

## ACD/Spectrus Processor Review

**A**CD/Spectrus Processor is a commercial suite of programs for the analysis of NMR, MS, optical, and chromatographic data.<sup>1</sup> Many readers are likely familiar with an earlier version of the program, ACD/NMR Processor, which only handled NMR data and is still freely available to academics.<sup>2</sup> ACD/Spectrus Processor is a newer, commercial version of this software that is much more user-friendly. This review is restricted to the NMR-related capabilities of ACD/Spectrus Processor and an associated program, ACD/NMR Predictor.

Processing NMR spectra is a bit like heading out to lunch during a work day. Most of the time, one simply wants to grab a quick bite. In ACD/Spectrus Processor, one can simply drag and drop a file, click print, and have a nicely processed spectrum to go. There is no need to adjust any curves or input any esterotic-sounding coefficients. (Of course, the “dining in” option of attending to these fine adjustments is still available.) The “smart” autoprocessing feature is particularly useful for two-dimensional (2D) NMR spectra because the optimal processing procedure varies significantly by experiment and can significantly affect the resultant signal/noise.<sup>3</sup> Another important improvement is that the 2D phasing algorithm is now a robust one, though experts may still want to phase spectra with lower signal/noise manually.

The user workflows for several other useful tasks have also been streamlined. For example, merely dragging the mouse across a multiplet will automatically locate its maxima, integrate it, and determine its coupling constants, ready for incorporation in a journal-formatted report of the form “3.81 (1H, tt,  $J = 7.71, 5.33$  Hz).” Although this can be done automatically for the whole spectrum at once, better results are still obtained manually for anything but the least-crowded of spectra. Still, the multiplet-recognition algorithm is quite good and parses complex first-order patterns correctly most of the time, while rejecting higher-order patterns.

One of the best features of ACD/Spectrus Processor is its ability to generate publication-quality reports (see Figure 1) through an interface with ACD/ChemSketch (freely included). For example, one can copy and paste a “bird’s eye view” spectrum, and then append an inset expansion. Chemical structures and labels are also easy to attach. One particular advantage of using ACD/ChemSketch, as opposed to a third-party application, is that the spectra remain in vector form at a high resolution and do not consume inordinate amounts of memory (which would not be the case if one were to copy spectra as JPEG files, for example). Because the native ACD/Laboratories metadata are retained, it is possible to adjust the display properties of the spectra in ACD/ChemSketch (e.g., add or remove a scale bar), even if the original file in ACD/Spectrus Processor has been lost. Although this may sound like something of a trivial feature, it will come as a considerable relief to those who have struggled with clipboard issues and ChemDraw.

One feature that probably needs more development is the ability to overlay several 1D NMR spectra. This is a common requirement in the organic laboratory, where one often needs

to identify subtle changes between the resonances of the starting materials and products. Although the overlay process itself is quite easy in ACD/Spectrus Processor, a subtle unresolved problem is that the vertical scale within each overlaid spectrum cannot be adjusted independently. This can be a problem when the spectra have very different dynamic ranges. This actually occurs quite frequently. One can have a nice spectrum of starting material with little solvent, and consequently a small dynamic range. In contrast, a reaction aliquot may contain a lot of solvent, and therefore a large dynamic range. When the spectra are overlaid, the solvent resonances may overwhelm the remaining signals. One workaround is to use the ability of ACD/Spectrus Processor to remove solvent residual signals—in effect, deleting part of the spectrum. However, it would be nice to see the ability to adjust the vertical scale of each spectrum independently in the future.

Another useful feature is the ability to process a series of spectra representing the time course of a reaction for a kinetic study. This area is one where the considerably simplified workflow will be well-appreciated by the harassed physical-organic chemist. One can integrate a region in a set of spectra automatically with a wave of the mouse and generate a graph of the resulting integrals with only a couple of clicks. There is even a “brush tool” that will correct for the drift in some peaks over time. The data can then be exported to a text file for further analysis in a spreadsheet program.

ACD/Spectrus Processor can also be integrated with ACD/NMR Predictor. I currently teach a graduate course in NMR spectroscopy, and I find that it is often useful to generate “sanitized” spectra that emphasize certain salient features of a spectrum. In particular, spectra without solvent residual signals, long-range couplings, or other artifacts are often easier for students to interpret. ACD/NMR Predictor is ideal for this task. Most readers will probably find its proton and carbon prediction capabilities to be the most relevant, although some will find its capabilities for predicting other heteronuclei useful as well. The prediction algorithm returns both chemical shifts and coupling constants, so the resulting spectra look fairly authentic. The chemical shifts can either come from a database prediction, or be user-defined if they are known. This latter feature is useful for problem set generation. The predictor can also generate second-order multiplet patterns from a given set of chemical shifts and couplings. However, the predictions are limited to rather small systems, and the reverse process, i.e., fitting of a second-order pattern to some couplings, is not supported. Additionally, it is not possible to adjust the isotopic abundances of the constituent nuclei; for example, one cannot predict the spectrum of a  $^{13}\text{C}$ -labeled compound.

