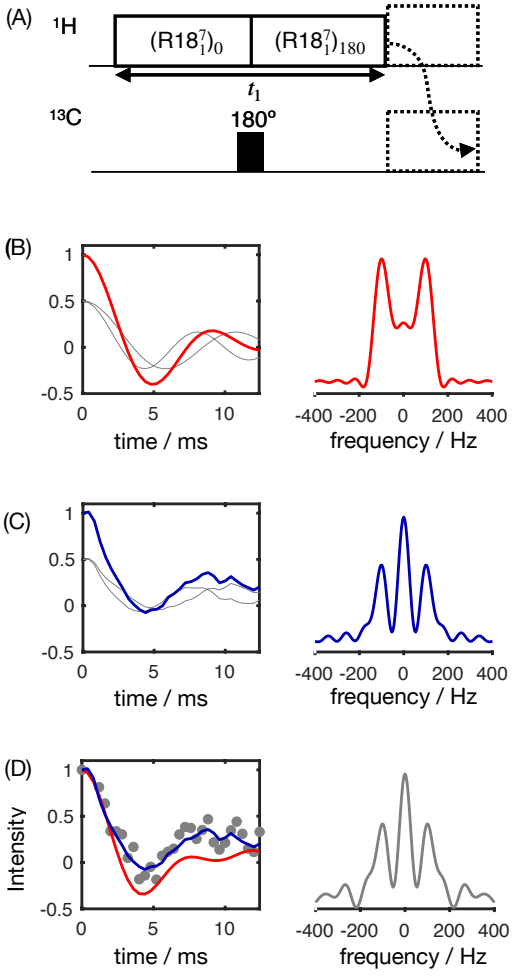

Figure 3. Simulation of the effect of RF spatial inhomogeneity on R-PDLF dipolar modulation and illustration of the advantage of time-domain over frequency-domain analysis of the data. (A) R-PDLF pulse sequence used in this work (Dvinskikh et al., 2004). (B) Ideal R-PDLF dipolar modulation with two components having C−H bond order parameters equal to 0.03 and 0.04 (grey lines display the individual components used). In the frequency domain, the two splittings can not be distinguished, due to the limited number of points used in the time domain. (C) The same as in (B) but including the effect of RF spatial inhomogeneity taken as a gaussian distribution that reflects the RF inhomogeneity of the coil used in this work (details in the SI). (D) Simulation of an experimental result with low signal-to-noise ratio by addition of random noise to the simulated curve in (C). The red and blue curves on the bottom plot show the result of fitting the data with two components using numerical simulations performed with ideal settings and accounting for the RF spatial inhomogeneity profile, respectively.

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Open Access MAGNETIC RESONANCE Discussions

with ideal settings or by taking the RF spatial inhomogeneity profile into account. The fit performed with NMR simulations having ideal settings yields values of 0.01 and 0.034, precluding the use of such fitting procedure for accurate analysis under such conditions. In contrast, the fit performed based on NMR simulations accounting for RF spatial inhomogeneity matches the data almost perfectly - as expected since these simulations were used to generate the original data - giving order parameters values of 0.03 and 0.038, very close to the original values 0.03 and 0.04 used. This suggests that, if the (coil dependent) RF spatial inhomogeneity across the sample is measured with reasonable accuracy, one may simulate a set of realistic data for the complete range of dipolar couplings (0-22 kHz for ^{1}H-^{13}C) which better describes experimental measurements and therefore enables a more accurate time-domain analysis.

