

No. 497 February 2000

Cool Carbohydrates .					•		. Batta, (3. 2	2
Structure Refinement of Mul	tiple, Ra	pidly In	terconve				and James, T.	L. 5	5
Sharing NMR Data and Maki	ng NMR	Report	s.				Williams, A.	J. 7	,
Determination of Network Pr	operties	Throug	h Trans	verse (T	²2) Relax		nents .	. 11	
Stereochemical Endo/Exo Pr	eference	of 3-Cy	ano-2-o	xofuro[2,3- <i>b</i>]ir				
	Moral	es-Rios	, M. S.,	Suárez	-Castil	lo, O. R., and J	oseph-Nathan, F	. 13	\$
8th Annual "Advances in NMI	R Applica	ations" (Symposi	ium	•		.Nalorac Corp	. 17	7
NMR Analysis of Alginates							. Cheng, H. N	ı. 18	3
Other Uses of MAS .				٠		Miknis, F. P.,	and Netzel, D. A	. 23	3
¹³ C Solid State NMR of Polyn	nerized C	270				Soldatov, A.	, and Johnels, I	. 25	5
DEPT: What Most Textbooks	Do Not	Mention	ı .	1	٠	. Schorn,	C., and Bigler, I	. 30)
Off-Line Processing of Bruke	r Digital	ly Filter	ed NMR	Data	٠		. Golotvin, S	3. 33	3
Renewable Resources .							. Batta, C	. 36	5

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THE NMR NEWSLETTER		NO.	497, 1	FEBRUARY 2000	AUTHOR INDEX
Batta, G 2, 36 Bigler, P 30 Botto, R. E 11	Görler, A James, T. L Johnels, D	. 5	5	Morales-Rios, M. S. 13 Netzel, D. A 23 Schorn, C 30	Stec, D. F 11 Suárez-Cas'o, O.R. 13 Ulyanov, N. B 5
Cheng, H. N 18 Golotvin, S 33	Joseph-Nathan, Miknis, F. P			Soldatov, A 25	Williams, A. J 7
THE NMR NEWSLETTER		NO.	497, 1	FEBRUARY 2000	ADVERTISER INDEX
Advanced Chemistry Develop Aldrich Chemical Company, I AMT	nc	 	27 9 31	Programmed Test Source Varian, Inc	outside back cover ces, Inc. inside front cover 21

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FORTHCOMING NMR MEETINGS

Biennial Meeting of the Australian and New Zealand Society for Magnetic Resonance (ANZMAG2000), Mt. Buller, Victoria, Australia; **February 13-17, 2000**; Contact: Dr. Jenny Wilson, Victorian College of Pharmacy, Monash University, Parkville, Victoria 3052, Australia; E-mail: anzmag@edda.vcp.monash.edu; vcp.monash.edu.au/chemistry/anzmag2k.

PITTCON 2000, New Orleans, LA, March 12-17, 2000; Contact: The Pittsburgh Conference, 300 Penn Center Blvd., Suite 332, Pittsburgh, PA 15235-5503; Phone: 412-825-3220; Fax: 412-825-3224; Email: expo@pittcon.org.

8th Scientific Meeting and Exhibition, International Society for Magnetic Resonance in Medicine, Denver, CO, April 1-7, 2000; Contact: ISMRM, 2118 Milvia Street, Suite 201, Berkeley, CA 94704. Tel. 510-841-1899; Fax. 510-841-2340; E-mail: info@ismrm.org; http://www.ismrm.org.

Symposium on Advances in NMR Applications, Naval Postgraduate School, Monterey, CA. Shuttle service to and from Asilomar will be provided. **April 9, 2000**; Contact: V. Davies, Nalorac Corporation, 837 Arnold Drive, Suite 600, Martinez, CA 94553; 925-229-3501; Fax: 925-229-1651; Email: victoria.davies@nalorac.com; http://www.nalorac.com. See Newsletter 495, 28.

41st ENC (Experimental NMR Conference), Asilomar Conference Center, Pacific Grove, CA, April 9-14, 2000; Contact: ENC, 1201 Don Diego Avenue, Santa Fe, NM 87505; (505) 989-4573; Fax: (505) 989-1073; E-mail: enc@enc-conference.org. Web: enc-conference.org

15th European Experimental NMR Conference, Leipzig, Germany, **June, 2000**. For information, see http://eenc. uni-leipzig.de.

SMASH-2000, Argonne, IL, **July 16-19, 2000**. Contact: G. E. Martin (garv.e.martin@amu.pnu.com). See Newsletter 493, 21.

XIX International Conference on Mag. Res. in Biological Systems, Florence, Italy, August 20-25, 2000. Contact: Profs. Ivano Bentini or Lucia Banci, Magnetic Resonance Center, Univ. of Florence, Via Luigi Sacconi 6, 50019 Sesto Fiorentino (Firenze), Italy; Phone: +39-055-2757600; Email: icmrbs@cerm.unifi.it; Fax: +39-0554-209253; http://www.cerm.unifi.it/icmrbs.html.

