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Non-uniformly sampled Maximum Quantum spectroscopy

Martial Piotto [a], G.N. Manjunatha Reddy [b], Stefano Caldarelli [b,*]

[a] BrukerBioSpin, 34 rue de l'Industrie, 67166 Wissembourg, France
[b] Aix Marseille Université, ISm2 UMR 6263, Campus de Saint Jérôme, Service 512 F-13013 Marseille, France

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ABSTRACT

Maximum-Quantum (MaxQ) NMR is an approach that exploits the simple lineshape (a singlet) of the highest possible coherence quantum order for a given spin system to help resolving the interpretation of the spectrum of complex mixtures. In this setup, resolution in the indirect, multiple-quantum, dimension is crucial, and it may be linked to a long duration of the signal acquired along this axis. We explored if this boundary on the length of the indirect dimension could not necessarily translate into extended experimental times by applying Non-Uniform Sampling (NUS) schemes in conjunction with Recursive Multi-Dimensional Decomposition (R-MDD) data processing. The actual value of the MaxQ order depends on the size of the spin system, so that for a mixture several MQ correlation spectra must be recorded to detect all possible molecular fragments. As the sparseness of the MQ datasets vary dramatically in going from higher (sparser) to lower (denser) coherence orders, the optimal compressing conditions and the fidelity of NUS/R-MDD scheme may vary along the series of MQ spectra. The NUS-MaxQ approach is demonstrated on the aromatic region of the ^{1}H spectrum of a mixture of 10 simple aromatic molecules.

1. Introduction

Maximum-Quantum NMR spectroscopy is a strategy for the investigation of mixtures of small molecules, in which individual spin systems are singled out by excitation of their highest possible quantum coherence [1–3]. The core aspect of this technique is that the spectral complexity is unfolded due to the progressive simplification associated to the excitation of higher and higher order *p*-quantum coherences. For a given spin system, this process culminates in a simple singlet for the maximum possible quantum (MaxQ) order [4]. Accordingly, a correlation spectrum of the MaxQ order with the 1Q spectrum isolates the signals of the molecular fragment hosting the spin system. The method can simplify greatly the analysis of crowded spectral regions, provided the resonance position of the fragment in the MaxQ dimension (the sum of the chemical shifts of the participating spins) can be distinguished. Demonstrations have been provided on the challenging case of mixtures of aromatic compounds (PAH, phenolics), where signals differing by less than 4 Hz (0.001 ppm) in the MaxQ dimension could be distinguished [1–3]. Resolution in the indirect dimension is thus a key aspect of MaxQ analysis, even more so than for most other homonuclear 2D NMR experiments. Moreover, the *p*-quantum coherence lifetime can reach values of the order of the second, which justifies the resolving power mentioned earlier on. Nonetheless, to best capitalize on this property it is necessary to sample extensively the indirect dimension. The demand in spectral resolution of the MaxQ experiment is further reinforced by the likely presence, in a given mixture, of spin systems of different size. Because of this, no single spectrum will provide a complete analysis, but rather a series of *p*-quanta spectra covering all options will be required. The complication proceeds from the fact that for a mixture low-order *p*-quanta spectra are progressively denser in signals, due to the decreased efficiency of the coherence order filter. Altogether, long experimental times (of the order of the hour for mM concentrations) are thus required to obtain a complete analysis, even using PFG coherence order selection and samples providing good signal-to-noise ratios. In the interest of improving the resolution obtained for unit of time of the technique, alternative ways of performing the experiment should be sought. It is noteworthy that multiplex acquisition of all *p*Q order of interest, the first method proposed towards this direction, although being a possible solution for recording all MQ spectra at once, [4–6] is impractical here as each of them requires a very specific and sensitive parameter optimization.

All in all, an approach that has a good probability of reducing the duration of the analysis without significantly altering the multiscale resolution of the experiment is to resort to Non-Uniform Sampling and adapted processing. Indeed, non-linear sampling schemes are finding an increasing utilization due to the intrinsic sparse nature of NMR multidimensional experiments. The effectiveness of sampling grids constructed this way has been demonstrated for a number of cases, either in heteronuclear and homonuclear experiments [7,8].