2.1 Results / Discussion

2.2 Time-domain fitting enables higher accuracy and shorter experiments

From the description shown in the preceding section it is clear that the RF spatial inhomogeneity affects the dipolar modulation in R-PDLF experiments. Therefore, for accurate fits of experimental data, this effect needs to be taken into account. In this and the following section we demonstrate that accounting for the effect of RF inhomogeneity in time-domain fits of experimental data indeed leads to highly accurate fits of the experimental data and consequently to a considerable improvement of the accuracy of the C–H bond order parameters determined. Figure 4 shows the application of this time-domain analysis to a sample of 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphoethanolamine (POPE) MLVs, illustrating the analysis method on the β carbon of the POPE headgroup. POPE is one of the most abundant lipids in cellular membranes and has recently been investigated with R-PDLF NMR in the context of the NMRlipids project aiming to resolve the atomistic molecular structure of the most abundant lipids in nature by means of a combination of solid-state NMR experiments and all-atom molecular dynamics simulations (Bacle et al., 2021). The time-domain curve fitted to the experimental dipolar modulation measured for the β carbons gives an estimation of S_{CH} =0.032 $\pm$0.006 for this C$-$H bond order parameter magnitude using only the first 8 points along the indirect dimension. Such fit enables to predict the experimental dipolar spectrum that one would obtain using a higher number of indirect dimension points as shown in Figures 4B and 4C. Figure 4D shows how the time-domain fit procedure enables to estimate an accurate order parameter using much shorter experiments in comparison to the use of the typical Fourier transform methodology. As it will be shown in a later section, this is particularly useful for complex systems for which only a limited number of indirect dimension points can be measured. Moreover, the fit procedure enables one to estimate an uncertainty of the value measured (the detailed description for defining the error bar is given as SI) which is more difficult to define with the Fourier transform method. Based on previous ^{2}H NMR measurements, the β methylene carbon is expected to have the equivalent order parameters for the two C$-$H bonds (Gally et al., 1975). In the next section we demonstrate the usefulness of R-PDLF time-domain fits to analyse cases of two-component dipolar modulations and estimate the accuracy of the order parameters determined with the proposed method by comparison with ^{2}H NMR quadrupolar splittings.

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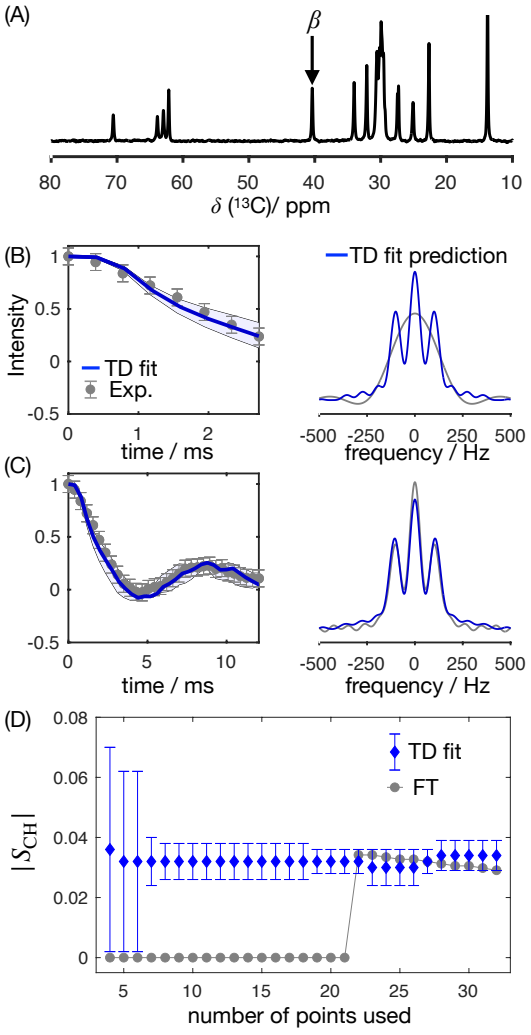

Figure 4. The proposed methodology applied to a sample of POPE MLVs. (A) ^{13}C rINEPT spectrum of the POPE MLVs. (B) Time-domain (TD) fit accounting for RF inhomogeneity of the dipolar dimension of a R-PDLF experiment with a total of 8 points (thick solid line). The experimental dipolar spectrum is shown on the right together with the fit prediction of the experimental dipolar spectrum (using a total of 32 time-domain points). The thin lines show the time-domain curves that correspond to the error limits as defined in the SI. (C) The same as in (B) but fitting a total of 32 experimental points in the indirect dimension. A single-exponential decay of 14 Hz was multiplied to the simulated data. (D) The dependence of the order parameter estimated by the time-domain fit (blue) and from the dipolar splitting in the Fourier transform of the experimental data (gray) on the total number of points in the indirect dimension.