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e-mail: batta@tigris.klte.hu, fax: (36) 52 512 914 tel: (36) 52 512 900 ext. 2370 or 2234

January 10, 2000 (received 1/11/2000)

Professor B. L. Shapiro The NMR Newsletter 966 Elsinore Court Palo Alto CA 94303-3410 USA

Cool Carbohydrates

Dear Barry,

Well behaving proteins have resolved NH signals in water solution, which is invaluable for any stuctural studies. This is not the case with the OH groups in oligo-and polysaccharides since their exchange with solvent water is generally too fast.

Studying highly concentrated (1-2M) oligosaccharides in D₂O-H₂O mixtures we observed that the ¹H resolution improves (simultaneously with sharper deuterium lock signal) if the temperature is decreased to ca. 264K (just above freezing point) and OH signals exhibit resolved couplings. High concentration of carbohydrates has twofold benefit. Freezing temperature is decreased without supercooling, and NMR sensitivity is sufficient to measure homo and heteronuclear couplings of hydroxyl protons in simple 1D spectra or recent SE-HETLOC or HECADE spectra at natural isotopic abundance. Sensitivity is an issue, since the resolution is better at low H₂O content (3-10 %), and water suppression is not a must. Concerning the two polysaccharides we studied recently, in one we observed the OH groups, however, coupling constant analysis seems more difficult.

Yours truly,

Gyula Batta

1. L. Poppe, H. van Halbeek, *Nat. Struct. Biol.* 1(1994) 215-216, 2. Gy. Batta and K. E. Kövér, *Carbohydr. Res.* 320(1999) 267-272

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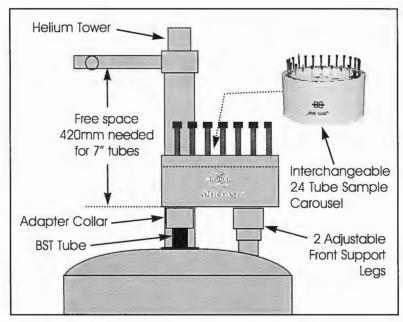
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SANTA BARBARA · SANTA CRUZ

Department of Pharmaceutical Chemistry SAN FRANCISCO, CALIFORNIA 94143-0446

January 26, 2000 (received 1/28/2000)

Dr. B.L. Shapiro The NMR Newsletter 966 Elsinore Court Palo Alto, CA 94303-3410

Structure refinement of multiple, rapidly interconverting conformers

Dear Barry:

Recently, we proposed a new approach for refining structural conformers and determining their populations based on NMR data [1].

When distinct multiple conformers exchange rapidly on the NMR time scale, they give rise to a single set of NMR lines. In such a situation, plain inspection of spectra may give no clues about the presence of such conformers. Experimentally measured NMR parameters (such as NOE or scalar coupling data) correspond, nevertheless, to appropriate averages over all structures contributing to the signal. Conventional structural refinement using such data may lead to incorrect or even sterically impossible structures. If no single conformation can satisfy all experimental restraints, this can be an indication of the presence of multiple conformers. Furthermore, contradictions between experimental restraints and the theoretical force field used in structure refinement can serve as a basis for determination of high-resolution structures of individual conformers. But this task requires, of course, special approaches for refinement.

Several refinement tools have been proposed in the past to deal with this situation. We mention here the ensemble-average (or multiple-copy) molecular dynamics (MD) [2,3], because our own approach is similar to it in its main idea. Similar to conventional refinement schemes, multiple-copy MD refinement is driven by a pseudoenergy. The pseudoenergy is a sum of two terms: conformational energy defined by a theoretical force field, and a penalty term, which enforces the agreement between calculated and observed NMR parameters (such as NOE-derived inter-proton distances). The difference from the conventional restrained MD is that multiple-copy MD refines several copies of a molecule simultaneously. Individual molecules do not interact with each other during the MD simulation, but theoretical NMR parameters are calculated as appropriate averages over all copies. As a result, experimental restraints are not enforced for each individual molecule, but only for the ensemble as a whole. If a set of experimental restraints cannot be satisfied by any single conformation, multiple-copy MD will produce a set of distinct structures that satisfy experimental restraints as an ensemble.

