## Supplement of

# Various facets of intermolecular transfer of phase coherence by nuclear dipolar fields 

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Four additional figures and a simulation program.

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Figures


Figure S1. Same as fig. 1a-c in the main text, except that the rf pulse-train was GARP instead of DIPSI-2. All other conditions for the simulations were identical.


Figure S2. Results of an experiment similar to the one of fig. 3 of the main text. The sole differences were a repetition time of about 3 s instead of 11 s , a DIPSI-2 irradiation time of 100 ms instead of 200 ms , and 1 scan per increment instead of 4. This results in an experimental time of about 12 minutes instead of 3 hours.



Figure S3. Calculated line shapes resulting from the experiment of fig. 2 of the main text. (a) The profile that characterizes the $B_{0}$ inhomogeneities, which is considered in the calculations. For a spin species $S$, the experiment results in:
$\operatorname{sig}(S)=\int c I_{i n h} e^{\left(-i \omega_{i n h}-R_{2}^{A}\right) t_{1}} e^{\left(i \omega_{i n h}+i \omega_{0}^{S}-R_{2}^{S}\right) t_{2}} d \omega_{i n h}$,
where $c$ is a constant that depends on several factors such as the spin-density and transfer and detection efficiencies. $R_{2}^{A}$ and $R_{2}^{S}$ are the transverse relaxation times of the $A$ and $S$ spins. The signal $\operatorname{sig}(S)$ has been calculated for proton spin $S$ with $\omega_{0}^{S}=3 \mathrm{ppm}, R_{2}^{A}=2 \mathrm{~s}^{-1}$ and $R_{2}^{S}=2 \mathrm{~s}^{-1}$ at a field of $B_{0}=18.8 \mathrm{~T}$ ( 800 MHz proton frequency). $12 \times 1024$ complex points for a bandwidth of 12 ppm were used in the direct $t_{2}$ dimension and 1024 indirect $t_{1}$ increments for a bandwidth of 1 ppm (more points have been used than in the experiments of fig. 3 in the main manuscript and fig. S2 to avoid truncation effects). In the center row the real part of the 2D Fourier transform of eq. S1 for three different scenarios is plotted: (b) a homogeneous $B_{0}$ field $\left(\Delta \nu_{i n h}=0\right)$, (c) a moderately inhomogeneous field ( $\Delta \nu_{i n h}=0.03 \mathrm{ppm}$ ), and (d) a substantially inhomogeneous field ( $\Delta \nu_{i n h}=0.3 \mathrm{ppm}$ ). The spectra zoom in on the region of interest and the lowest contour levels are at $2 \%$ of the maximum intensity of each spectrum. Since only 1 coherence pathway is recorded, the spectrum cannot be phased to pure absorption mode, as evidenced by the severe phase twist in (b). However, due to the symmetry of these distortions, the phase twists do not appear in the sum of the rows as shown in (e). The phase-twists are attenuated with increasing $B_{0}$ inhomogeneities, and are not visible in the sum, after shearing of the 2D spectra, of the rows as shown below the spectra (c) and (d) in (f) and (g). The sum spectra in (e-g) have the same normalization factor. Thus increased inhomogeneities do not reduce the signal intensity, but, since the signal is spread out over more rows, lead to a decrease of the signal-to-noise ratio. The line-width in (e) depend on $R_{2}^{S}$, the line-width in (f) and (g) on the sum $R_{2}^{A}+R_{2}^{S}$.
Sucrose



Figure S4. Spectrum obtained with a pulse-acquire experiment preceded by saturation of the solvent signal $\left(\mathrm{H}_{2} \mathrm{O}\right)$. The sample, 0.5 mM DSS and 2.0 mM sucrose in a $90 \% / 10 \%$ mixture of $\mathrm{H}_{2} \mathrm{O} / \mathrm{D}_{2} \mathrm{O}$, has been used for all experiments in this work. The assignments come from the Spectral Database for Organic Compounds, SDBSWeb, https://sdbs.db.aist.go.jp (National Institute of Advanced Industrial Science and Technology, date of access: 05-09-2023).

```
    '''
2: modified: 21-07-2023
3: Parameter file for simul_df_tocsy_01.py
For fig. Id use:
5: iniDSS = "zed"
6: VDF = 1.84
7: order = [-1, 1]
8: we look at the 'planeabs' results
9: For fig. 5b use:
10: iniDSS = "MH2O"
11: }\quadvDF=1.84 or - 0. 5*1.8
12: order = [2]
13: we look at the 'zabs' results
14: '' '
15: B0 = -800.13 # main field (minus sign for positif gyrom.)
16: vDSS = -4.85 # chemical shift difference wr H2O (ppm)
17: vDF = 1.84 # amplitude dipolar field
18:
19: mixing = "Dipsi2" # "Dipsi2", "Garp","CW" or "Waltz16"
20: tau90 = 30.e-6 # duration 90 pulse, defines rf power mixing
21: maxcyc = 120 # maximum number of mixing cycles
22:
23: ngrid = 36 # number of equidistant (in angles) gridpoints for
24: # the dephased solvent magnetization (MH2O)
25: iniDSS = "MH2O" # "iks", "why", "zed" or "MH2O"
26: # MH2O is initially dephased in the plane, MDSS (the solute
27: # magnetization) can be along one of the axis or initially
28: # aligned with MH2O
29: order = [2] # indicates the ratio beween the pfg before acquisition
30: # and the dephasing pfg
31: plot = True
32: plotopt = {'plane':False, 'planeabs':True,'z':False,'zabs':True}
33: # 'zed' plots the magnetization in the plane after:
34: # pfg-mixing-spoiling-90-pfg*order
35: # 'plane' plots the magnetization in the plane after:
36: # pfg-mixing-pfg*order
37: plotcol = ['blue','red','green','orange','cyan']
38: savedata = False
```