* Corresponding author.
E-mail address: s.caldarelli@univ-cezanne.fr (S. Caldarelli).

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It should be noted in passing that, besides the interest in reducing their experimental duration, MaxQ experiments on mixtures could prove a solid workhorse for testing NUS schemes, due to the large variation of the degree of sparseness observed along the series of MQ correlation spectra.

Among the recent approaches that appear to produce stable processing of NUS nD NMR data with reasonable computing time, Multi-Dimensional Decomposition (MDD) is among the most tested algorithms [7,8]. Moreover, one of its specific declinations, the Recursive MDD (R-MDD) is suitable for treating bidimensional NMR experiments acquired non-uniformly in the indirect dimension.

In the following, we demonstrate Non-Uniform Sampling, associated with the R-MDD processing approach, on a mixture of ten aromatic compounds containing spin system of between two and five protons, to assess the potential and possible pitfalls of NUS in the context of MaxQ NMR.

2. Experimental

2.1. Nmr

All experiments were performed on a Bruker AVANCE III spectrometer, at a B_0 field of 14.1 T, using a TXI probehead. 5Q and 3Q correlation spectra of a test mixture (Table 1) containing 10 aromatic molecules were recorded using a classic pulse sequence 90_x-τ-180_x-τ-90_ϕ-t_1-90_x ($\phi = x$ or y for even or odd order excitation respectively), [4,5,9,10].

2.2. MDD

The built-in functions of Topspin 3.0 (Bruker Biospin) software were applied to setup the NU sampling schedules and the R-MDD processing for the indirect dimension. Subregions of 0.15 ppm were chosen. See the text below for a discussion on the selection of the number of components of the fit. The sampling followed a random scheme, with a positive bias towards the beginning of the FID for optimal S/N behavior.

2.3. Methodology

This specific data processing has been discussed at length in recent reviews, so that in the following only the basic layout will be outlined [7,8]. Multiway decomposition or PARAFAC is an algorithm designed to separate the sources that make up a complex signal, using a specific model function [11,12]. In synthesis, for a nD NMR the objective of the algorithm is to search the optimal number of signals in the NUS sampled dimensions. Several algorithms have been proposed to perform this operation, and we shall be following the method proposed by Orekhov, based on the Alternate Least Squares approach, [13] which has been demonstrated in several cases.

Table 1
Relevant ^{1}H NMR parameters of the molecular systems in the test mixture.

No.	Molecule (pQ)	1Q chemical shifts	Max-Q chemical shifts
1	Phenol (5Q)	7.25(2), 6,93(1), 6,85(2)	6.96
2	o-Terphenyl (5Q) 4Q	7.22(*), 7.19(*), 7.14(*)	7.13
3	Dibenzyl (5Q)	7.31(*), 7.21(*)	7.18
4	Acetanilide (5Q)	7.61(2), 7.45(2), 7.36(1)	7.43
5	Benzophenone (5Q)	7.83(2), 7.61(1), 7.50(2)	7.59
6	Fluoranthene (4Q)	7.93(2), 7.40(2)	7.70
7	Naphthalene (4Q)	7.61(2), 7.49(2)	7.72
8	Anthracene (4Q)	8.02(2), 7.48(2)	7.78
9	Phenanthrene (4Q)	8.71(1), 7.91(1), 7.67(1), 7.62(1)	8.01
10	Triphenylene (4Q)	8.68(2), 7.68(2)	8.21

The time-domain bidimensional signal associated to a multiple-quantum correlation experiment can be modeled as:

$$S_{MDD}(t_1,t_2) = \sum_1^{N_{MQ}} \alpha(\tau)\mathrm{F}_1(\mathrm{TD}_1)\otimes \mathrm{F}_2(\mathrm{TD}_2) = \sum_1^{N_{MQ}} \alpha(\tau)\mathrm{F}_{11}(\mathrm{d})\otimes\cdots\otimes \mathrm{F}_{1\mathrm{TD}_1/\mathrm{d}}(\mathrm{d})\otimes \mathrm{F}_2(\mathrm{TD}_2) \quad (1)$$

where the sum runs over all resonances involved in the multiple-quantum transitions under scrutiny, $\alpha(\tau)$ being their associated transfer function that takes into account the combined efficiency of excitation and reconversion of higher coherence orders into observable ones. F_1 and F_2 are normalized vectors, describing the shape of the signal in the relative dimension. The labels TD_1 and TD_2 refer to the length of the model shape, and are the acquisition vectors in the respective dimensions.