One problem with this approach is the assumption that all members of the ensemble have equal populations, which somewhat limits its possible applications. In one variant of this method [4], individual structures are weighted with the Boltzmann factors derived from their conformational energies. However, relative free energies rather than conformational energies determine populations of conformers; attempts to calculate free energies during refinement would make this method impractical. We wanted to modify this method in such a way that populations of conformers are determined by experimental data rather than by theoretical force field. This can be done using the PDQPRO program, a part of the PARSE procedure [5]. For a given set of conformations, PDQPRO calculates their optimal populations by fitting theoretical ensembles' NMR parameters to the observed parameters. The fitting is done by a quadratic programming algorithm, which imposes a limitation on the type of NMR parameters that can be used: they must average in a linear fashion over the

ensemble. Suitable parameters are, e.g., scalar coupling constants and dipolar relaxation rates. It is relatively straightforward to calculate dipolar cross-relaxation rates for a theoretical ensemble of structures; experimental rates can be derived iteratively from NOE data, using, e.g., the program MARDIGRAS [6]. Derivation of experimental dipolar relaxation rates from NOE data is done independently of (prior to) refinement, so the required CPU time is not an issue here. Calculation of theoretical rates and PDQPRO calculations are relatively fast and they can be done at each refinement step.

For practical implementation of this idea, we used the DNAminiCarlo program [7] as the refinement engine, because we have the source code of this program in our hands. Instead of MD simulations, DNAminiCarlo performs energy minimization and Metropolis Monte Carlo calculations for nucleic acid systems. This choice limits, of course, possible applications of this method to nucleic acids. However, the calculations are very effective for these systems because of the use of highly specialized internal coordinates, generalized helical parameters. We modified DNAminiCarlo to handle multiple copies; dipolar relaxation rates are calculated for each ensemble-snapshot by invoking subroutines of the RELAX program [8]; "floating" populations are calculated for each snapshot by invoking subroutines of PDQPRO.

We extensively tested this approach using simulated data for DNA oligonucleotides [1]. We assumed that we have measured NOE data corresponding to typically observed cross-peaks for this type of molecule, and we did not use scalar coupling data. These data were sufficient to recover correct structures and correct populations for simulated equilibria involving two major conformers of sugar moieties: C2'endo and C3'endo. However, the same data were not sufficient to define reliably three-conformer equilibria with C2'endo, C3'endo, and an intermediate O4'exo conformers. This exercise showed that our approach can work successfully, but only if the system is defined sufficiently by experimental data. If all experimental data can be explained with a single structure, the method will produce a single "average" structure, even if multiple conformers contributed to observed data. Currently we are applying this method to an experimental RNA system. Also, we are interested in extending our approach to protein systems, but this will require using a different refinement engine.

Sincerely,

Nikolai B. Ulyanov

Nileda Wlyanor

Adrian Görler

Thomas L. James Professor & Chair

^{1.} A. Görler, N.B. Ulyanov & T.L. James, J. Biomolec. NMR, in press (2000).

^{2.} A.M. Bonvin & A.T. Brönger, J. Mol. Biol., 250, 80-93 (1995).

^{3.} J. Kemmink & R.M. Scheek, J. Biomolec. NMR, 6, 33-40 (1995).

^{4.} J. Fennen, A.E. Torda & W.F. van Gunsteren, J. Biomolec. NMR, 6, 163-170 (1995).

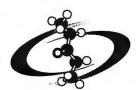
^{5.} N.B. Ulyanov, U. Schmitz, A. Kumar & T.L. James, Biophys. J., 68, 13-24 (1995).

^{6.} B.A. Borgias & T.L. James, J. Magn. Reson., 87, 475-487 (1990).

^{7.} V.B. Zhurkin, N.B. Ulyanov, A.A. Gorin & R.L. Jernigan, *Proc. Natl. Acad. Sci. U.S.A.*, **88**, 7046-50 (1991).

^{8.} A. Görler & H.R. Kalbitzer, J. Magn. Reson., 124, 177-188 (1997).





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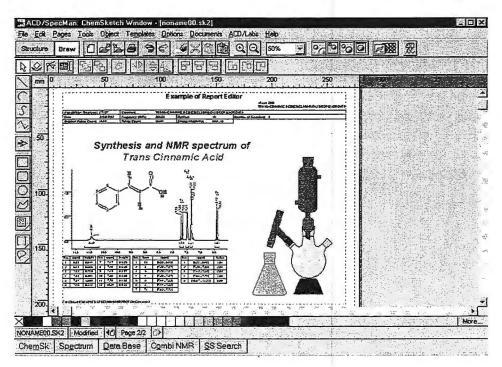
Sharing NMR Data and Making NMR Reports

January 11th, 2000 (received 1/12/2000)

Dear Barry,

During recent months I have been watching a large number of contributions which have been made to the NMR Newsletter and wonder whether or not there is an awareness regarding the ease of graphics inclusion in word processing documents. Recently there was a report regarding the movement of NMR data from a spectrometer through a desktop NMR processing package to a commercial graphics package From here an image file was generated for moving into a word processor. I would like to suggest that modern software packages offering standard OLE capabilities are more than sufficient for these tasks and that spectrometer vendors include such functionality in their standard software, especially when providing access to the data at the desktop whether it be via X-Windows emulation or Java tools.

