The TSAR mechanism:

A family of new solid-state NMR recoupling techniques

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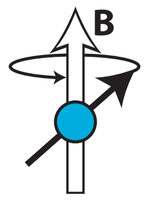
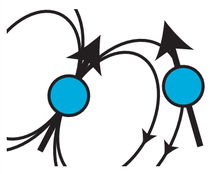
Introduction

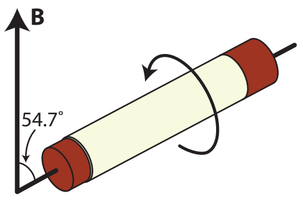
NMR: When a nuclear spin is placed in a magnetic field it precesses at a characteristic frequency. The spin will absorb and re-emit electromagnetic radiation resonant with this frequency. The way in which it does this tells us about the spin's chemical environment.





Dipolar coupling: Spins possess magnetic dipole moments that can interact mutually. This coupling can be used to measure internuclear distances due to its inverse cube dependence.

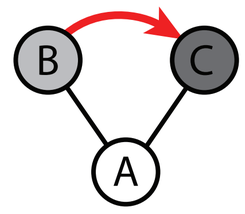
Magic angle spinning (MAS): Dipolar coupling and other interactions lead to the broadening of spectral lines. These interactions can be decoupled by physically spinning the sample at an angle of 54.7˚ to the field.

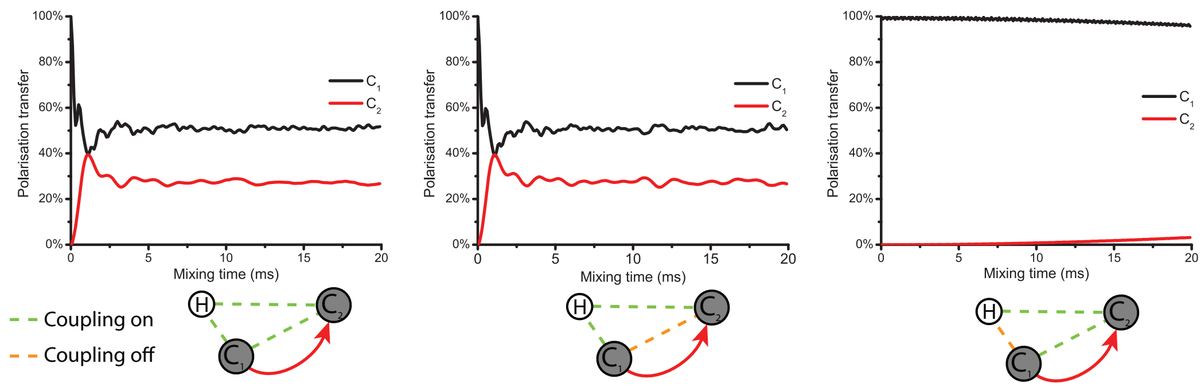


Protein structure determination: We can re-introduce the dipolar couplings using recoupling sequences, allowing us to measure internuclear distances. These can be used to determine the structure of proteins. However, existing techniques suffer from dipolar truncation and sample heating. This project investigated a new mechanism which does not suffer from these problems.

The TSAR mechanism

Mechanism: Third spin assisted recoupling (TSAR) is a new MAS dipolar recoupling mechanism. It gives polarisation transfer between spins B and C, assisted by a mediating heteronuclear spin A. It uses a second order cross term involving the dipolar couplings B-A and C-A. [1]



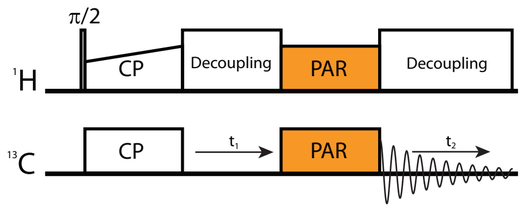


PAR and PAIN: Protons are highly abundant in proteins and have a large gyromagnetic ratio, so can be used as the mediating spin A to facilitate large transfer. If B=C then we have PAR transfer. If B≠C then we have PAIN transfer.