The right-hand side of Eq. (1) constitutes a further decomposition that exploits the regular expression of the NMR signal to divide it in section of length d, the original indirect dimension being represented as the direct product space of these shorter functions. This step transforms effectively the problem in a (TD_1/d + 1) ways decomposition, thus assuring the existence of a unique solution, which would not be the case for a purely bidimensional problem. To adapt the scheme to Non-Uniform Sampling, the model is multiplied by a mask matrix, g, that has elements 1 in correspondence to sampled points and 0 otherwise.

The approach described above is the basis of the Recursive MDD data processing scheme, which searches the minimization, over all lineshapes F_i and the transfer function α, of the deviation between the model function and the actual data, S,

$$\min_{\{\mathrm{F_i}\},\alpha} \|g(S - S_{\mathrm{MDD}})\|_2 \quad (2)$$

It has been proposed that the computational burden of R-MDD can be eased by Fourier transforming the direct dimension first, and subsequently dividing this section of the model in N subregions corresponding to spectral sections.

$$\sum_{i=1}^{N}\sum_1^{N_{MQ}^R} \alpha(\tau)F_{1,1}(d)\otimes\ldots\otimes F_{1,TD_1/d}(d)\otimes F_{2,i}(TD_2/N) \quad (3)$$

The advantage in the calculation efficiency stems from the fact that the new number of components to fit, N_{MQ}^R, is reduced (see Ref. [8] for a more detailed discussion).

Qualitatively the combination of Recursive MDD and Fourier transform of direct dimension exploits the power of signal dispersion of multidimensional NMR, i.e. its sparseness. Indeed, as the 2D dimensional signals spread over the grid, the density of resonances dilutes. If the direct dimension is first transformed and then cut in strips, fewer components will be required to fit the indirect dimension relative to each subregion, whence the reduced computational burden. This is equivalent to say that the number of components in this reduced frame, N_{MQ}^R, is dramatically reduced. In fact, the maximum compression factor tolerated by a given experiment without significant loss of resolution will depend on the sparseness of the dataset. The estimation of this quantity depends on the details of the lineshapes and it is often left to the appreciation of the experimentalist, but it can be approximated by the number of expected resonances in the undersampled dimensions.

3. Results and discussion

3.1. Resolution per unit time

The molecular set analyzed here consists of mono- and polyaromatic hydrocarbons (Table 1 and Fig. 1), with spin systems ranging from two to five coupled protons, so that a maximum of five coupled protons, corresponding to monosubstituted rings, can be expected [1]. Consequently, a series of 5Q–2Q correlation spectra are required to complete the assignment of all compounds. Indeed, such a strategy was demonstrated in the original work in which MaxQ was introduced [1]. Here, we just focus on the 5Q and 3Q correlation spectra, as they summarize well the extreme situation that can be encountered in MaxQ spectroscopy, namely a well-resolved layout with a few signals. Indeed, the specificity of MaxQ NMR is to detect the singlet associated to the highest coherence order available to a spin system to extract its associated 1Q subspectrum. The number of transitions associated to the given quantum coherence orders relevant to this study are summarized in Table 2. For instance, a monosubstituted aromatic ring will contribute one single resonance to the 5Q spectrum, but as many as 45 to the 3Q spectrum. Table 2 allows therefore a first estimate of the expected complexity of the various MQ order spectra, although only a selected few, the MaxQ ones, are of interest to the analysis. In a given MQ correlation spectrum, MaxQ and not-MaxQ signals can be easily distinguished on the basis of their shape in the indirect dimension, the latter ones presenting a more complex multiplet structure, and by comparison with higher quantum order spectra [1]. For instance, the 3Q–1Q correlation is a MaxQ-one for fluoranthene fused rings, but not for third one, with this latter possessing eight 3Q transitions (Table 2) and thus a more complex spectrum [1].