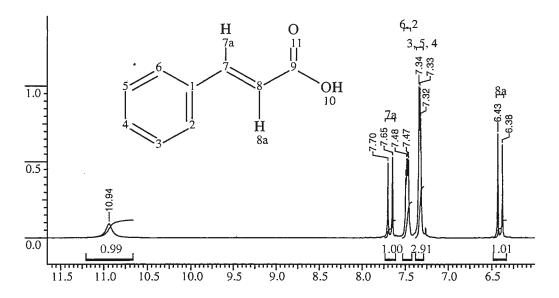
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January 11, 2000 (received 1/15/2000)

Bernard L. Shapiro The NMR Newletter 966 Elsinore Court Palo Alto, CA USA 94303

Determination of Network Properties through Transverse (T₂) Relaxation Measurements

Dear Barry,

We have extended the scope of our investigation into solvent transport behavior to include transversal 1H NMR relaxation studies. During the past decade, studies on polymeric networks have shown this method to be a useful tool for characterizing molecular dynamics. Since transverse 1H relaxation times are dependent upon interand intramolecular dipolar interactions of protons, useful properties such as crosslink density, molecular mobility and chain dynamics can be determined. Typically, rigid fractions such as crosslinks and physical entanglements are characterized by short T_2 relaxation times while mobile fractions such as dangling end chains are characterized by longer T_2 .

The samples used in our initial investigation were cross-linked copolymers of poly(isobutylene)-co-poly(paramethyl-styrene) (PIB/PMS) (see *The NMR Newsletter* 478, 25, July 1998).

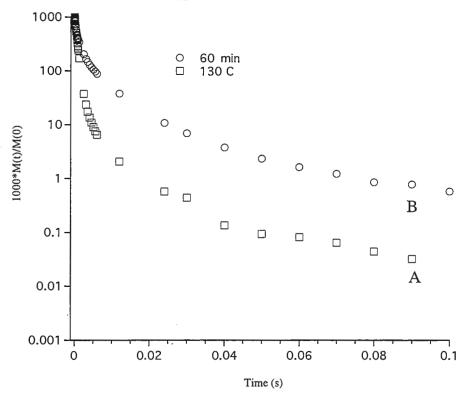
 T_2 relaxation curves for a sample of PIB/PMS heated to 130 °C (squares) and the same sample swollen in d_{12} -cyclohexane for 60 minutes (circles) are shown in Figure 1. The relaxation measurements were acquired using the Carr-Purcell-Meiboom-Gill (CPMG) pulse sequence with typical delay times between pulses in the range of 1 μ s to 500 ms. Three distinct regions can be observed from the relaxation curves; an initial fast decaying component, an intermediate component and a slowly relaxing tail. The two inserts provide expanded views of regions between 0-100 μ s and 200-1000 μ s respectively. Although the samples have similar decay rates initially (up to 200 us), the sample heated to 130 °C appears to decay much quicker than the sample swollen in d_{12} -cyclohexane.

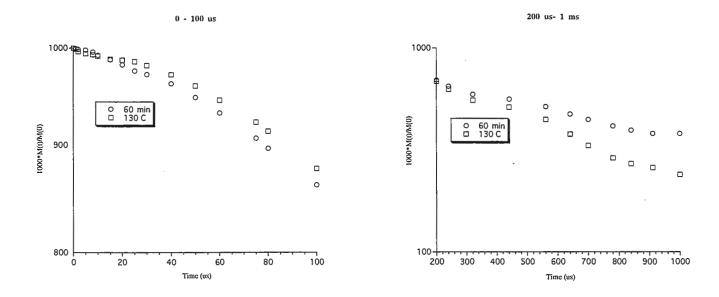
We have attempted to extract values for the fraction of inter-crosslink chains and dangling chain ends, in addition to determining the crosslink density as reported by Simon et al. (Rubber Chemistry and Technology, 65, 1, 1992). However, initial attempts at extracting these values using their empirical approach, based on second moment analysis, have been unsuccessful. One possible explanation for this maybe be due to the complex, multicomponent nature of our samples. We are currently investigating new theoretical approaches that will enable useful parameters such as crosslink density to be determined for complex polymeric materials. The ultimate goal is to determine the reliability and accuracy of relaxation measurements in relating physical structure to the energetic state of polymer systems such as rubbers and coals.

Sincerely,

Donald F. Stec Chemistry Division Robert E. Botto Chemistry Division

Figure 1. ¹H transverse relaxation curves for PIB/PMS heated to 130 °C and swollen with d₁₂-cyclohexane for 60 min.







CENTRO DE INVESTIGACION Y DE ESTUDIOS AVANZADOS DEL I.P.N.

