MAGNETIC RESONANCE IN CHEMISTRY, VOL. 36, 135–136 (1998)

Note

A Post-processing Method for Clean-up of t_1 Noise in HMBC Spectra

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Received 27 June 1997; revised 29 September 1997; accepted 30 September 1997

ABSTRACT: A simple post-processing method for clean-up of t_1 noise in HMBC spectra based of scaling individual F_1 traces is described. The method does not address the origin of t_1 noise but improves the presentation of the spectra and facilitates manual interpretation and automatic peak picking. © 1998 John Wiley & Sons, Ltd.

KEYWORDS: NMR; HMBC; t_1 noise scaling

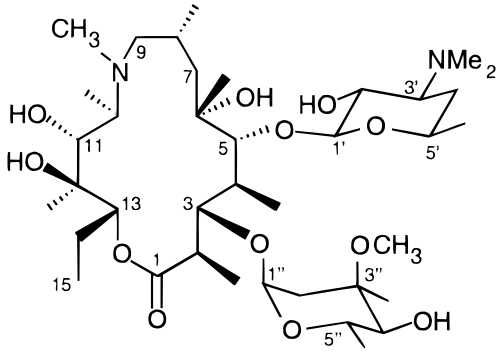
INTRODUCTION

The HMBC (heteronuclear multiple bond correlation) experiment[1–3] has become one of the cornerstone techniques for the structure determination of unknown organic molecules. HMBC spectra, however, are usually marred by strong t_1 noise, which complicates their interpretation especially around strong signals such as those of isolated methyl groups. The use of a pulsed-field gradient (PFG) version of HMBC[4–6] has resulted in a dramatic improvement in spectral quality. Many spectrometers, however, are still not capable of performing PFG experiments. In this paper we present a simple post-processing scheme for improving the appearance of HMBC spectra, facilitating their analysis.

RESULTS AND DISCUSSION

Post-processing schemes for reduction of t_1 noise in HMBC spectra have been proposed previously. One such scheme is based on subtraction of a projection of a noise region.[3] Another more elaborate scheme is based on the method of reference deconvolution.[7,8] Other related methods have been applied to different kinds of spectra.[9–12] The present scheme relies on differential scaling of each trace along the F_1 dimension by a factor proportional to the r.m.s. noise of that trace. It takes advantage of the fact that t_1 noise is usually associated with intense peaks which can be scaled down without significant loss of information content.

A typical result of the present scheme is shown in Fig. 1, an HMBC spectrum of the macrolide antibiotic azithromycin (**1**)[13,14] before and after applying the proposed scheme. As can be seen, the ridges are no longer visible and the display gain could be increased to show weak correlations on the same plot. Furthermore, the spectrum is now amenable to automatic peak picking with minimal user intervention.



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We implemented this scheme for use with Varian data as a C program which is called from within Vnmr (the source code is available upon request). The user surrounds a noise region along the F_1 dimension by two cursors and types a single command. The exact choice of the noise region is not very critical.

The scheme presented here has been applied advantageously to HMBC spectra of a wide variety of compounds. It can also be applied to other types of spectra such as HMQC or HMQC-TOCSY although t_1 noise in these spectra is less of a problem than in HMBC spectra. Unlike the method of reference deconvolution,[7,8] it does not address the origin of t_1 noise. It is, however, simpler to implement and has no special requirements for data acquisition, and thus can be applied to old data. In our hands, it gave better results than subtracting noise projection.[3] As with any other non-linear post-processing scheme, treated spectra should be labeled as such.

EXPERIMENTAL

The spectrum shown in Fig. 1 was collected on a Varian Unity-500 spectrometer on a sample of 7.5 mg in $CDCl_3$ using 32 transients per increment and a delay optimized for a long-range ^1H–^{13}C coupling of 5 Hz.

