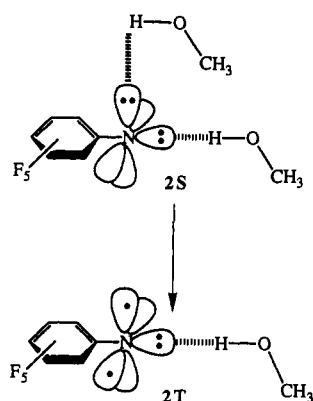


bending modes and can thereby catalyze the ISC process. Alternatively methanol may preferentially stabilize the singlet state of the nitrene which forms two hydrogen bonds, relative to the triplet state which forms only a single hydrogen bond.¹⁹ Reducing the singlet-triplet energy gap is expected to result in an increased rate of ISC.¹⁸ Experiments are in progress with other nitrenes to establish the generality of the alcohol effect.



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Supplementary Material Available: A matrix spectrum of **2T**, a solution-phase transient spectrum of **2S** or **7** in acetonitrile, the matrix spectrum of ³PN, and a transient spectrum of KET (4 pages). Ordering information is given on any current masthead page.

(19) Effects of this type are responsible for shifting $n \rightarrow \pi^*$ absorption maxima of ketones. The absorption maximum of acetone is shifted from 279 to 264.5 nm between hexane and water, an amount corresponding to 5 kcal/mol; $n \rightarrow \pi^*$ excitation destroys one hydrogen bonding interaction. See: Jaffé, H. H.; Orchin, M. *Theory and Applications of Ultraviolet Spectroscopy*; Wiley: New York, NY, 1962; p 187.

Correlation Spectroscopy at a Bargain: SIMPLE-COSY[†]

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Correlation spectroscopy (COSY) of J -coupled spins was the first representative^{1,2} of multidimensional experiments, which have revolutionized NMR spectroscopy.³ Various methods have been developed to get pure-phase spectra with quadrature detection in both dimensions. Multiple-quantum filtering is frequently used⁴ resulting in diagonal peaks also of pure absorption phase, as well as reduced cross-peak multiplet structure.⁵ Attempts have been made to suppress diagonal peaks in homonuclear correlations.⁶

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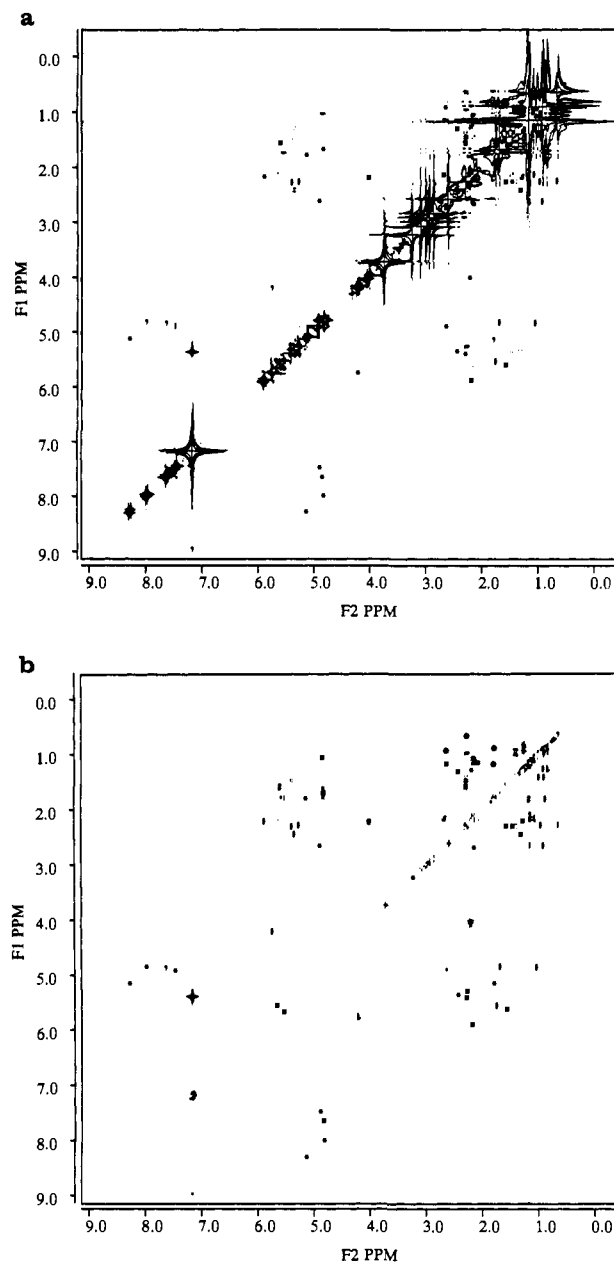