In the following we first analyze the simpler 5Q–1Q correlation (Fig. 2). Obviously, the 5Q order will provide the sparsest of all possible correlation spectra, being the highest filter level, all signals being MaxQ layouts, which will not be the case of lower quantum correlations. A series of spectra were recorded with the same experimental time, but varying the length of the acquisition in the indirect dimension. To keep the time constant, this extension in length was compensated for by skipping the adequate number of increments. The uniformly sampled 5Q spectrum shows five resonances, as expected from the number of fragments that contains five coupled spins (Fig. 1 and Table 1). All five have MaxQ characteristics, that is to say they are a singlet that correlates to the entire ^{1}H spectrum of the molecular fragment that originates them, and are well resolved. This and the rest of the assignment of the MaxQ signals to a molecular structure is typically straightforward in light of the easy recognition of the associated ^{1}H chemical shifts and signal multiplicity [1]. As in this spectrum the maximum separation between resonances is of 147 Hz, a good discrimination of all MQ signals can be achieved, in principle, already with a signal length in the indirect dimension of the order of 7 ms. However, a priori it is not possible to predict what is the optimal resolution required for this experiment for an unknown mixture, as differences in the order of 4 Hz have been observed for MaxQ signals in mixtures of natural origin, relatively to compounds of the same structural family. Thus, we set to seek for the best possible resolution achievable. Fig. 2A illustrates the resolution enhancement in the 2D spectrum obtained by simultaneously increasing eight times the length of the signal in the MQ dimension and compressing the number of acquired data point by a reciprocal factor. A more precise visual impression of the variation associated to different acquisition/processing scheme is further depicted in Fig. 1B, which reports the projections along the 5Q dimension of four different test cases. Line narrowing in going from the shortest time to the longest vector in the indirect dimension is observed.

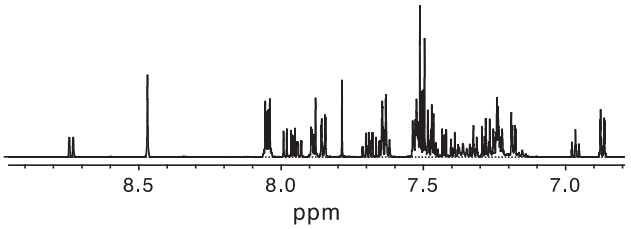

Fig. 1. Aromatic section of the ^{1}H NMR spectrum at 600 MHz of the test mixture. See Table 1 for details on the composition of the mixture.

Table 2
Number of expected resonances in the spin systems of relevance. From Ref. [10].

	0Q	1Q	2Q	3Q	4Q	5Q
ABC	6	15	6	1		
ABCD	27	56	28	8	1	
ABCDE	110	210	120	45	10	1

Processing artifacts generated from R-MDD are introduced, as expected, in the form of t_1-noise. This is exemplified in the spectrum acquired with 4096 data points and 6.25% compression factor (Fig. 1B), where a number of spurious peaks appears. Analysis of the corresponding 2D diagram (not shown) reveals that this anomalous spectral intensity in the indirect dimension does appear in correspondence of the most intense peaks in the discretely acquired spectrum. This kind of spurious peaks is a typical artifact observed in association to the use of a large number of components in the fit and to the high compression factor, but in the case of MaxQ NMR these artifacts can be easily recognized as they do not have a resonance in the MQ dimension that is the sum of the 1Q participating signals. As discussed above, the intrinsic resolution required to achieve perfect separation of all 5Q signals in this mixture is not very high, so that all signals are distinguished even for the shortest time vector. The observed line narrowing stems thus from the extension of the time dimension, so that a similar outcome could be achieved by linear prediction (Fig. 1B). Indeed, the increased resolution obtained by both methods is, in this case is just due to an extrapolation of the signal shapes, and more specifically the extended sampling in the indirect dimension bears no advantage over linear prediction.