Given that the predicted NMR spectra look so good, one might worry that the software could be used for nefarious purposes. However, any detailed examination of the raw data would almost certainly reveal the difference between genuine

Published: June 19, 2012



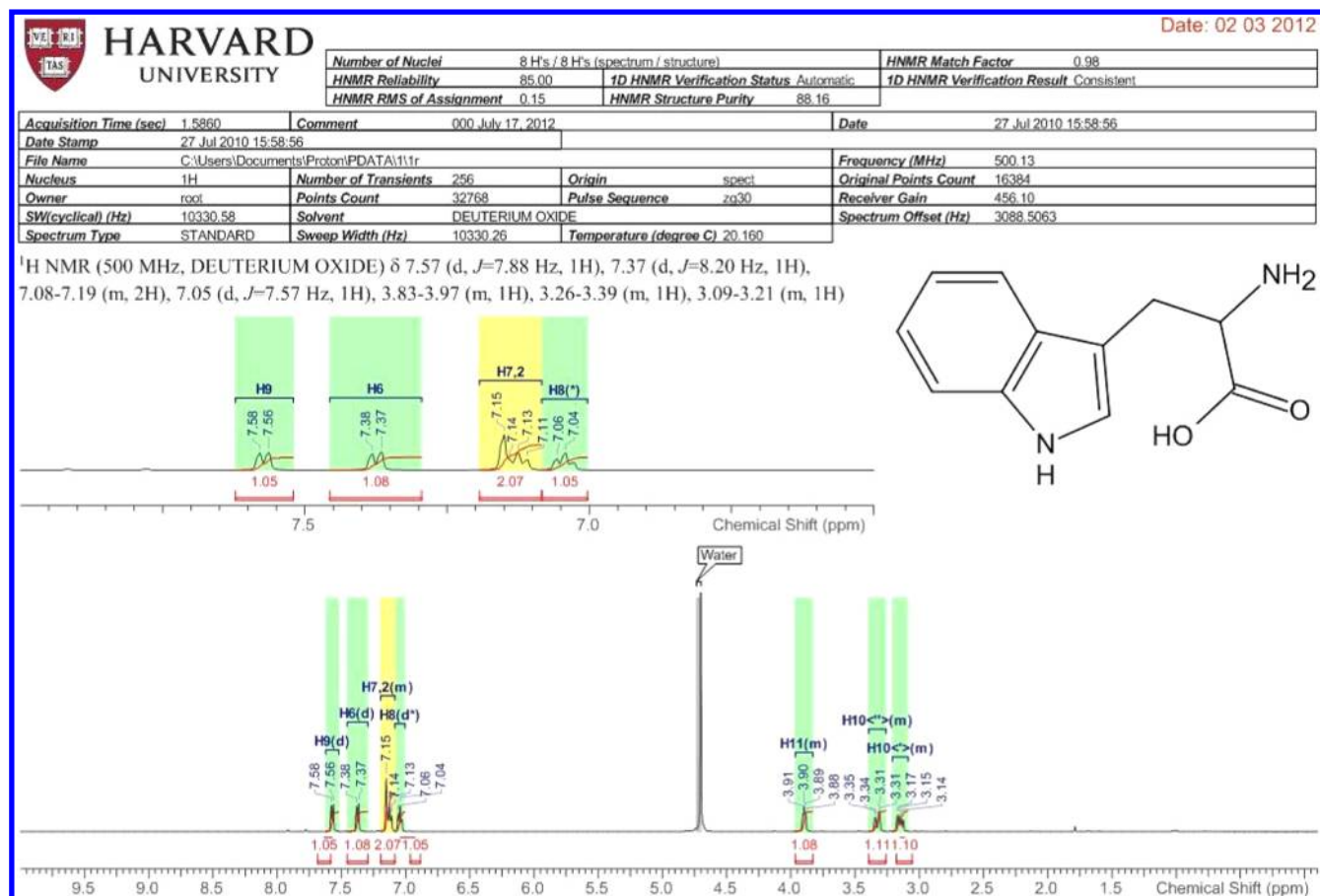


Figure 1. Typical ACD/Spectrum Processor report. Courtesy of Mr. Arvin Moser, ACD/Labs.