Figure 1. Two stages of the SIMPLE-COSY procedure for cyclosporin A, measured in C_6D_6 at 303 K at 500.1 MHz on a GN-500 spectrometer: (a) pure-phase spectrum with huge dispersive diagonal peaks, (b) which are removed via the method described in the text. One percent of the full spectrum was zeroed along the diagonal. Some residual intensities at higher fields are due to incompletely suppressed truncation of more intense overlapping signals.

However, each of these experimental modifications results in a more complicated acquisition scheme and increases the minimum number of scans to be acquired.

Recently, a witty simplification has been introduced to substitute MQ filtering with subtraction of a reference 2D set containing only the diagonal peaks.⁷ Marion and Bax have improved this approach by synthesizing the latter reference 2D from a carefully adjusted 1D spectrum.⁸ This P.COSY has been proven to be the most economical and fastest way to get a pure absorption phase COSY spectrum, so far.

We present here an even faster and the most simple way to create a full-power pure-phase COSY spectrum (SIMPLE-COSY or S.COSY). This approach does not need extra care in setting up the experiment and requires less effort in computation in

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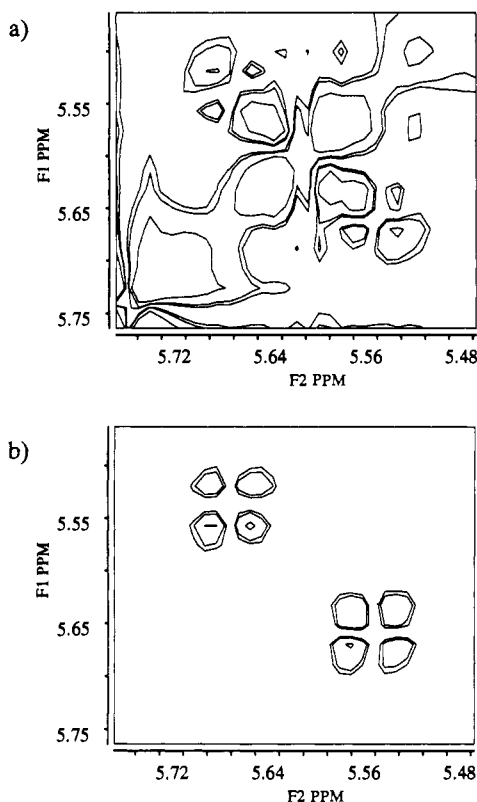


Figure 2. Enlarged section of the correlation region for H- ϵ and H- ζ protons of the MeBmt residue¹¹ (a) before and (b) after appropriate data handling. For all the figures, the same positive and negative contour levels were plotted without discrimination. All data processing was accomplished by the NMR2 software (New Methods Research, Inc., Syracuse, NY).

comparison with other methods. The essential step is selective removal of the 90° out-of-phase diagonal peaks from the familiar pure-phase two-dimensional spectrum through simple data processing maneuvers. It can be accomplished by successive absorptive-dispersive phase setting, deletion of unwanted signals, and reconstruction of imaginaries by Hilbert transformation⁹ for

rephasing. This approach minimizes the necessary number of scans to one in the ultimate case,¹⁰ when sign discrimination is achieved by setting the carrier at one end of the region of interest. The data processing procedure includes the following major steps: phasing the diagonal peaks to pure absorption in both dimensions, removal (or, alternatively, scaling) of the diagonal, replacement of imaginary data using Hilbert transformation, and rephasing in both dimensions by 90°. All this is straightforward to automate if simple autophase routines are provided. The ultimately simple experimental setup and automated computation make the overall procedure extremely user-friendly.