January 6, 2000 (received 1/18/2000)

Dr. Bernard L. Shapiro Editor/Publisher The NMR Newsletter 966 Elsinore Ct. Palo Alto, CA 94303 USA

Streochemical endo/exo preference of 3-cyano-2-oxofuro[2,3-b]indoles

Dear Professor Shapiro:

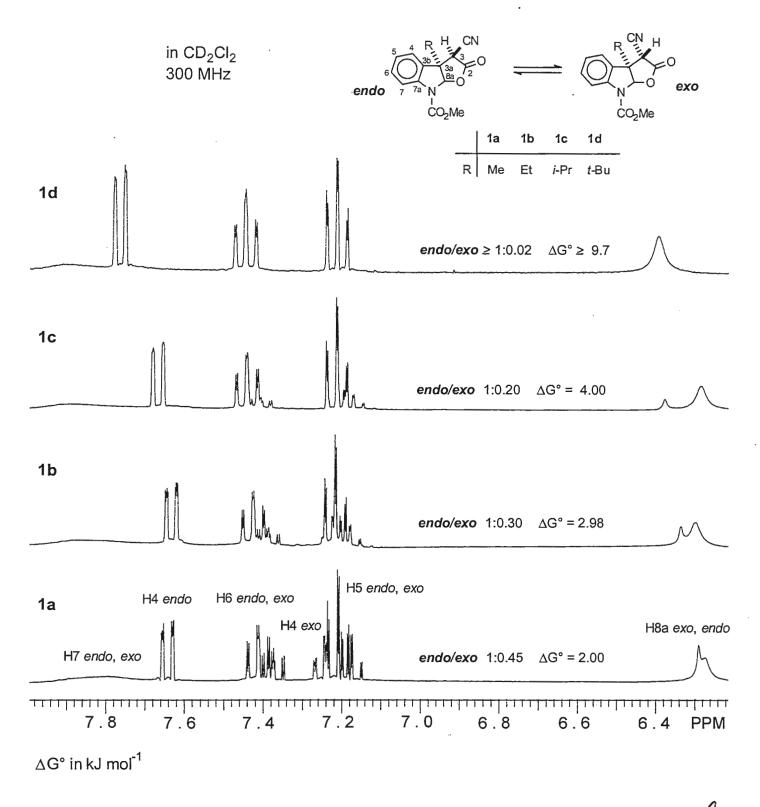
3a-Alkyl-3-cyano-2-oxofuro[2,3-b]indoles 1a-d are an important class of compounds, because they may be easily transformed into the corresponding fused furans, lactams, pyrroles, etc. These compounds are useful intermediates for the synthesis of biologically active natural products, which have been isolated from diverse origins such as the *Physostigma* and *Flustra* alkaloids. Preliminary investigations about the configuration of 1a-d demonstrated that compound 1a-c exist as mixtures of endo/exo epimers in solution and undergo fast H-3 deuterium exchange with D₂O. In contrast, although H-3 in 1d slowly exchanges with D₂O, a single diastereoisomer is present in solution.

The NOE experiments allowed unequivocal *endo/exo* assignment (Figure). For *endo* epimers NOEs of 17-27% were observed for the H-3 and H-8a protons, upon irradiation at the C(3a) methyl protons of the alkyl group of the major epimer in 1a, and for the single epimer in 1d. Whereas, a NOE was not detected for H-3 when the methyl protons of the minor *exo-1a* epimer were irradiated.

Concerning the furoindole 1a, ab initio calculations performed at the HF/3-21G* level predict that the most stable structure corresponds to the endo epimer with a relative energy difference ($E_{\rm rel}$) between the endo and exo epimers of 2.1 kJ mol⁻¹. Furthermore, if it is assumed that the entropic and solvation contributions are not important in the equilibrium between these epimers, the calculated difference in free energy (2.1 kJ mol⁻¹) means a value of 2.4 for the corresponding equilibrium constant, in agreement with the ΔG° value ($\Delta G^{\circ} = -RT \ln K$, 25 °C) derived from the observed endo/exo populations in the ¹H NMR spectra measured in CD₂Cl₂ solvent.