The US 3Q spectrum (Fig. 3) is largely more crowded with more resonances than their higher quanta homologue, as in this spectrum can be found contributions from any spin system with at least three coupled spins. Notably, fragment with four or more coupled spins will not produce a MaxQ effect in this spectrum, but rather a more complex pattern, presenting regular multiplets in both dimensions. Thus, it is crucial for a good discrimination of MaxQ vs non-MaxQ resonances not to lose signals in low-order pQ spectra, as this alteration of the patterns would interfere with the global analysis. Thus, although this parameter can be allowed to vary in order to improve the quality of the results, an educated choice is in order. Table 3 summarizes estimates of the N^R_{MQ} for the mixture under analysis, considering that we elected to separate the 1Q dimension, after FT, in subregions of 0.15 ppm, i.e. about 10 sections for the cases under study here. It should be noted that perfect overlap of some signals in the indirect dimension would further reduce the reported values, while the same behavior in the direct dimension would produce the opposite effect. Analysis of Table 3 shows that the 5Q correlation spectrum is almost compressible at will, while, on the other hand, the 3Q one presents a low degree of sparseness. For this latter case a large number of components, of the order of 30, is required to properly describe the signal density.

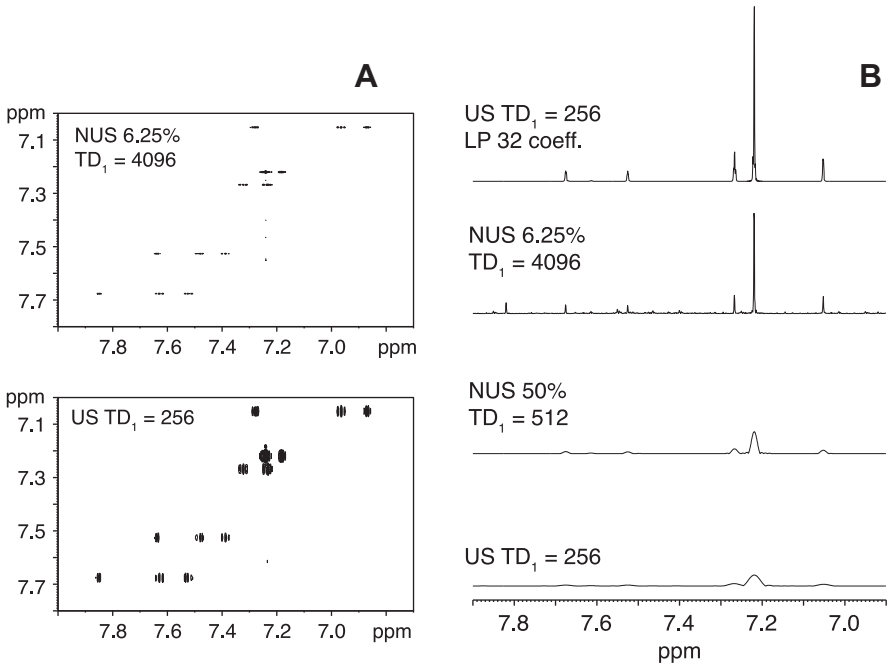

Fig. 2. Comparison of 5Q–1Qs ^{1}H NMR experiments under different US and NUS processing conditions. All spectra were recorded with the same duration and Fourier Transformed to 2048 points in the indirect dimension. All spectra are shown in magnitude. (A) 2D diagrams of a US (bottom) and NUS spectrum, showing the five MaxQ signals. (B) Projections of the 5Q spectra, recorded and processed as indicated, all transformed with 2048 points in the frequency domain.

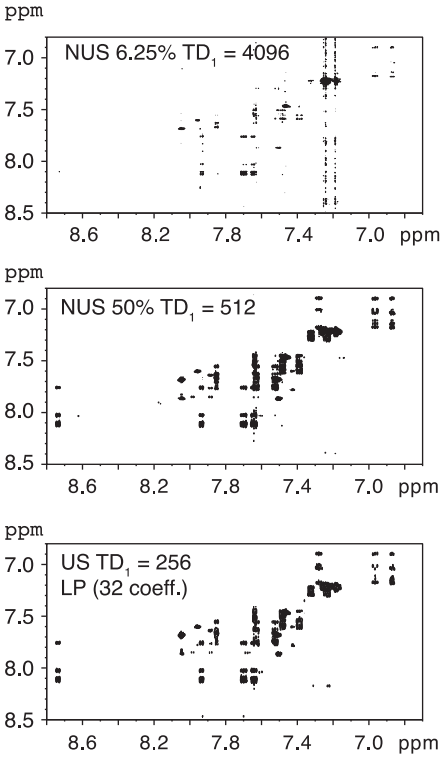

Fig. 3. Comparison of 3Q–1Q correlation spectra recorded and processed with different US and NUS schemes. All spectra were Fourier transformed to 2048 points in the indirect dimension and are shown in magnitude mode.

