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Simultaneously Enhancing Spectral Resolution and Sensitivity in Heteronuclear Correlation NMR Spectroscopy**

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A method for acquiring pure shift heteronuclear single quantum correlation (HSQC) NMR spectra in real time is described. A windowed acquisition scheme consisting of trains of bilinear rotation decoupling (BIRD) refocusing elements is used to acquire chunks of data with refocused J modulation while suppressing J resolution in the spectra of complex species. It has recently been shown that it is possible to extend the pure shift methods currently used, which rely on stitching together separate measurements of short periods of decoupled signal, to real-time acquisition, in which homonuclear couplings are periodically refocused, by applying appropriate spin manipulations during the acquisition of a single free-induction decay. Such J-refocusing sequence elements are generally designed to be broadband, as distinct from classical selective or band-selective homodecoupling; in the case of HSQC J-refocusing uses a BIRD pulse sequence element and a hard (nonselective) 180° pulse. The BIRD sequence element, which, as its name suggests, was originally intended for broadband homonuclear decoupling, has, until recently, been used almost exclusively for decoupling in the indirect dimension of heteronuclear 2D experiments. Here, the combined effect of the BIRD sequence and the hard 180° pulse is to invert only those protons not directly coupled to 13C, thus refocusing the effects of couplings between the latter protons and protons that are directly coupled (bonded) to 13C and whose signals are recorded in HSQC. The great advantage of the BIRD method here is that, in contrast to Zangger–Sterk type methods, it incurs no extra sensitivity penalty; indeed, the sensitivity is generally increased.

The BIRD sequence element has already been very effectively used to obtain pure shift 1H–13C HSQC spectra and pure shift 1D proton spectra of strongly coupled...
species. In both cases, the pure shift dimension was constructed from multiple separate acquisitions of short chunks of data, requiring ancillary software for the generation of decoupled spectra. Here we demonstrate how pure shift HSQC data with comparable resolution may be obtained much more quickly (to the point where a pure shift spectrum can require less time to acquire than a conventional spectrum) and without the need for any extra data processing. The one restriction is that the nucleus observed indirectly, generally $^{13}$C, should not itself show homonuclear coupling; thus, for example, the proposed sequence is not suitable for fully $^{13}$C-labeled compounds.

The pulse sequence used is shown in Figure 1. The initial part of the sequence is a conventional gHSQC, with the J-refocusing element. More frequent J-refocusing gives cleaner spectra, but at the expense of some extra line broadening owing to imperfect refocusing and $T_2$ relaxation. The BIRD real-time acquisition scheme differs slightly in timing from that previously proposed, requiring fewer J-refocusing elements for a given spectral quality. Heteronuclear couplings are suppressed as usual by broadband irradiation (denoted CPD in Figure 1); the intermittent nature of the decoupling limits the types of modulation favored. Because BIRD selects protons directly bonded to $^{13}$C, one class of coupling is not refocused, that between geminal protons. Spectra thus show singlet signals for all $^1$H sites except for nonequivalent methylene protons, for which doublet signals are seen (full details of the sequence are given in the Supporting Information).

Figure 2 illustrates the application of the new real-time pure shift method to $^1$H-$^{13}$C correlated spectra. The conventional gHSQC spectrum (Figure 2a) of $^1$H-$^{13}$C HSQC spectra of d(+)-fucose in D$_2$O with TSP as internal reference: a) conventional gHSQC; b) real-time pure shift gHSQC. 1D traces are integral projections onto the $F_2$ ($^1$H) axis. Data were acquired, processed, and plotted with equivalent parameters, to allow quantitative comparison.

The second part of the sequence is a conventional gHSQC, $^{[21]}$. The data acquisition window, with small delays (ca. 20 $\mu$s) flanking the hard 180° proton pulse set to refocus the chemical shift. The first and last chunks are half in size ($at/2n$) relative to the rest of the chunks ($at/n$). Phase cycling: $\phi_1 = [1 3 5], \phi_2 = [0 2], \phi_3 = [0 2 1]$. All other pulses are of phase 0 (for the explicit phase table, see Table S1).