2.3 Comparison with ^{2}H NMR quadrupolar splittings

To further test the accuracy of the proposed methodology, we used a water/DMPC/DMPCd54 liquid crystalline system (L_α phase) such that the ^{2}H NMR spectrum of the perdeuterated acyl chains of the DMPCd54 molecules could be measured and

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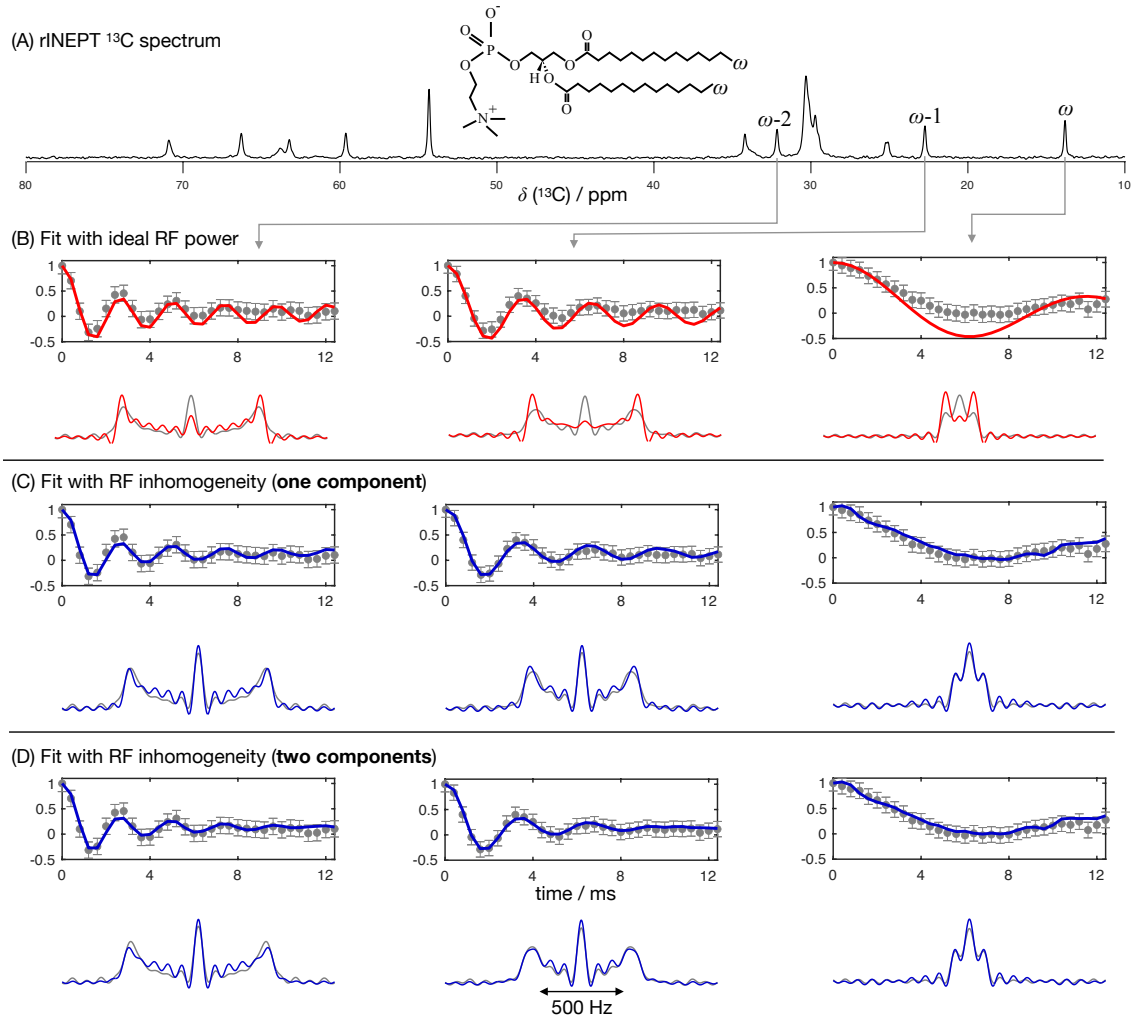

Figure 5. The proposed methodology applied to a sample of a DMPC/DMPCd54 liquid crystalline system. (A) ^{13}C rINEPT spectrum and labels used to identify different carbons. (B) Time-domain fits neglecting the RF inhomogeneity across the sample. (C) Time-domain fits accounting for the RF inhomogeneity across the sample using one single dipolar coupling as fit parameter. (D) The same as in (C) but using two dipolar couplings as fit parameters assuming a two-component dipolar modulation.