data and fake data. Still, there is the question of just how accurate the predictions are. Bally and Rablen have shown that the chemical shift predictions are good for an increment-based method, but not as good as those that can be produced by even relatively low levels of DFT.<sup>4</sup> For a large set of proton chemical shifts in small molecules, the unscaled rms error for ACD/NMR Predictors (0.185 ppm) is significantly less than that of ChemDraw (0.329 ppm), but larger than the linearly scaled error of the empirically parametrized WP04 functional at 6-31G(d,p)/gas phase (0.140 ppm). (Interestingly, without linear scaling, the same level of theory actually performs *worse* than ACD/NMR Predictors: 0.196 ppm.) One thing to note is that the rms error metric hides the fact that the performance of the predictions can vary significantly by the kind of molecule being considered. One should expect poor performance for molecules that lie outside the scope of the database (the database can be augmented manually). Additionally, because the ACD/Laboratories algorithm has a fairly primitive understanding of stereochemistry, its predictions are not appropriate for distinguishing between diastereomers. Nonetheless, the prediction of routine molecules gives uncannily accurate results, takes virtually no time or expertise in computations, and is very useful for understanding the shifts one might see at the bench.<sup>5</sup>

A pared-down form of the predictors is present in the standalone form of ACD/Spectrum Processor (\$450 US, North American academics, for a one year license) to assist in the automated assignment of a spectrum. The explicit ability to create simulated 1D NMR spectra adds \$350 to the price (there are plans to include 2D NMR prediction in the future). At the time of writing, representatives from ACD/Laboratories

informed me that the older ACD/NMR Processor academic edition will continue to be offered free of charge, but that there are no plans to offer ACD/Spectrum Processor free of charge. These prices are on par with its competitor programs of comparable feature sets. An incomplete list follows (USD prices for academics as of March 2012): Acorn NUTS Professional (\$1000, perpetual license); iNMR (\$200, perpetual license); Mnova NMR (\$150 for one year; \$400 for a perpetual license). To the best of my knowledge, only the Mnova Suite also offers comparable prediction capabilities (\$315 for one year; \$810 for a perpetual license).

Overall, I would highly recommend ACD/Spectrum Processor to anyone who deals with NMR spectra on a day-to-day basis. Researchers will like how easy it is to process spectra, create journal-formatted multiplet reports and nice-looking figures. They will also appreciate the accuracy of ACD/NMR Predictor, which is significantly better than that of ChemDraw. Instructors will find that the ability of ACD/NMR Predictor to generate crisp simulated spectra very useful for generating problem sets for students. The software is well-supported and is continually being improved. Most queries to technical support are ably answered within hours. The biggest drawback to the software is the lack of Mac support. Although the software can be run in an emulation environment, anecdotal evidence suggests that the software can become somewhat unstable. (At the time of writing, there are no plans to release a Mac version in the near future.) Nonetheless, its performance in its native Windows environment is quite good; in my experience, it functions quickly and as expected about 99% of the time. The bottom line is that if you want to spend more time thinking

about chemistry and less time wrestling with your NMR software, this is the way to go.

**Eugene E. Kwan\***

Harvard College Fellow, Department of Chemistry and  
Chemical Biology, Harvard University, 12 Oxford Street,  
Cambridge, Massachusetts 02138, United States

## ■ AUTHOR INFORMATION

### Corresponding Author

\*E-mail: [ekwan@fas.harvard.edu](mailto:ekwan@fas.harvard.edu).

### Notes

The author received a free copy of this software in exchange for writing this review but declares no other competing interests.

## ■ REFERENCES

- (1) Advanced Chemistry Development, Inc., Toronto, Canada. <http://www.acdlabs.com/products/spectrus/> (accessed June 12, 2012).
- (2) <http://www.acdlabs.com/resources/freeware/> (accessed June 12, 2012).
- (3) Reynolds, W. F.; Enriquez, R. G. *J. Nat. Prod.* **2002**, 65, 221–244.
- (4) (a) Bally, T.; Rablen, P. R. *J. Org. Chem.* **2009**, 74, 4017–4023.  
(b) Jain, R.; Bally, T.; Rablen, P. R. *J. Org. Chem.* **2011**, 76, 4818–4830.
- (5) Perez, M.; Peakman, T. M.; Alex, A.; Higginson, P. D.; Mitchell, J. C.; Snowden, M.; Marao, I. *J. Org. Chem.* **2006**, 71, 3103–3110.