Figure 1. Pulse sequence for real-time pure shift gHSQC using BIRD. Narrow rectangles are 90° RF pulses, wide are 180° pulses, and wide with a diagonal line are either hard 180° pulses or composite 180° pulses. Gradient pulses $G_1$, $G_2$, $G_3$, follow the normal pattern for gHSQC, and $\tau = 1/(4J_{HC})$. The dotted proton RF pulse (0–2 times the duration of 90° pulse) centered between $\delta_1$ delays is for multiplicity editing; for edited spectra this pulse is 180° and $\delta_1 = 2\tau$, which causes methylene protons to appear with opposite phase to methine and methyl; for unedited spectra this pulse is removed and $\delta_1$ is set to $\delta_2$ plus associated stabilization delay. The second $\delta_2$ delay precedes a delay equivalent to a hard proton 180° pulse, which compensates for the evolution during the 180° pulse in middle of the $t_1$ evolution. Each BIRD/180° J-refocusing block consists of a BIRD element, a hard 180° pulse, and a data acquisition window, with small delays (ca. 20 $\mu$s)...

Figure 2. Selected regions (indicated with dashed lines in the full spectra of Figure S1) of $^1$H-$^{13}$C HSQC spectra of d(+)-fucose in D$_2$O with TSP as internal reference: a) conventional gHSQC; b) real-time pure shift gHSQC. 1D traces are integral projections onto the $F_2$ ($^1$H) axis. Data were acquired, processed, and plotted with equivalent parameters, to allow quantitative comparison.
Similar results were obtained for quinine (Supporting Information, Figure S3); in this case the wider range of \(^{13}\)C chemical shifts means that some degradation in performance is seen at the edges of the spectrum. Any discontinuities in the decoupled signal, such as those caused by \(T_2\) relaxation during the BIRD sequence element, mismatch between the BIRD timing and \(\frac{1}{2}C_{138}\), or a breakdown of the condition \(n \gg (at \times J_{1H})\), will lead to small \(F_2\) sidebands at multiples of \(n t_1\). In the current work, the level of these sideband artifacts is typically around 1% (Figure S5).

The proposed method is also applicable to \(^{1}H\)-\(^{15}\)N correlation, either at natural abundance or in labeled systems where the labels are too far apart for \(^{13}\)N-\(^{15}\)N coupling to be significant (as is generally the case in peptides and proteins). Figure 3 compares conventional and real-time pure shift pure shift \(g\)HSQC spectra for \(^{15}\)N-labeled beta-amyloid peptide 1-42 (\(\alpha\)). The shaded region in the conventional HSQC spectrum (Figure 3a) shows doublet resonances, which are collapsed to singlets in the pure shift HSQC spectrum (Figure 3b). As shown in the spectra, this collapsing of multiplets again improves both the resolution and sensitivity of the signals. Overcrowding in the shaded region is reduced; for example, with overlap between the signals of isoleucines 32 and 41 much reduced in the pure shift spectrum.

In conclusion, the pure shift \(g\)HSQC method described here leads to complete collapse of multiplet resonances into singlets (except for nonequivalent methylene signals, which collapse to doubles). This homonuclear decoupling produces signals with increased intensity and better resolution, lowering detection limits, speeding up experiments, and improving the ability to distinguish between signals in complex spectra. This method is potentially well-suited to automated spectral analysis, as a single signal is seen for each distinct chemical site or correlation.