compared with the ^{1}H-^{13}C dipolar couplings determined from the acyl chains of the molecules with natural abundance of isotopes. Figure 5 shows the R-PDLF dipolar modulation for a number of resolved carbons from the liquid crystalline system and their corresponding fits with and without accounting for RF inhomogeneity. The improvement of the fits by accounting for RF inhomogeneity is evident, especially for the smaller couplings. Moreover, since each of the three carbon peaks analysed is a sum of components from the two individual acyl chains, sn-1 and sn-2, we also performed the time-domain fits of the dipolar modulations using two components. In the case of the acyl chain methyl groups ω, a single dipolar coupling minimizes the root

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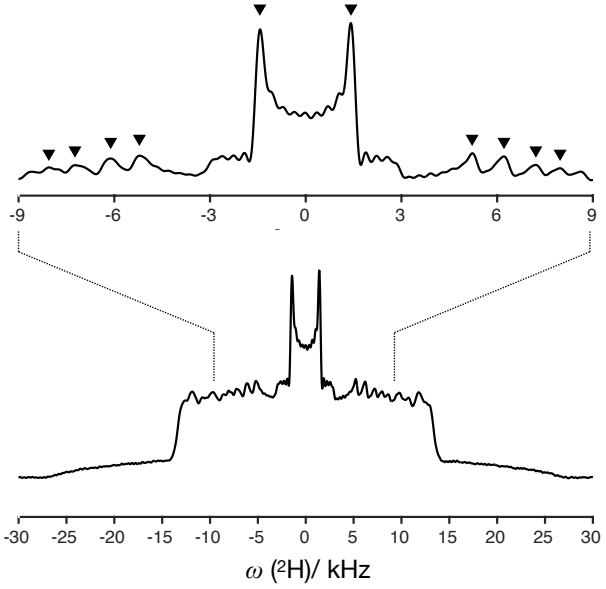

Figure 6. ^{2}H NMR spectrum of the DMPC/DMPCd54 liquid crystalline system and symbols showing the positions used to determine order parameters.

mean square deviation (RMSD). On the other hand, for the $\omega - 1$ and $\omega - 2$ methylenes, two dipolar couplings enable a better fit than a single value which suggests a distinct motional geometry in the sn-1 and sn-2 acyl chains for these methylenes (a detailed analysis is given in the SI). The nonequivalence of the order parameters from the distinct chains is in agreement with previous investigations of specifically deuterated DPPC molecules (Seelig and Niederberger, 1974).

The ^{2}H NMR spectrum measured from DMPCd54 molecules is shown in Figure 6. The five lowest quadrupolar splittings were used to calculate C–D bond order parameters. The results are included in Table 1 together with the results from the time-domain fits of the dipolar modulations from the molecules with natural abundance of isotopes. The agreement between the values obtained by using the different techniques is striking. The maximum difference between the order parameter magnitudes determined with the methodology proposed and the values determined from the ^{2}H NMR spectrum is below ± 0.005, much below the errors reported previously (up to ± 0.02) when doing similar comparisons between dipolar recoupling experiments with ^{2}H NMR spectroscopy (Gross et al., 1997; Dvinskikh et al., 2005; Ferreira et al., 2013). Here, we used values taken from previous studies for the rigid ^{1}H-^{13}C dipolar and ^{2}H quadrupolar couplings, namely 22 kHz and 126 kHz, respectively (Dvinskikh et al., 2004; Davis et al., 2009). We may therefore exclude a significant isotope effect on the molecular dynamics of the acyl chains in the water/DMPC/DMPCd54 liquid crystalline system. Moreover, we can unambiguously assign the C–D order parameters measured with ^{2}H NMR.

https://doi.org/10.5194/mr-2022-19
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Table 1. Comparison of the order parameter magnitudes, $|S_{\mathrm{CH}}|$, determined from the DMPC/DMPCd54 liquid crystalline sample for the ω, $\omega-1$ and $\omega-2$ carbons from using the observed splitting in the frequency domain (FT) of the R-PDLF experiment, from time-domain (TD) fits with numerical simulations accounting for the effect of RF inhomogeneity on R-PDLF experiments using one and two components, and from quadrupolar splittings observed with a ^{2}H quadrupolar echo.