1: ' ' '
2: modified: 21-07-2023
3: Simulation program transfer of phase coherence from abundant spins (H2O)
4: to solute (DSS) by dipolar field during TOCSY.
5: Only with mixing sequences along one axes with constant rf amplitude.
6: The solvent magnetization evolves as described in the main article.
7:
8: Program uses numba for jit compilation. Uses para02.py file for parameters
9: so that numba can use cache.
10 :
11: The program has been run with versions:
12 :
13: Python 3.11.3
14: Numpy 1.25.1
15: Numba 0.57 .1
16: Matplotlib 3.7.2
17:
18: This code is provided for the purpose of checking and/or reproducing the
19: simulations of the main article and comes without any warranty. If you use
20: (part of) this code for your own work, please cite the original publication.
21:
22: 2023 Philippe Pelupessy
' ' '
24:
25: \# Import necessary libraries
26: import numpy as np
27: import matplotlib.pyplot as plt
28: from numba import njit,prange
import para02 as pa \#import parameter file
import importlib
importlib.reload(pa) \#reload parameter file, needed if rerun from ipython
32:
33: \# Evolution of the solute magnetization
34: @njit(parallel=True, cache = True,fastmath=True)
35: def evolveDSS (MDSS, ngrid,maxcyc,MH2O, SupCyc,Angle,Phase, IA, sA, cA, rfA, wDSS, lA, lS, unit):
'''Rotation around an axis during spinlock sequence along the $x$-axis. The axis of rotation for DSS is determined by the rf field and by the MH2O. $R F$ power is constant but sign may alternate. On-resonance for abundant solvent spins, while magnetization of the off-resonant sparse spins is calculated. Optimized for numba just in time compilation. Gains in speed using fastmath=True depend strongly on computer.'''
pil $=n p . p i /(180 * u n i t)$
mixing = pa.mixing
tau90 $=$ pa.tau90
maxcyc $=$ pa.maxcyc
\#main field (minus sign for positive gyrom.)
\#chemical shift difference with H2O (ppm)
\#spin-lock seq. "Dipsi2","Garp","cw" or "Waltz16"
\#duration 90 pulse spinlock
\#maximum number of cycles spin-lock

88:

```
ngrid = pa.ngrid #H20 magnetization is phasemodulated number of phases
```

