Manchester Experiments

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Section: liquids

Abstract We provide pulse programs, au macros, parameter files for a set of experiments including various pure shift (i.e. homodecoupled) and diffusion NMR methods. Where selective or adiabatic pulse waveforms are used, the experiments are compatible with automatic update by WaveMaker. Installation is in three stages. First, copy the contents of the par.catalog folder to %USERPROFILE%/.topspin1/par.catalog (creating this folder if necessary), where %USERPROFILE% is typically C:/<yourusername> for windows, or your home directory for Linux. This ensures the new experiments will remain available from the Experiment Selector in future TopSpin installations. Second, copy the contents of each of the other folders in the zip archive to the corresponding folder in the TopSpin directory. Finally, set up the software by one or other of the methods (1) to (4) below.

1) Open a standard proton parameter set in TopSpin and run the au macro < kp_makepars_r1 y > to create a complete set of experiments. This automatically calls a setup au-macro for each of the experiments in turn, saving par files with default parameters when, as above, the argument y is used. Once the par files have been saved, all experiments are available from the Experiment Selector under the Manchester_Sequences tab in the Personal Library (see Fig.1).

2) Take the parameter sets provided and manually convert them to be compatible with your spectrometer routing.

3) To implement a single experiment from the package, open a standard proton parameter set in TopSpin and run the appropriate setup au macro (kp_set_XX where XX is the pulse program name after kp_) to convert your proton dataset to the desired experiment. You may then want to save a copy of the converted parameter set for use in automation.

4) This is not recommended, but it is also possible to open a standard proton

parameter set and simply change the pulse program to one of those provided. In this case it is your responsibility to manually choose sensible values for all the parameters required for the experiment.

We recommend that you use the first of these methods.

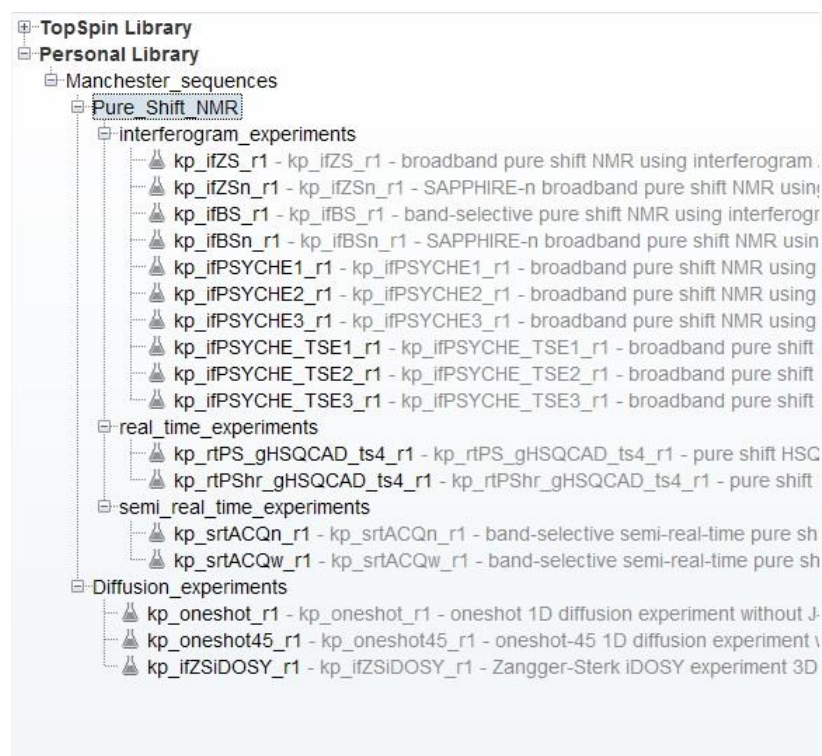**List of pulse programs in this package:**

Fig. 1 The Manchester sequences package can be accessed from the Experiment Selector

Interferogram pure shift experiments: These use 2D style acquisition; results are processed using the au macro pshift4 to create a 1D homodecoupled spectrum in a new experiment number.

kp_ifZS_r1: broadband homodecoupling by the Zangger-Sterk method.

kp_ifBS_r1: band-selective homodecoupling, to observe one or more protons of interest (that are not mutually coupled) in a chosen frequency band.

kp_ifZSn_r1: SAPPHIRE version of broadband homodecoupling by the Zangger-Sterk method. This experiment uses 3D acquisition, in which F2 defines the SAPPHIRE steps. This costs no additional experiment time (it only affects the minimum number of scans needed) and is recommended for high dynamic range problems as it gives very clean spectra. Homodecoupling sidebands can be cancelled progressively by using increasing numbers of steps in F2. The current TopSpin version and this implementation support the use of any even number, but 4 will normally suffice. The resulting 3D data should be processed using the au macro pshift4n. This will create two additional experiment numbers, one for the final 1D

pure shift spectrum and one containing the individual pure shift spectra for each of the SAPPHIRE steps defined in F2. The final pure shift 1D fid is the sum of the fids in the latter ser file.

kp_ifBSn_r1: SAPPHIRE band-selective homodecoupling. See comments on SAPPHIRE above.

kp_ifPSYCHEi_r1 (i=1,2,3): broadband homodecoupling by the PSYCHE method, with the following options for the small flip angle chirp/wurst pulses: 1) two chirp pulses with opposite sweep directions; 2) two saltire pulses; or 3) a single saltire pulse.

kp_ifPSYCHE_TSEi_r1 (i=1,2,3): broadband homodecoupling by the PSYCHE method, using the triple spin echo method for improved strong coupling tolerance, with the same three PSYCHE element options as before.