**Experimental Section**

All experimental data were obtained using a Varian VNMRS 500 MHz spectrometer equipped with a triple resonance (\(\hat{1}\)H/\(^{15}\)C/\(^{15}\)N) triple axis gradient probe of maximum \(z\) gradient 68.5 G cm\(^{-1}\), using GARP\(^{8}\) homonuclear decoupling (\(\gamma_B/2\pi = 4.2\) kHz for \(^{13}\)C, 1.3 kHz for \(^{15}\)N) during data acquisition and BIRD\(^{20}\) composite pulses. The spectra in Figure 2 were acquired at 20°C using a 100 mM sample of \(\alpha\)-(R)-fucose in deuterium oxide, containing trimethylsilyl propionic acid (TSP) as internal reference. The unusually high concentration was used in order to confirm that clean results are obtainable, with artifact signals at around the 1% level. The following experimental and processing parameters were used: a hard 90° \(\hat{1}\)H pulse of duration 10.9 \(\mu\)s, a hard \(^{13}\)C 90° pulse of duration 15.2 \(\mu\)s, a BIP composite 180° pulse (for Figure 2b) of duration 125 \(\mu\)s and bandwidth 25 kHz; INEPT transfer delays \(\tau = 1.66\) ms and BIRD delays \(2\tau = 3.31\) ms (equivalent to \(J_{1H} = 151\) Hz); homospoil gradient pulses of 23.0 G cm\(^{-1}\) (\(G_h\)) and 13.8 G cm\(^{-1}\) (\(G_s\)) of durations 4.0 ms (\(h_s\)) and 2.4 ms (\(h_h\)), respectively; and coherence selection (CTP) gradients of 33.4 G cm\(^{-1}\) (\(G_c\)) and 16.8 G cm\(^{-1}\) (\(G_s\)) of durations 2.0 ms (\(h_s\)) and 1.0 ms (\(h_h\)), respectively; \(\hat{1}\)H spectral width (\(sw\)) was 3592.0 Hz; 4 transients were averaged for each of 2\(\times\)512 free induction decays in which \(t_1\) was incremented to provide a \(^{13}\)C spectral width of 11 467.9 Hz (\(sw\)) in the \(F_1\) dimension; total number of points (\(np\)) stored per FID was 4104, and for Figure 2b \(np = 27\). Data were zero filled to 16 384 \(\times\) 8192, and Gaussian weighting was applied before double Fourier transformation. The total experiment times were 4.2 h for Figure 2a and 4.4 h for Figure 2b, the slightly greater duration for the latter arising from the 27 extra BIRD/180° elements in each FID.

For Figure 3, data were acquired at 25°C using a solution of \(^{15}\)N-labeled \(\alpha\beta\) in [\(D_8\)]dimethylsulfoxide containing H\(_2\)O (5%). Experimental and processing parameters were: a hard 90° \(\hat{1}\)H pulse of duration 12.8 \(\mu\)s, a hard \(^{15}\)N 90° pulse of duration 44 \(\mu\)s, a BIP composite 180° pulse (for Figure 3b) of duration 400 \(\mu\)s and bandwidth 6.5 kHz; INEPT transfer delays \(\tau = 2.78\) ms and BIRD delays \(2\tau = 5.56\) ms (equivalent to \(J_{1H} = 90\) Hz); homospoil gradient pulses of 23.0 G cm\(^{-1}\) (\(G_h\)) and 13.8 G cm\(^{-1}\) (\(G_s\)) of durations 4.0 ms (\(h_s\)) and 2.4 ms (\(h_h\)), respectively; and coherence selection (CTP) gradients of 33.4 G cm\(^{-1}\) (\(G_c\)) and 16.9 G cm\(^{-1}\) (\(G_s\)) of durations 2.0 ms (\(h_s\)) and 0.4 ms (\(h_h\)), respectively; \(\hat{1}\)H spectral width (\(sw\)) was 10.0 kHz; 32 transients were averaged for each of 2\(\times\)64 free induction decays in which \(t_1\) was incremented to provide a \(^{15}\)N spectral width of 3.0 kHz (\(sw\)) in the \(F_1\) dimension; number of points (\(np\)) sampled per FID was 4096, and for Figure 3b \(np = 8\). Data were zero filled to 16 384 \(\times\) 512 and then Fourier transformed without weighting. The total experiment time was approximately 2.7 h in each case.

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