Carbon label	FT	TD fit with RF inhomogeneity		^{2}H NMR
		1 comp.	2 comp.	
ω	0.0023	0.0023±0.006	0.0023±0.004	0.0023
	-	-	0.0023±0.004	-
ω-1	0.083	0.090±0.009	0.096±0.009	0.098
	-	-	0.085±0.009	0.083
ω-2	0.114	0.118±0.01	0.122±0.011	0.127
	-	-	0.115±0.011	0.115

The agreement between the ^{2}H NMR and R-PDLF values obtained highlights the usefulness of the methodology described here over the conventional frequency-domain analysis: Such distinct dipolar couplings cannot be observed in the dipolar spectrum due to the limited number of points measured as described previously.

In contrast to the POPE case described in the preceding section, for the DMPC/DMPCd54 system, including an exponential decay to account for relaxation effects affects the RMSD less significantly (detailed comparison in the SI). We believe that this relates to the different membrane curvatures of the samples. While the POPE MLVs where prepared at excess hydration, the DMPC/DMPCd54 MLVs were prepared by placing the dry lipid film into a desiccator for about one day. The reduced hydration of the DMPC/DMPCd54 MLVs is expected to yield long range flat membranes eliminating relaxation effects from the reorientation motion due to the lateral diffusion of the lipid molecules. The POPE MLVs at excess hydration may have a higher curvature with lateral diffusion contributions to the spin relaxation during the dipolar recoupling dimension. However, for some other lipid systems, such as POPC and POPC/cholesterol that were prepared at excess hydration, a slower relaxation during the indirect dimension of the R-PDLF experiment was observed as well (results not shown). We refrained from investigating such relaxation effects in this work.

2.4 Application to a brain lipid extract

To showcase the applicability of the presented methodology we investigated the molecular structure of a complex membrane system composed of a brain lipid extract with several lipid types present. The complex lipid mixture consists of the chloroform:methanol extract of porcine brain tissue as purchased from AVANTI LIPIDS.

Figure 7 shows the ^{13}C spectrum of the brain lipid extract at excess hydration together with spectra acquired from single phospholipid model systems. Due to the much higher complexity of the brain lipid extract sample in comparison to model

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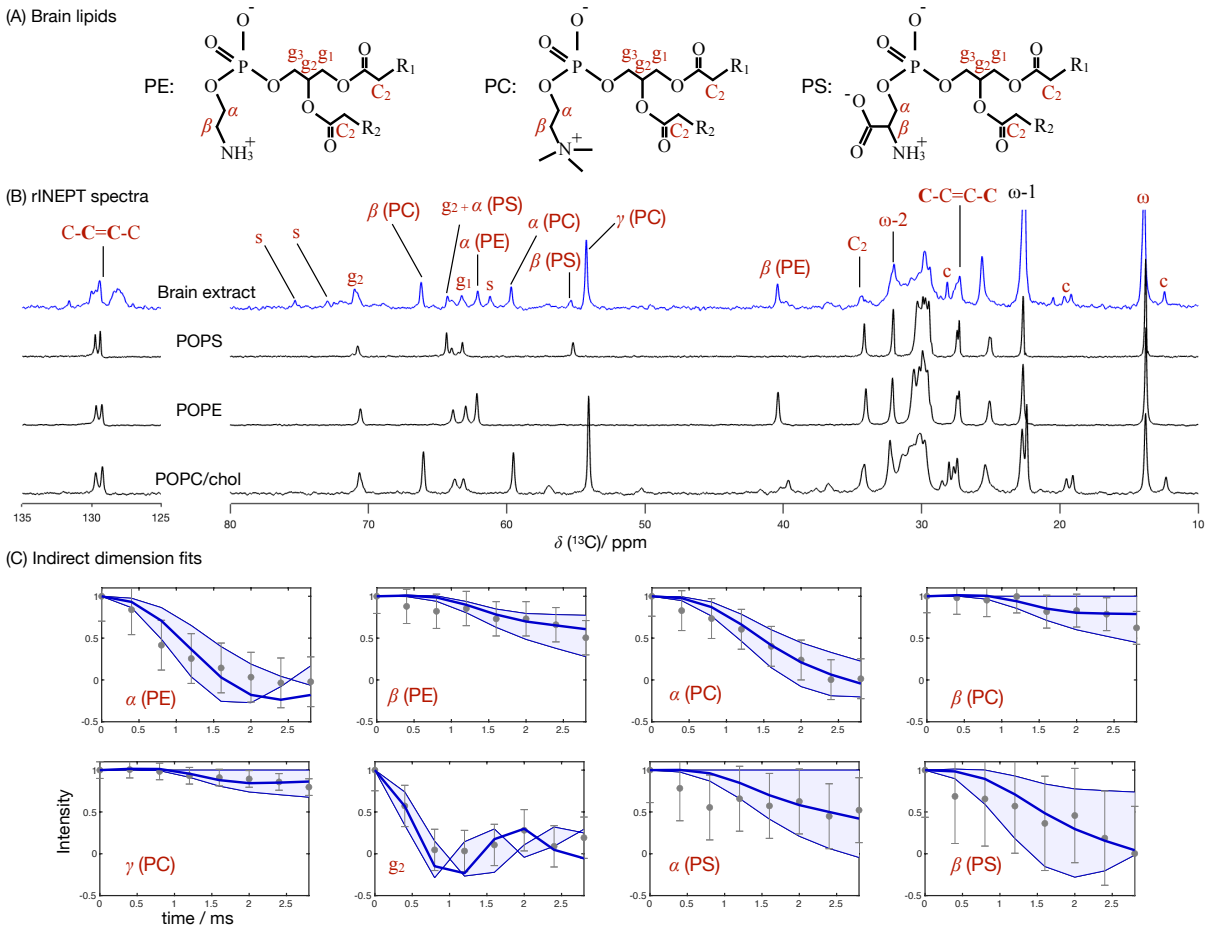