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Martha S. Morales-Ríos

Oscar R. Suárez-Castillo

Sincerely yours,

Pedro/Joseph-Nathan

pjoseph@nathan.chem.cinvestav.mx

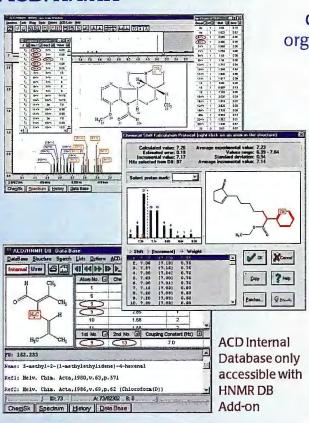


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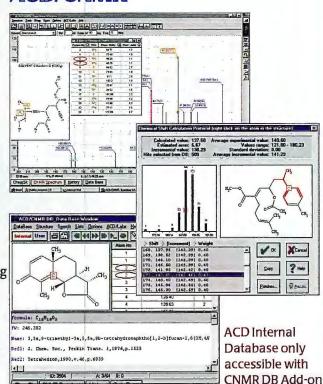
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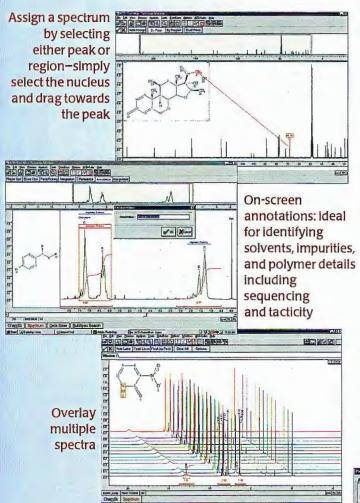
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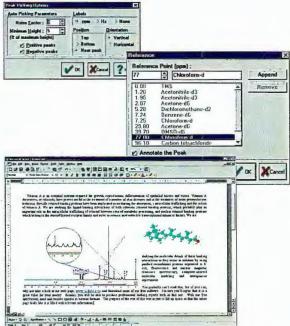
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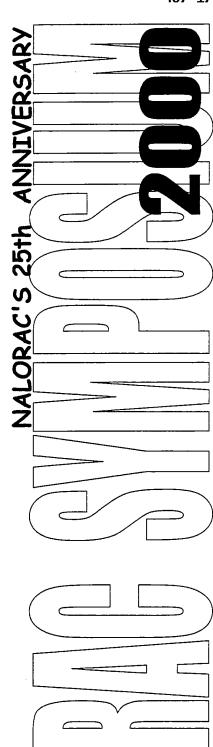
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January 8, 2000 (received 1/15/2000)

Dr. B. L. Shapiro The NMR Newsletter 966 Elsinore Court Palo Alto, CA 94303-3410

Dear Dr. Shapiro:

NMR Analysis of Alginates

Alginates are natural polysaccharides extracted from brown algae and used commercially as thickeners, binders, encapsulants, stabilizers, film-formers, and suspending agents¹. Structurally, they are unbranched copolymers of (1-4)-linked β -D-mannuronic acid (M) and α -L-guluronic acid (G) residues.

These comonomers are known to form both blocky and alternating sequences in alginates, and the polymeric microstructure is essential for their properties.

Alginates have been extensively studied by NMR²⁻⁶, especially by Grasdalen, Larsen, Smidsrod, Skjak-Braek, and their coworkers³⁻⁶. They have provided spectral assignments and also recommended a computational procedure to obtain M-and G-centered triads. Analysis has often been done with the help of conventional statistical models, viz., Bernoullian, first- and second-order Markovian models^{1,6}. Because alginates are compositionally heterogeneous, Bernoullian and Markovian models may not be appropriate. I have recently⁷ used alternative models to analyze the NMR data of alginates.

As an example, the NMR triad data (I_{obsd}) of an alginate sample, taken from a paper in the literature³, are shown in column 2 of Table 1. It is clear (from columns 3 and 4 in Table 1) that single-component Bernoullian (B) and first-order Markovian (M1) models⁸ do not fit the data very well (mean deviation > 1.0). Two analytical methodologies were then employed⁷ to analyze this data set: 1) perturbed Markovian (continuous) model, and 2) multicomponent (discrete) model.

Table 1. NMR data of alginate and analysis by different statistical models

		one-compo	nent models	perturbed Mar	kovian models	multicompone	ent models
triad	I _{obsd}	$I_{calc}(\mathbf{B})$	$I_{calc}(M1)$	$I_{calc}(EMG/B)$	$I_{calc}(EMG/M1)$	$I_{calc}(B/B)$	$I_{calc}(M1/M1)$
MMM	38	38.0	38.0	38.0	35.7	38.0	38.0
MMG	16	28.9	18.3	18.1	16.0	16.4	16.0
GMG	6	5.5	2.2	4.3	6.0	5.1	6.0
MGM	10	14.5	3.1	9.1	9.8	8.2	10.0
GGM	8	11.0	16.5	8.5	8.3	10.3	8.0
GGG _	22	2.1	22.0	22.0	24.2	22.0	22.0
mean de	v.	6.8	3.6	0.9	0.8	0.9	0.0
		$P_{M}=0.724$	$P_{GM} = 0.272$	$P_{M}=0.643$	$P_{GM} = 0.695$	component 1	component 1
		•	$P_{MG} = 0.194$	$\sigma = 0.294$	$P_{MG} = 0.437$	$w_1 = 0.344$	$w_1 = 0.344$
				$\tau = -0.039$	$\sigma = 0.367$	$P_{M}=0.143$	$P_{GM} = 0.144$
					$\tau = -0.042$		$P_{MG} = 0.996$
						component 2	component 2
						$w_2 = 0.656$	$w_2 = 0.656$
						$P_{M}=0.833$	$P_{GM} = 0.970$
							$P_{MG} = 0.174$

