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Direct-Detect HETCOR V.2

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We use this protocol and it's working

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Abstract

Purpose

To collect a 2D through-space correlation spectrum between ^{1}H and a spin-1/2 nucleus.

Scope

This protocol is focused on the basic Frequency Switched Lee Goldberg (FSLG) heteronuclear correlation (HETCOR) experiment. There are more advanced modifications and experiments which can provide various benefits, but the basic sequence is generally adequate, robust, reliable, straightforward to set up, and can be run on a wide variety of hardware configurations.

Guidelines

As the experiment is CP-based, correlations are through-space. Setting a very short CP contact time will de-emphasize, but not necessarily eliminate, remote couplings transferred via ^{1}H homonuclear coupling. Setting a long CP contact time will allow for long-range correlations to be observed.

This protocol assumes that the user has substantially optimized a cross-polarization transfer prior to beginning. CP optimization is best performed using a 1D sequence.

HETCOR has similar sensitivity to CPMAS experiments. It may be preferable to perform significant optimization on an isotopically enriched set-up sample if available. The ^{1}H, Hartmann-Hahn CP condition, and FSLG parameters are all largely transferrable from sample to sample if the probe configuration is unchanged.
However, if there is a serious difference in the tuning and matching between samples, re-optimization may be required.

Samples with very poor CP transfer efficiency (e.g., highly dynamic environments) or small heteronuclear dipolar couplings will not perform well using this protocol.

Materials

Definitions:

1. CP: Cross polarization
2. MAS: Magic Angle Spinning
3. rf: Radiofrequency
4. HH: Hartmann-Hahn
5. FSLG: Frequency Switched Lee Goldberg
6. t_1: Evolution time

Safety warnings

Unless low-power proton decoupling is used, user must ensure that the total high-power time is less than 50 ms or the limit of the probe, whichever is less.

Before start

User should be familiar with the power, duty cycle, and decoupling limits of the probe.

Unless low-power proton decoupling is used, user must ensure that the total high-power time is less than 50 ms or the limit of the probe, whichever is less.

Expected amount of time SOP will use: 1 hour to 1 day, depending on sample sensitivity.

Procedure

1 Begin with an optimized ^{1}H pulse width and power and CP condition.

2 Load the **lghetfq** pulse program. It will need to be immediately converted to a 2D experiment before proceeding.

3 Set the following initial parameters. These will likely not require significant additional optimization.

3.1 **aq**: Set to 50 ms or less. This is required for the safety of the probe.

3.2 **d1**: Set to 1.3 × $T_1(^{1}H)$. Ensure that the time is at least 20 times longer than **aq**; for example, if **aq** is 50 ms, **d1** should be at least 1 s.

> Note
>
> If significant t_1 noise is encountered, **d1** can be reduced from 1.3 × $T_1(^{1}H)$ as long as it remains 20 times longer than **aq**.

3.3 **o1**: Set the X transmitter frequency to the desired center of expected X chemical shift range.

3.4 **o2**: Set the ^{1}H transmitter frequency to the low-frequency edge of the ^{1}H chemical shift range.

3.5 **p15**: Set to the previously optimized CP contact pulse length. This will likely be longer than optimal for probing short-range correlations, but will allow for greater sensitivity during the optimization process.

3.6 **plw1**: Set to the previously optimized X power for CP.

> Note
>
> Note that the sequence inherently uses a square pulse for the X channel CP contact pulse. If your CP condition was previously optimized using a shaped pulse on the X channel, you will need to reoptimize your condition.

3.7 **cpdprg2**: Set to an appropriate decoupling sequence such as SPINAL64.

3.8 **pcpd2**: Set the decoupling pulse length as appropriate for the chosen decoupling sequence. This pulse uses **plw12** for power.

3.9 **p3**: Set to a previously optimized ^{1}H excitation pulse width at **plw12**.

3.10 **plw12:** Set to a previously optimized ^{1}H pulse power for the excitation pulse **p3** and decoupling pulse **pcpd2**.

3.11 **spnam0**: Set to the previously optimized ^{1}H CP contact pulse shape.

3.12 **spw0**: Set to the previously optimized ^{1}H CP contact pulse power.

4 Set the following initial FSLG parameters.

4.1 **cnst24**: Set to 0. This parameter is used to shift the ^{1}H axis away from the transmitter frequency to avoid artefacts and can be adjusted later.