Real-time pure shift experiments: Unlike interferogram methods these take no more time than the parent experiment, acquiring data with broadband homodecoupling using the BIRD method. Note that this does not suppress geminal methylene couplings and only works for protons directly bonded to carbon, and that relaxation losses cause some additional broadening of the homodecoupled signals.

kp_rtPS_gHSQCAD_ts4_r1: HSQC with adiabatic carbon pulses and gradient selection. AQ duration is limited to avoid probe damage, but decoupling parameters are similar to standard adiabatic decoupling.

kp_rtPShr_gHSQCAD_ts4_r1: HSQC with adiabatic carbon pulses and gradient selection. Decoupling power level is more limited, allowing longer AQ for higher proton resolution. The decoupling parameters should be adjusted according to the needs of the sample, e.g. limiting the bandwidth of the adiabatic pulse to cover only the relevant region.

Semi-real-time pure shift experiments: These allow time-efficient band-selective observation of one or more protons of interest (that are not mutually coupled) in a chosen frequency band. Experiment time is twice that of the parent experiment and there is little or no additional line broadening, in contrast to real-time experiments. See the specific manual for these experiments, submitted to the Bruker Users' Library as srtACQ.zip in Nov 2018. Step-by-step instruction for using semi-real-time experiments are given in the srtACQ_README.pdf file.

kp_srtACQn_r1: Passive spin frequency list has to be created for this version.

kp_srtACQw_r1: No need for prior knowledge of passive spins, but a slight signal broadening appears, less than for real-time experiments.

Diffusion experiments:

kp_oneshot_r1: DOSY Oneshot experiment. This is a good general purpose DOSY sequence, and provides more reliable diffusion data than other methods when used with small numbers of scans because it uses the diffusion encoding pulses to enforce selection of the desired magnetisation. For optimum performance a minimum of 8 scans is recommended.

kp_oneshot45_r1: DOSY Oneshot experiment using a 45° purge pulse to suppress the effects of J-modulation. Again for optimum performance a minimum of 8 scans is recommended. This version is recommended for coupled spin systems where the combined duration of the diffusion encoding pulse and stabilization delay is sufficient to cause substantial J-modulation effects, distorting multiplets.

kp_ifZSiDOSY_r1: This is a 3D experiment in which F1 is used for interferogram Zangger-Sterk pure shift and F2 for diffusion encoding. The au macro pshift4d is provided to concatenate the pure shift chunks and create 2D DOSY data that can be processed as normal. Diffusion calculation has to take into account the additional diffusion-encoding effect of the ZS sequence element.

Additional notes:

The ZS experiments use the combination of a p12/sp12 selective pulse and gpz0 gradient for active spin refocusing. The shaped pulse parameters can be easily changed and updated by using cnst50 for the effective bandwidth definition; ideally this should be less than the minimum difference in frequency between coupled spins. In manual mode the wvm –q command will then update the shape parameters, in automation (xaua) the au_wvm macro provided automatically calls WaveMaker. Any valid WaveMaker waveform definition can be used (e.g. userA1 = rsnob). The slice-selection weak gradient (gpz0) is typically 1-3%, and for optimum sensitivity can be adjusted to cover only the chemical shift range of interest.

The difference [±10-50 µs] between the positive short delays d18 and d19 allows adjustment of the relative timing of the selective pulse and the weak gradient, to correct for the probe-dependent gradient rise and fall times. To set the timing, select a strong sample containing both aromatic and aliphatic protons that cover a representative range of chemical shifts, run the experiment with equal values for d18/d19 (e.g. 16 µs), and process the resulting broadband pure shift spectrum. Adjust the difference between d18 and d19 to minimize the PHC1 needed; this procedure does not need high resolution, and can be usually done quickly with no more than 4 chunks and NS = 2. It is advisable to keep the PHC1 value below 30° to minimise baseline distortions. The optimal difference between d18 and d19 depends on the probe and gradient amplifier used, but not on the sample.

After acquisition of interferogram pure shift raw data, the chunks need to be concatenated by the pshift4 au macro provided. This has been developed for the native double precision data acquisition used in Neo spectrometers. If automatic sertoint conversion is applied (which we do not recommend) or data were acquired with an Avance spectrometer and TopSpin 3, then pshift4 will convert the integer

data to double format.

The SAPPHIRE experiment allows any even user-chosen number of SAPPHIRE steps TD2. Higher order sidebands can be suppressed by using more SAPPHIRE steps. For optimum results SW3/(TD2 SW1) should be an integer, but this is not critical. The default parameters provided should be fine for general use; unusually wide multiplets may need a higher SW1, conversely if all multiplets are narrow than a lower SW1 will reduce experiment time.

The HSQC pure shift experiments include a hardware protection feature that may not be appropriate for non-Neo spectrometers. High resolution results, with a long AQ, are needed to take full advantage of pure shift acquisition, but this can be dangerous due to the use of high power broadband decoupling. Using WaveMaker and appropriate parameter settings, adiabatic ^{13}C decoupling can be optimised to minimise sample heating. The pulse program files and setup au macros include a maximum limit for the power used, which should be adjusted to the safe limit for a given spectrometer. The parameters supplied are optimised for a TBI room temperature probe; two experiments are provided, one with conservative and one with more ambitious decoupling.

Keywords: pure shift, homodecoupling, broadband, Zangger-Sterk

Contents: pulse program (/pp), au-macros (/au), parameter file (/par), and README file.

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Compatibility: The pulse program code was developed using on an Avance Neo spectrometer running TopSpin 4, but with the exception of the real-time HSQC and semi-real-time pure shift experiments it is expected to be compatible with legacy Avance systems and TopSpin 3.

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