Perturbed Markovian Model

Previously the perturbed Markovian models have been developed to treat compositionally heterogeneous polymers, using symmetric function⁹, non-symmetric functions¹⁰, or a function-free approach¹⁰. For convenience, the exponentially modified Gaussian (EMG) function has been used for alginates⁷. Thus, the Bernoullian probability is represented not by one value (P_M), but by a distribution:

$$f(z) = \frac{N}{\tau \sigma \sqrt{(2\pi)}} \int_{0}^{\infty} \exp \left[-\frac{(z - P_{M} - z')^{2}}{2\sigma^{2}} - \frac{z'}{\tau} \right] dz'$$
 (1)

where z is the Bernoullian probability, N the area under the Gaussian, σ the standard deviation, τ the skew factor, z' the dummy variable of integration, and P_M the average value of Bernoullian probability without the exponential modification. Equation 1 gives the Bernoullian EMG function (EMG/B). The EMG function for the first-order Markovian probabilities (EMG/M1) can be expressed similarly 10 .

The experimentally observed sequence intensities can be fitted to the theoretical sequence intensities to obtain P_M (or P_{MG} and P_{GM}), σ , and τ . The results are shown in columns 5 and 6 of Table 1. Indeed both perturbed models (EMG/B and EMG/M1) produce acceptable goodness-of-fit (mean deviation $\leq 1.0\%$, comparable to experimental precision). Although the EMG/M1 function introduces one additional probability parameter, the improvement in the fit over EMG/B function is only marginal (mean deviation 0.8 versus 0.9). Using the values of the EMG/B function, we can plot the chemical composition distribution (CCD) curve for this polymer (Figure 1).

Multicomponent Model

In the multicomponent models^{11,12}, the polymer is considered to be the mixture of two or more discrete components. No assumption is made of the nature of the components: they may be separate chains or joined together as block copolymers. In this case, each experimentally observed sequence (composition, diad, triad, or higher n-ad) is the weighted average of the corresponding sequences of all the components. For a two-component polymer, the observed intensity for each triad (I_{i,obsd}) is:

$$I_{i,obsd} = w_{1i} f_{1i} + w_{2i} f_{2i}$$
 (2)

where $w_{\alpha i}$ is the weight factor, and $f_{\alpha i}$ is the intensity for triad i and component α .

This discrete two-component model has been used to analyze the alginate data (Table 1, columns 7 and 8). The two-component B/B model provides a good fit to the data, and the two-component (M1/M1) model gives even a better fit. Thus, this alginate sample contains at least two components. The two M1/M1 components can be depicted in the chemical composition distribution plot (Figure 1).

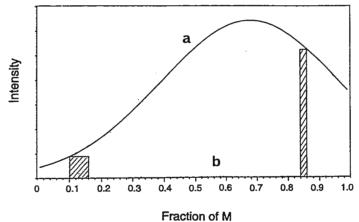


Figure 1. Calculated chemical composition distribution (CCD) for alginate isolated from *Laminaria digitata*: (a) continuous function approach, (b) two-component approximation (discrete model); each component is shown as separate polymer chains for convenience. The area under each bar corresponds to the weight factor.

It is of interest that the same sample can be represented in two different ways (continuous versus discrete functions). For a polymer with a complex microstructure, often the NMR data on the polymer alone do not enable us to tell if one representation is preferred over another. Additional data from other analytical techniques (e.g., fractionation and molecular weight) are needed. In the case of alginates, it is useful to fractionate the polymer and to analyze the NMR data of polymer fractions. This has indeed been done⁷; interested readers may consult the recent paper⁷ for more detailed studies.

In summary, alginates are compositionally heterogeneous, and the NMR data reflect this heterogeneity. The NMR data should therefore be analyzed not by conventional single-component models, but by alternative methods, e.g., multicomponent and perturbed Markovian models.

Very truly yours,

H. N. Cheng

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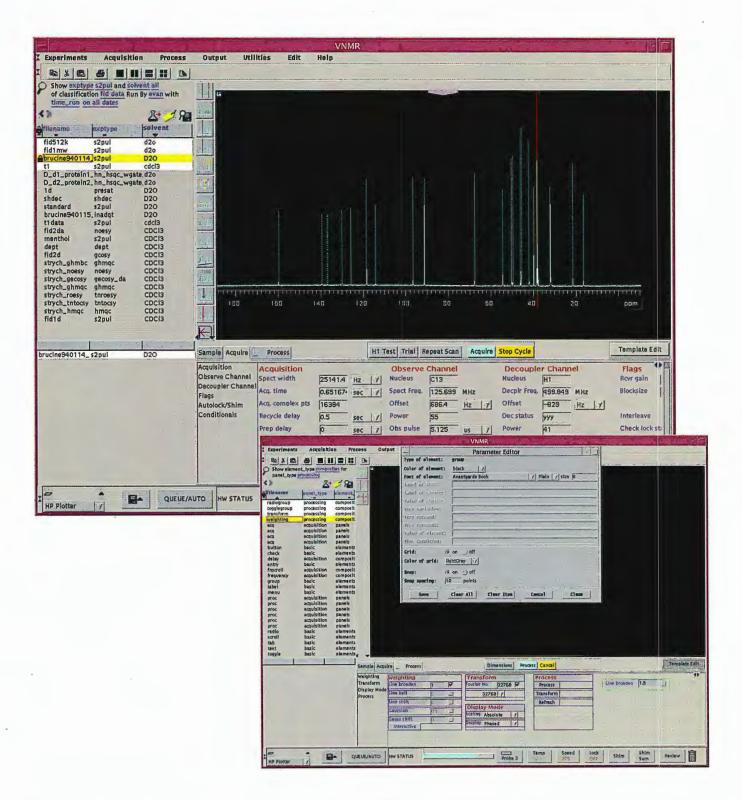
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January 14, 2000 (received 1/18/2000)