4.2 **plw13**: Set to a previously optimized ^{1}H pulse power. This can be the same value as the ^{1}H excitation pulse power **plw12**.

4.3 **cnst20**: Set to the ^{1}H rf field strength at **plw13**, as expressed in Hz. This value is used to calculate the FSLG pulse widths and frequency offsets. Starting with a well-calibrated ^{1}H pulse power will minimize the amount of optimization of **cnst20** that is required. Higher power usually provides better resolution, particularly when run on higher field magnets.

5 Set the following 2D parameters using **eda** and **edp**:

5.1 **1 sw:** Set an initial value of sw to ensure that the F1 sweep width is large enough to observe the expected ^{1}H chemical shift range. Note that because **o2** is set to the low-frequency edge of the ^{1}H spectrum, peaks will only appear in half of the spectral width. 30 to 40 ppm is a reasonable default value. Note the value of **in_f** for later reference.

5.2 **1 td**: set to a short value for initial calibration of the sequence, e.g., 4.

5.3 **FnMode:** set to States-TPPI.

5.4 **mc2**: Set to States-TPPI.

6 Run the **ased** command to compile the pulse sequence. Change the value of **l3** such that **dwellf1** is close to the desired value of **in_f**. Set **in_f** to the same value as **dwellf1**.

Note

l3 adjusts the number of FLSG pulse pairs per t_1 increment, effectively setting the F1 spectral width. The value of **dwellf1** adjusts the F1 chemical shift axis for the 0.578 scaling factor inherent to FSLG chemical shifts, which should assist with assigning ^{1}H resonances.

7 With a minimal number of scans and **1 td** points, acquire a 2D spectrum. This should only take a few seconds.

7.1 Ensure that the F1 spectral width encompasses the desired chemical shift range. Adjust **o2p** and **l3** as needed.

7.2 If there is a significant artefact in F1 along the ^{1}H transmitter **o2** which is overlapping with peaks of interest, set **cnst24** to -1000 or -2000. This adds an offset to the LG frequencies which should reduce the overlap.

8 If sensitivity permits, **cnst20** can be optimized to maximize resolution:

8.1 Increase **1 td** to a sufficiently high value that ^{1}H resolution is not limited by the digitization.

8.2 Create multiple experiment environments. In each experiment, change **cnst20** slightly. An error of 0.05 µs in the ^{1}H power calibration corresponds to about 2 kHz in **cnst20**.

8.3 Run the experiments in series. Compare the F1 resolution and select the value of **cnst20** with the best performance.

8.4 If the ^{1}H power is substantially mis-set, recalibration via a ^{1}H 1D or X{^{1}H} CPMAS experiment may be more efficient than via **cnst20**.

9 Once FLSG performance is satisfactory, prepare to run the actual experiment:

9.1 Increase **1 td** to minimize truncation artefacts in sharp peaks.

9.2 Reduce **p15** to a short value, typically between 50 µs to 250 µs. Shorter values will reduce signal originating from distant protons.

9.3 Increase **ns** to best make use of experiment time, recognizing that the reduction in **p15** will reduce overall sensitivity.

10 Acquire the experiment. Reference the ^{1}H axis by comparison to a well-resolved peak in a ^{1}H 1D experiment.

Protocol references

van Rossum, B. J.; Förster, H.; de Groot, H. J. M. High-Field and High-Speed CP-MAS 13C NMR Heteronuclear Dipolar-Correlation Spectroscopy of Solids with Frequency-Switched Lee–Goldburg Homonuclear Decoupling. Journal of Magnetic Resonance 1997, 124 (2), 516-519. DOI: 10.1006/jmre.1996.1089.

Bruker Solid State NMR User Manual Z4D10641B, Section 8

Protocol

NAME

CPMAS

CREATED BY

NMRFAM Facility

Preview

Example Data at 1.1 GHz: usnan.org/ark:/83454/e1b940ec4e-f072-4483-b63a-6b441d95b989
Example Data at 900 MHz: usnan.org/ark:/83454/e1c0445eb4-375e-4890-b15b-d2f203376ade
Example Data at 600 MHz: usnan.org/ark:/83454/e1f63b7c63-cd75-4b5e-830f-17f1237f0f39