Indeed, Fig. 3 demonstrates that the R-MDD reconstructed 3Q spectrum acquired with NUS using half of the grid points of the reference spectrum and $N_{MQ} = 30$ is visually similar to the US analogue. Conversely, experiments performed with higher compression factors (and thus longer overall acquisition times) could not reproduce faithfully even some of the main features of the spectrum (Fig. 3, top spectrum).

Table 3
Estimate of the sparseness for the relevant *p*-quantum order for the test mixture.[a]

	5Q	3Q	1Q
Transitions[a]	5	276	1345
Estimated no. of components, N^R_{MQ}[b]	1	28	

[a] Using Table 2 and the number and type of relevant spin systems in the mixture.
[b] Calculated assuming a uniform distribution of the resonances over about 10 spectral regions.

Besides the added complexity, a complete analysis of the faithfulness achieved by compressed acquisition schemes should consider that the signal intensity in a same MQ order for different fragments may vary dramatically on the basis of the concentration but also of the transfer function, [2] so that weak MaxQ singlets may be partially masked by overlapping, more intense, non-MaxQ resonances. This aspect is discussed below.

3.2. Noise level and sensitivity

According to experiments performed on proteins, Non-Uniform Sampling schedules adapted to follow the exponential decay of the NMR resonances maintain the signal density per unit of measurement time, that is to say they decrease as the square root of the experimental time, if the maximum acquisition time is kept the same [13]. A different situation could be expected if the objective of NUS is to increase the resolution per a given amount of time, i.e. keeping constant the number of points acquired while extending the length of the recorded signal (along the indirect dimension). In this case, a degradation of the signal to noise ratio is expected to some extent, as points recorded a longer times have relatively stronger contribution by the noise. Indeed, for variable values of the maximum acquisition time in the indirect dimension, T_{MAX}, the signal-to-noise ratio evolves according to the approximation

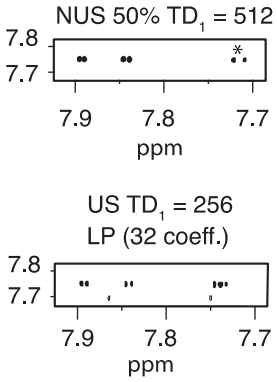

Fig. 4. Comparison of the 3Q spectra of fluoranthene acquired with US (bottom) and NUS (top) schemes. The star indicates a processing artifact.

$$S/N \propto \frac{T_2(1-e^{-T_2/T_{MAX}})}{T_{MAX}} \approx \frac{T_2}{T_{MAX}} \quad (4)$$

which holds for sampling durations in excess of $3T_2$. This effect can be compensated, however, if the sampling is biased towards early points of the FID, although the specific contribution to the S/N of any given point in the acquisition grid should be assessed [14]. An alternative approach, not used here, has been demonstrated recently and it concerns the redistribution of the information over the two dimensions as a function of the result of the fit [15]. In light of all of the above, we explored this issue experimentally by comparing the S/N figures for intense reference peaks in both the 3Q and 5Q spectra. For this latter the degradation of the S/N for a constant time of acquisition is visible for Fig. 2B, recorded with a T_{MAX} of more than 500 ms. As discussed above, high compression levels introduces significant signal losses in the 3Q spectrum.

Further insight comes from monitoring a specific low intensity MaxQ resonance in the 3Q spectrum, located at 7.70 ppm in the MQ dimension, corresponding to fluoranthene, as shown in Fig. 4, which is not recovered faithfully in the NUS spectrum. This signal has the lowest detectable intensity, with a signal-to-noise ratio of about 2.5 in the US experiment and 1.9 in the NUS analogue. However, the presence of a processing artifact in this latter severely misdirect the MaxQ analysis. Indeed, the interest of this experiment is that it facilitates the discovery of molecular fragments in a mixture as it is capable of separating along the indirect dimension the signal of entire spin systems. The assignment of each one of these spin system traces is based on their chemical shifts, which are the same as the regular 1D spectrum, and multiplicity, which may be distorted due to the use of the absolute value in the processing. For mixtures of unknown nature, the appearance of artifacts would thus severely interfere with the discovery process.