As an example, applying this strategy in two dimensions, the S.COSY spectrum of cyclosporin A¹¹ is shown (Figure 1). The presented data were previously acquired as the measured 2D counterpart for a P.COSY experiment. All the information involved in a pure-phase spectrum is retained. Cross peaks, even very close to the diagonal, are well seen and easy to analyze (Figure 2).

In conclusion, an ultimately simple and easy to automate overall procedure (SIMPLE-COSY) has been developed for acquisition and data processing of *J*-correlation spectra. In the presented approach, only a single dataset needs to be acquired, which is processed by using successive absorption-dispersion phasing, removing the diagonal, and rephasing data by the help of Hilbert transformation. The strategy is applicable in more than two dimensions, too, and could be useful in all cases when diagonal and cross peaks have a uniform phase difference.

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Note Added in Proof. Recently a closely related approach has been published (Tsang, P.; Wright, P. E.; Rance, M. *J. Magn. Reson.* **1990**, *88*, 210), focusing on 1D applications.

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Computer Software Reviews

Alchemy II for Macintosh. Version 1.00. Tripos Associates Inc.: 1699 S. Hanley Road, Suite 303, St. Louis, MO 63144. List price \$950.00; educational discounted price \$650.00.

At long last, action on the Macintosh molecular modeling front is heating up, and several very useful packages have recently become available. These include Chem3D Plus from Cambridge Scientific Computing, PC Model for the Macintosh from Serina Software, Microchem by Anthony Hopfinger (University of Illinois at Chicago), and the subject of this review, Alchemy II from Tripos Associates. A recent review of Alchemy II published in *MacWorld* (Charles Seiter, *MacWorld*, October 1990 issue, p 235) provides a brief comparison of the capabilities of Alchemy II and Chem3D (the latter includes "MM2 with pi-electron calculation and a basic molecular dynamics capability").

This review focuses upon the capabilities and limitations of Alchemy II for Macintosh, which requires an 8-bit color Mac system with a minimum of 2 Mb of RAM (the review was done using a Mac II with 8 Mb of RAM, and giving Alchemy II a 1Mb MultiFinder partition, System 6.0.5, and 32 bit quickdraw installed). In brief, this is a very stable, professional program, which would be highly useful for practicing lab chemists and educators. It sports an interesting, very easy to use 3D drawing interface, a minimizer for obtaining reasonable conformations, and outstanding, essentially real time rotation and translation of color

framework models. It also provides very nice color space-filling models and ball-and-stick models at a useful speed, though far from real time (converting a DNA duplex framework model to an 8-bit shaded color graphic such as those used to create the half-tones presented below took about 6 s).

Aside from the excellent features mentioned above, Alchemy II provides the following.

The manual is concise, informative, and very well written. It gives an especially good account of the force field method and provides all the information necessary for creation of custom atom types and parameters. The minimizer included with the program is not the standard MM2, but rather the proprietary Tripos force field. This force field seemed quite useful to me, giving very reasonable minima and strain energies for standard molecules and showing better than VAX 11-780 speeds on the 16-MHz Mac II. There is no capability, however, for dealing with charges, or for minimizing intermolecular interactions. Thus, while one may display many molecules on the screen, it is only possible to minimize one at a time, and the energy obtained is that for the isolated molecule. While it is possible to monitor six interatomic distances for atom pairs in separate molecules in real time during rotation or translation of one of the molecules, I found this approach to "docking" to be very cumbersome.