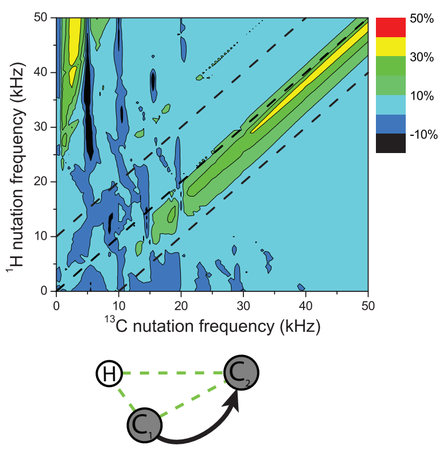
Proton Assisted Recoupling (PAR)

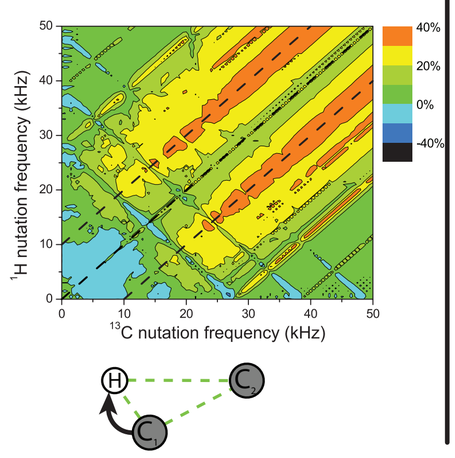
The pulse sequence

This can be used to produce two-dimensional homonuclear correlation spectra [1]. Cross polarisation (CP) is used in order to transfer the proton magnetisation to the less sensitive ^{13}C nuclei.



By varying the power on the two channels during the PAR recoupling (which determines the nutation frequencies of the nuclei), we can find the conditions for optimum transfer. Dashed lines are Hartmann-Hahn conditions for CP.

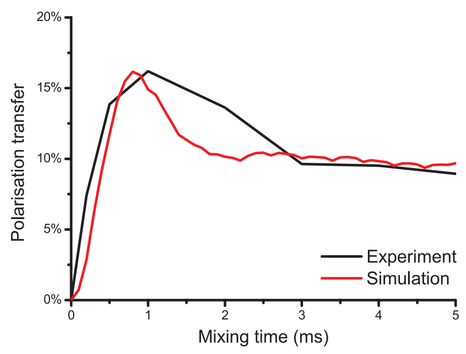


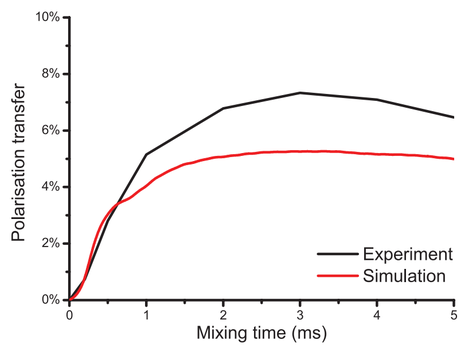


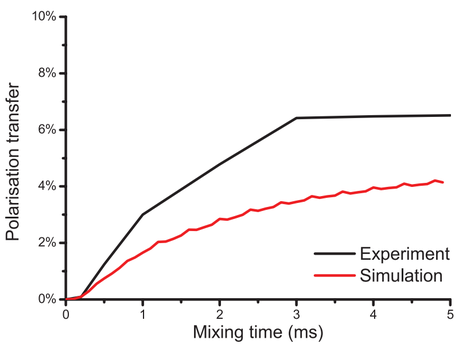
Experiment and simulation

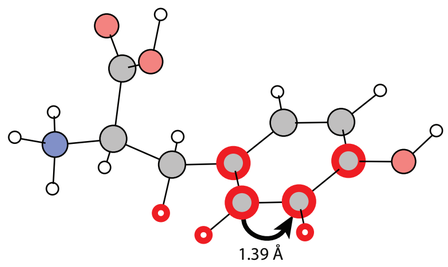
By recording ^{13}C-^{13}C spectra of tyrosine at different PAR mixing times and integrating the peaks, we measured how the polarisation transfer between different pairs of nuclei varied with time.

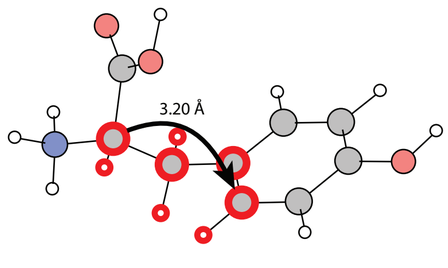
Each transfer was simulated using density matrix simulations [2], using the spin systems circled below each graph. The simulated transfers were much more accurate and required smaller spin systems than competing techniques [3]. Also, as the internuclear distance increases, the peak in the buildup curve occurs later. This demonstrates a potential method of distance measurement.