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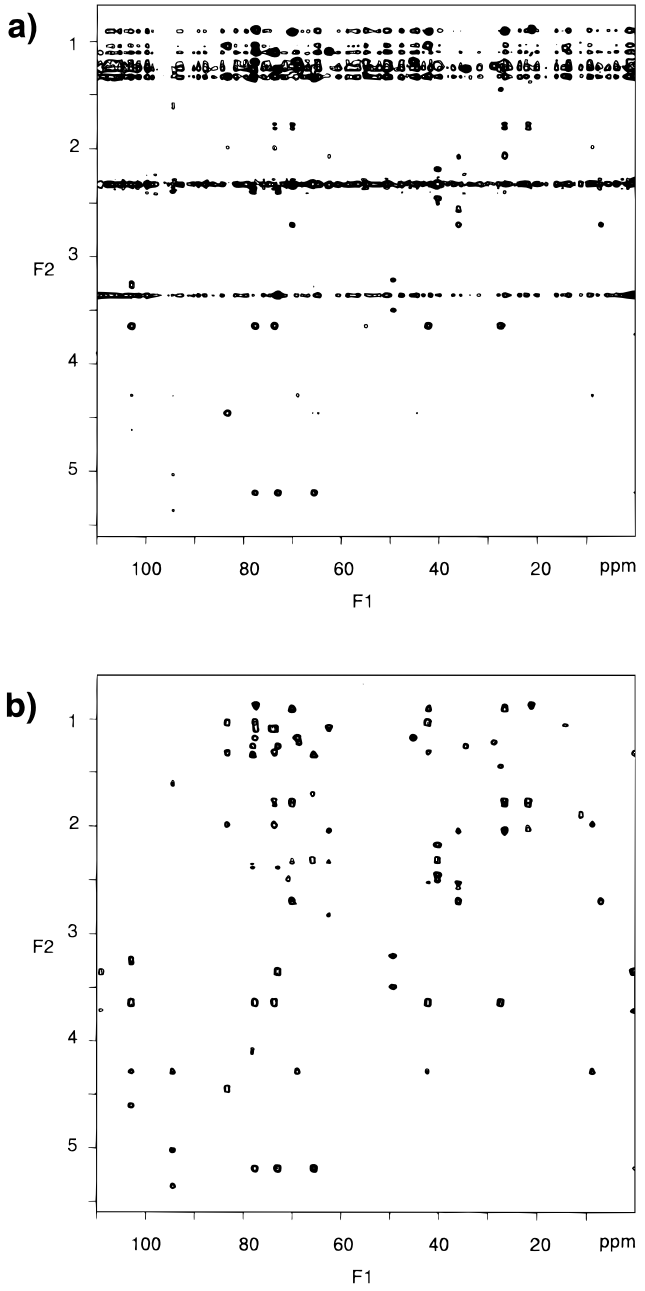

Figure 1. (a) HMBC spectrum of the macrolide antibiotic azithromycin (**1**) showing intense t_1 noise. (b) The same spectrum after t_1 noise clean-up using the scheme described.

The acquisition times in F_1 and F_2 were 0.1 and 0.01 s, respectively. The size of the final matrix was 1024 × 1024 points. The carbonyl signal (178.8 ppm) was allowed to fold over in F_1 at 68.8 ppm.

Acknowledgement

I thank Dr Ronald W. Ratcliffe for proving a sample of azithromycin.

REFERENCES

1. A. Bax and M. F. Summers, *J. Am. Chem. Soc.* **108**, 2093 (1986).
2. M. F. Summers, L. G. Marzilli and A. Bax, *J. Am. Chem. Soc.* **108**, 4285 (1986).
3. A. Bax and D. Marion, *J. Magn. Reson.* **78**, 186 (1988).
4. R. E. Hurd and B. K. John, *J. Magn. Reson.* **91**, 648 (1991).
5. P. L. Rinaldi and P. A. Keifer, *J. Magn. Reson. A* **108**, 259 (1992).
6. W. Willker, D. Leibfritz, R. Kerssebaum and W. Bermel, *Magn. Reson. Chem.* **31**, 287 (1993).
7. A. Gibbs, G. A. Morris, A. G. Swanson and D. Cowburn, *J. Magn. Reson. A* **101**, 351 (1993).
8. T. J. Horne and G. A. Morris, *J. Magn. Reson. A* **123**, 246 (1996).
9. G. Zhu, A. Renwick and A. Bax, *J. Magn. Reson. A* **110**, 257 (1994).
10. D. Uhrin, V. Varma and J.-R. Brisson, *J. Magn. Reson. A* **119**, 120 (1996),
11. A. Ziegler, M. Izquierdo, C. Remy and M. Decorps, *J. Magn. Reson. B* **107**, 10 (1995).
12. A. Ziegler and M. Decorps, *J. Magn. Reson. B* **102**, 26 (1993).
13. J. Barber, *Magn. Reson. Chem.* **29**, 740 (1991).
14. R. J. Brennan and J. Barber, *Magn. Reson. Chem.* **30**, 327 (1992).