Figure 7. Phospholipid headgroup C–H bond order parameter magnitudes determined from a brain lipid extract using time-domain fits accounting for B_1 inhomogeneity. The polarization transfer method used was rINEPT, recycle delay was 5 s, MAS rate was 5 kHz and a total of 4096 scans were acquired for each point in the indirect dimension which amounts roughly to 2 days of experimental time. (A) Chemical structures and carbon labels of the most abundant phospholipids in the brain lipid extract: phosphatidylethalonamine (PE), phosphatidylcholine (PC), and phosphatidylserine (PS).(B) ^{1}H-^{13}C rINEPT spectrum of the brain lipid extract membranes together with reference spectra for the most abundant lipids. The additional labels c and s were used to identify cholesterol and Galactose peaks, respectively. (C) Application of the proposed methodology for fitting the dipolar modulations and determining the corresponding order parameter magnitudes for selected carbons.

membrane systems (that are usually composed of 1-3 distinct components), the number of transients required to achieve a reasonable signal to noise ratio is considerably higher. The comparison of the spectra enables to identify a number of peaks from the different components in the extract, namely the α, β and γ segments of the headgroup of phosphatidylcholine (PC), the α and β segments of phosphatidylethanolamine (PE), the α and β segments of phosphatidylserine (PS), several cholesterol peaks and some galactose peaks most likely due to the presence of galactose cerebrosides in the mixture. Although only

https://doi.org/10.5194/mr-2022-19
Preprint. Discussion started: 8 November 2022


Open Access MAGNETIC RESONANCE Discussions

approximately 40% of the molar composition was known prior to the solid-state NMR experiments, from inspection of the ^{13}C rINEPT spectrum, and knowing the lipid composition of myelin that makes up most of the dry weight of brain tissue (Norton and Autilio, 1966), it is clear that most of the remaining unknown molar content is cholesterol plus a considerable fraction of galactose cerebrosides (GalCer).

Figure 7C shows the indirect time-domain modulation for a number of identified peaks in the spectra measured by R-PDLF spectroscopy. Only 8 points in the indirect dimension were acquired for the brain lipid extract sample due to the high number of transients required to achieve a a reasonable signal to noise ratio (4096 scans) with a total experimental time of about 48 hours. Within such an experimental setup the Fourier transform of these time-domain modulations does not enable resolution for determining dipolar splittings. However, application of time-domain fitting including RF inhomogeneity enables to determine the dipolar couplings and therefore estimate C–H bond order parameters. The estimated order parameters are presented in Table 2.