Note that such a fine comparison involving peaks of low intensity but of high significance will tend to be overlooked by typical measurements of similarity using n-order statistics and thus the trade-off between faster throughput and a degradation of the experiment sensitivity should be evaluated for each single mixture.

4. Conclusions

High-order MaxQ spectroscopy is particularly suitable for acquisition schemes exploiting sparse sampling, due to the very reduced number of signals populating these particular dimensions, which is devoid of interfering signals and to their simplest lineshapes. These conditions together make the experiment an ideal candidate for Non-Uniform Sampling schemes, which would allow major time savings for cases when the groups of MaxQ signals clusters in different spectral regions. This is a common situation for mixtures in which the components belong to the families with similar chemical structures. As lower order pQ-1Q correlation spectra become more crowded, the performance of acquisitions scheme relying on sparseness degrades accordingly, but still remains a possible alternative for a quick evaluation of the spectral layout, if the signal-to-noise ratio is adequate.

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References

[1] M.R.G.N.S. Caldarelli, Demixing of severely overlapping NMR spectra through Multiple-Quantum NMR, Analytical Chemistry 82 (2010) 3266–3269.
[2] G.N.M. Reddy, S. Caldarelli, Maximum-quantum (MaxQ) NMR for the speciation of mixtures of phenolic molecules, Chemical Communications 47 (2011) 4297–4299.
[3] G.N.M. Reddy, S. Caldarelli, Identification and Quantification of EPA 16 Priority Polycyclic Aromatic Hydrocarbon Pollutants by Maximum-Quantum (MaxQ) NMR, submitted for publication.
[4] A. Pines, D. Wemmer, J. Tang, S. Sinton, Bulletin of the American Physical Society 23 (1978) 21.
[5] A. Wokaun, R.R. Ernst, Chemical Physics Letters 52 (1977) 407.
[6] G. Drobny, A. Pines, S. Sinton, D. Weitekamp, D. Wemmer, Fourier transform Multiple Quantum NMR, Faraday Division of Chemical Society Symposium 8 (1979) 49–55.
[7] K. Kazimierczuk, J. Stanek, A. Zawadzka-Kazimierczuk, W. Kozminski, Random sampling in multidimensional NMR spectroscopy, Progress in Nuclear Magnetic Resonance Spectroscopy 57 (2010) 420–434.
[8] V.Y. Orekhov, V.A. Jaravine, Analysis of non-uniformly sampled spectra with multi-dimensional decomposition, Progress in Nuclear Magnetic Resonance Spectroscopy 59 (2011) 271–292.
[9] T.J. Norwood, Multiple-quantum NMR methods, Progress in Nuclear Magnetic Resonance Spectroscopy 24 (1992) 295–375.
[10] Richard R. Ernst, Geoffrey Bodenhausen, A. Wokaun, Principles of Nuclear Magnetic Resonance in One and Two Dimensions, Clarendon Press, Oxford, UK, 1990.
[11] J. Carroll, J. Chang, Analysis of individual differences in multidimensional scaling via an n-way generalization of "eckart-young" decomposition, Psychometrika 35 (1970) 283–319.
[12] R. Harshman, Foundations of the PARAFAC procedure: models and conditions for an "exploratory" multimodal factor analysis, UCLA Working Papers in Phonetics 16 (1970) 1–84.
[13] V. Jaravine, I. Ibraghimov, V.Y. Orekhov, Removal of a time barrier for high-resolution multidimensional NMR spectroscopy, Nature Methods 3 (2006) 605–607.
[14] H. Celik, A.J. Shaka, V.A. Mandelshtam, Sensitivity analysis of solutions of the harmonic inversion problem: are all data points created equal?, Journal of Magnetic Resonance 206 (2010) 120–126
[15] Y. Matsuki, M.T. Eddy, J. Herzfeld, Spectroscopy by integration of frequency and time domain information for fast acquisition of high-resolution dark spectra, Journal of the American Chemical Society 131 (2009) 4648–4656.