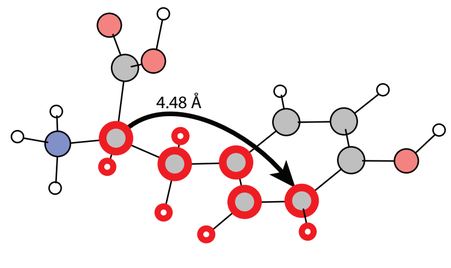








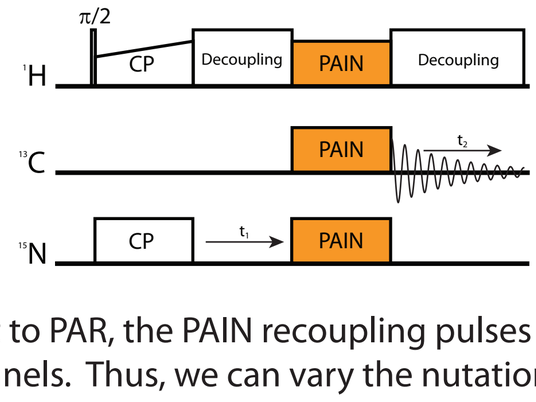




Proton Assisted Insensitive Nuclei Cross Polarisation (PAIN-CP)

The pulse sequence

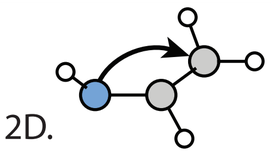
This can be used to produce two-dimensional heteronuclear correlation spectra [4].

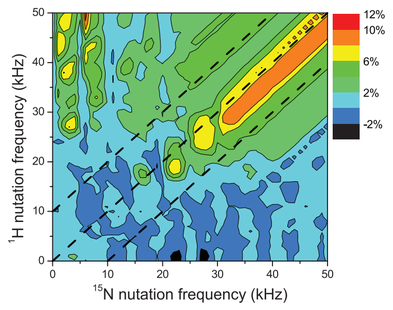


In contrast to PAR, the PAIN recoupling pulses are applied to three channels. Thus, we can vary the nutation frequencies of all three nuclei, giving three-dimensional optimisation maps.

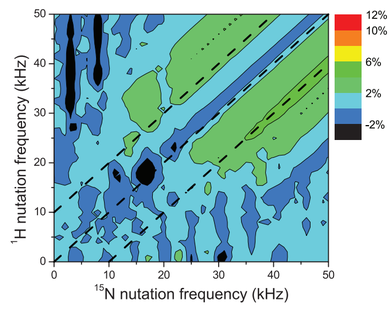
Optimising PAIN

Since we require good transfer from ^{15}N to ^{13}C nuclei, we utilise the ^{15}N-^{13}C Hartmann-Hahn (HH) conditions for cross polarisation (CP), reducing the maps to 2D.

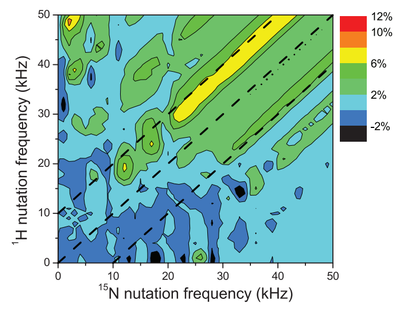




^{15}N-^{13}C $n = 0$ HH condition: transfer optimised near the ^{15}N-^{1}H $n = 0$ HH condition.



^{15}N-^{13}C $n = 0.5$ HH condition: not a true HH condition, so there is never good transfer.



^{15}N-^{13}C $n = 1$ HH condition: transfer optimised near the ^{15}N-^{1}H $n = 1$ HH condition.

Summary

I have investigated two recoupling techniques for use in solid-state magic angle spinning NMR experiments. Unlike competing techniques, they can be used in high field and fast spinning regimes, enabling higher resolution spectra to be taken. Also, their dipolar truncation is attenuated, making them ideal for protein structure determination.

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References

[1] G. De Paëpe, J. R. Lewandowski, A. Loquet, A. Böckmann and R. G. Griffin, J. Chem. Phys. **129**, 245101 (2008)
[2] M. Veshtort, R. G. Griffin, J. Magn. Reson. **178**, 248 (2006)
[3] Work done by Elizabeth Briggs and Caroline Selwood
[4] J. R. Lewandowski, G. De Paëpe and R. G. Griffin, J. Am. Chem. Soc. **129**, 728 (2007)