The headgroup order parameters determined from the set of different phospholipid types in the brain lipid extract are very much in line with what is observed in corresponding lipid model membranes. The only exception is the PS β order parameter with a rather small order parameter equal to 0.04. This suggests that the brain lipid extract may contain calcium ions that are known to significantly affect the PS headgroup orientation. A thorough analysis of the order parameters in terms of the molecular structure in the complex brain lipid extract system will not be given here. Such analysis should be done in combination with experiments and MD simulations on PC/PE/PS/cholesterol/GalCer model membranes which resemble the lipid extract composition, to investigate potential phase separation behavior, effects of distinct ions present in the system and pH, or ultimately the effect of macromolecules such as basic myelin protein, the most abundant protein in myelin. We believe that such a combined approach will lead to a more accurate description of the lipid/protein interactions in myelin, which may be important in the context of a number of diseases related to demyelination. The methodology proposed here will enable to perform such investigations with higher accuracy and without the requirement of isotopic labelling. Moreover, we envision applications to many other complex membranes such as bacterial membrane models, eukaryotic membrane models with cell type or organelle specific compositions, technological systems such as lipid-nanoparticles, as well as to address the molecular structure/orientation of drugs, peptides or other molecules with anisotropic motion in lipid membranes.

3 Conclusions

In summary, we have described a PDLF NMR methodology that consists of performing time-domain fits of the dipolar modulation with numerical simulations that account for the RF spatial inhomogeneity of the probe used. The proposed methodology enables one to determine C–H bond order parameters from simple model systems with a much higher accuracy than previously and enables to investigate complex lipid membrane systems that were so far inaccessible using the conventional PDLF NMR methodology. We believe that the method presented will be extremely useful in the future concerning molecular structural investigations of complex systems such as multi-component models, lipid extracts and lipid membranes with drugs, peptides

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Preprint. Discussion started: 8 November 2022

Open Access MAGNETIC RESONANCE Discussions

Table 2. Order parameter magnitudes determined from a brain lipid extract using the methodology proposed in this work compared to ^{2}H NMR values measured from phospholipid model systems reported previously. [a)] $T = 40°C$, [b)] $T = 30°C$ and [c)] $T = 23°C$

Carbon segment	Brain extract $\lvert S_{CH\rvert}$	Model system $\lvert S_{CD\rvert}$	model
α (PC)	0.044 ± 0.015	0.048^a	DPPC/chol (Brown and Seelig, 1978)
		0.049^b	DOPC (Ulrich and Watts, 1994)
		0.048^c	POPC (Bechinger and Seelig, 1991)
β (PC)	0.01 ± 0.015	0.024^a	DPPC/chol (Brown and Seelig, 1978)
		0.029^b	DOPC (Ulrich and Watts, 1994)
		0.044^c	POPC (Bechinger and Seelig, 1991)
γ (PC)	0.001 ± 0.016	0.008^a	DPPC/chol (Brown and Seelig, 1978)
α (PE)	0.066 ± 0.024	0.063^a	DPPE/chol (Brown and Seelig, 1978)
β (PE)	0.019 ± 0.012	0.020^a	DPPE/chol (Brown and Seelig, 1978)
α (PS)	0.026 ± 0.018	0.016^a	POPC/POPS (Roux and Bloom, 1990)
β (PS)	0.040 ± 0.039	0.091^a	POPC/POPS (Roux and Bloom, 1990)
		0.062^a	+ 1 M $CaCl_2$ (Roux and Bloom, 1990)

or other molecules incorporated. Moreover, the higher accuracy and farther reach of the method will also be fundamental to validate molecular dynamics simulations for which structural experimental data was not accessible so far.

Code and data availability. https://github.com/tfmFerreira/inhomogeneous-rf-nmr.git

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Preprint. Discussion started: 8 November 2022

Open Access MAGNETIC RESONANCE Discussions

Author contributions. T.M.F. idealized the project. T.M.F. and A.W. developed the code. T.M.F and A.W. performed experiments and processed the experimental data. T.M.F., A.W. and K.S. analysed and discussed the results and manuscript. T.M.F. wrote the manuscript.

Competing interests. no competing interests

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Preprint. Discussion started: 8 November 2022

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