ngrid = pa.ngrid \#H20 magnetization is phasemodulated number of phases
wDF = 2*np.pi*pa.vDF \#dipolar field amplitude
wDF = 2*np.pi*pa.vDF \#dipolar field amplitude
iniDSS = pa.iniDSS \#inital DSS magn. "iks", "why","zed" or "MH2O"
iniDSS = pa.iniDSS \#inital DSS magn. "iks", "why","zed" or "MH2O"
order = pa.order \#lists of initial orders, SQ, DQ, TQ...(+ or -)
order = pa.order \#lists of initial orders, SQ, DQ, TQ...(+ or -)
plot = pa.plot \#True or False
plot = pa.plot \#True or False
plotopt = pa.plotopt \#Dictionary of plotoptions (True or False):
plotopt = pa.plotopt \#Dictionary of plotoptions (True or False):
\#plane, planeabs,z, zabs
\#plane, planeabs,z, zabs
plotcol = pa.plotcol \#colors plot (each order has its color)
plotcol = pa.plotcol \#colors plot (each order has its color)
savedata = pa.savedata\#if True save data to text file
savedata = pa.savedata\#if True save data to text file
\#sequences consist of a sequence of pulses of rotation angle integer/unit
\#sequences consist of a sequence of pulses of rotation angle integer/unit
\#always along the x-axis, with positive or negative sign (0, 180),
\#always along the x-axis, with positive or negative sign (0, 180),
\#repated in a supercycle (e.g. for Dipsi2 a full cycle is 4*9= 36 pulses)
\#repated in a supercycle (e.g. for Dipsi2 a full cycle is 4*9= 36 pulses)
if mixing=="Dipsi2":
if mixing=="Dipsi2":
unit = 1
unit = 1
Phase = np.array([0,180,0,180,0,180,0,180,0])*(-1./90)+1
Phase = np.array([0,180,0,180,0,180,0,180,0])*(-1./90)+1
Angle = np.array([320,410,290,285,30,245,375,265,370])
Angle = np.array([320,410,290,285,30,245,375,265,370])
SupCyc = np.array([0,180,180,0])*(-1./90)+1
SupCyc = np.array([0,180,180,0])*(-1./90)+1
if mixing=="Waltz16":
if mixing=="Waltz16":
unit = 1
unit = 1
Phase = np.array([0,180,0])*(-1./90)+1
Phase = np.array([0,180,0])*(-1./90)+1
Angle = np.array([90,180,270])
Angle = np.array([90,180,270])
SupCyc = np.array ([0,0,180,180,180,0,0,180,
SupCyc = np.array ([0,0,180,180,180,0,0,180,
180,180,0,0,0,180,180,0])*(-1./90)+1
180,180,0,0,0,180,180,0])*(-1./90)+1
if mixing=="Dipsi20": \#to test unit = 10, gives same result a Dipsi2
if mixing=="Dipsi20": \#to test unit = 10, gives same result a Dipsi2
unit = 10
unit = 10
Phase = np.array([0,180,0,180,0,180,0,180,0])*(-1./90)+1
Phase = np.array([0,180,0,180,0,180,0,180,0])*(-1./90)+1
Angle = np.array([3200,4100,2900,2850,300,2450,3750,2650,3700])
Angle = np.array([3200,4100,2900,2850,300,2450,3750,2650,3700])
SupCyc = np.array ([0,180,180,0])*(-1./90)+1
SupCyc = np.array ([0,180,180,0])*(-1./90)+1
if mixing=="Garp":
if mixing=="Garp":
unit = 10
unit = 10
Phase = np.array([0,180,0,180,0,180,0,180,0,180,0,180,0,180,
Phase = np.array([0,180,0,180,0,180,0,180,0,180,0,180,0,180,
0,180,0,180,0,180,0,180,0,180,0])*(-1./90)+1
0,180,0,180,0,180,0,180,0,180,0])*(-1./90)+1
Angle = np.array([305,552,2578,2683,693,622,850,918,1345,2561,
Angle = np.array([305,552,2578,2683,693,622,850,918,1345,2561,
664,459,255,727,1195,1382,2584,649,709,772,
664,459,255,727,1195,1382,2584,649,709,772,
982,1336,2559,656,534])
982,1336,2559,656,534])
SupCyc = np.array([0,180,180,0])*(-1./90)+1
SupCyc = np.array([0,180,180,0])*(-1./90)+1
if mixing=="cw":
if mixing=="cw":
unit = 1
unit = 1
Phase = np.array([0])*(-1./90)+1
Phase = np.array([0])*(-1./90)+1
Angle = np.array([360*1]) \#multiples of 360
Angle = np.array([360*1]) \#multiples of 360
SupCyc = np.array([0])*(-1./90)+1

```
    SupCyc = np.array([0])*(-1./90)+1
```

174: print('Compilation and parallel calculation starts')
175: MDSS = evolveDSS (MDSS, ngrid, maxcyc, MH2O, SupCyc,Angle, Phase, IA, sA,

176:
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199:
200:
201:
202:

204: if savedata:
205:
206:
207:
208: if
209:
\#before the same pfg.
$\mathrm{c}=0$
for $o$ in order:
if plot:
c $+=1$
if savedata:
plt.show()
$\qquad$ main()
\#plot for different pfgs before acquistion. ' $z$ ' corresponds to, spoil-90
$c o=n p \cdot \cos (o * 2 * n p \cdot p i * n p \cdot$ arange(ngrid)/(ngrid))/ngrid
si $=n p . \sin (0 * 2 * n p \cdot p i * n p . a r a n g e(n g r i d) /(n g r i d)) / n g r i d$
MDSSbuX $=\operatorname{co.dot(MDSS[0])-si.dot(MDSS[1])~}$
MDSSbuY $=\operatorname{co} \cdot \operatorname{dot}(\operatorname{MDSS}[1])+$ si.dot (MDSS[0])
MDSSbuZx $=$ co.dot (MDSS[2])
MDSSbuZy $=$ si.dot(MDSS[2])
if plotopt['plane']:
plt.figure('plane')
plt.plot(time,MDSSbuX,color = plotcol[c])
plt.plot(time,MDSSbuY,color = plotcol[c],linestyle='--')
if plotopt['planeabs']:
plt.figure('planeabs')
plt.plot(time, np.sqrt(MDSSbuY**2+MDSSbuX**2), color $=$ plotcol[c])
if plotopt['z']:
plt.figure('z')
plt.plot(time, MDSSbuZx, color = plotcol[c])
plt.plot(time,MDSSbuZy, color = plotcol[c],linestyle='--')
if plotopt['zabs']:
plt.figure('zabs')
plt.plot(time,np.sqrt(MDSSbuZx**2+MDSSbuZy**2), color = plotcol[c])
\#can be saved to make own plots, especially to compare
np. savetxt('mag'+str(o) +'.txt', [time, MDSSbuX, MDSSbuY, MDSSbuZx,
MDSSbuZy]) ':