Dr. B. L. Shapiro The NMR Newsletter 966 Elsinore Court Palo Alto, CA 94303

Other Uses of MAS

Dear Barry,

We were expecting your missive about our not having sent in a contribution to the NMR newsletter. We've been in somewhat of a holding pattern while we got our FHWA asphalt contract in place, so have not been doing a lot of spectroscopy. Consequently, our contribution is only marginally related to NMR, but we hope it might be of interest to the readers just the same.

The seeds of this idea were planted about 20 years ago when we were working with Gary Maciel at Colorado State University on applications of CP/MAS ¹³C NMR to characterize fossil fuels. At that time, Vic Bartuska had built a large-volume spinner, ~14 mm in diameter, for this purpose. After Vic had used it to acquire spectra of oil shales and coals, we decided to look at tar sands. I remember one day Gary telling me how Vic had run a tar sand sample and when he took the cap off the spinner there was only sand left in the center, the bitumen having centrifuged out and coated the walls. Well 20 years later we are looking into whether we can use high-speed spinning as a way to study the adhesive properties of asphalt with aggregates.

We purchased a large-volume (14 mm dia) bench top spinning module from Varian/Chemagnetics and have been using it to test combinations of different asphalts on different aggregates. The results of one of our exploratory experiments are shown in the Figure. As you can see, a significant fraction of the asphalt can be removed by spinning, leaving the more tightly bound material coating the aggregate. In this case the glass beads. We have done similar experiments with pieces of aggregate (~1/4 inch).

This gives us an opportunity to now extract the remaining material from the asphalt to determine what classes of compound types and functional groups adhere most strongly to different aggregates. We found that the fraction of material remaining on the aggregate is different for different asphalts, but this may be just a viscosity effect as the asphalts have different viscosities at room temperature. Hopefully, we'll have more to report about these experiments in future contributions.

In the meantime we hope Y2K is a good one for the Newsletter,

Best regards,

Fran Miknis

Dan Netzel

a) b) c)

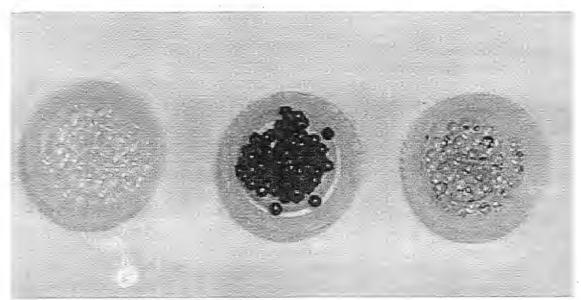


Figure 1. Asphalt coated onto 3 mm glass beads. a) glass beads, b) glass beads coated with asphalt, c) glass beads after spinning at 3 kHz for 30 min, then at 4 KHz for 60 min.

UMEÅ UNIVERSITET Kemiska Institutionen/Organisk Kemi Dan Johnels



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Dr. B. L. Shapiro The NMR Newletter 966 Elsinore Court Palo Alto, CA 94303 January 25, 2000 (received 1/26/2000)

¹³C solid state NMR of polymerised C70.

Many different fullerene derivatives have been prepared since the discovery of the fullerenes in 1985¹. These are prepared by chemical modifications, but also by subjecting the fullerenes to high temperatures and pressures². The structure and properties of the materials prepared by physical methods, starting from C60, were not fully understood until the materials were investigated by spectroscopic methods, where the application of solid state NMR spectroscopy clearly revealed that the fullerene units are linked together by covalent bonds to polymeric chains or sheets³. We are currently investigating the structure of high pressure/temperature treated C70, where several structural possibilities exist due to the reduced symmetry. The material we have investigated has been treated at 2.5 GPa and 580 K. The solid state ¹³C MAS NMR spectrum of this material, presented in Figure 1A, clearly show that the polymer again is formed by covalent bonds between the C70 units, as indicated from the signals at 67 and 71 ppm, stemming from sp³ carbons. The signal at 110 ppm arises from the end caps of the rotor. The sp² region corresponds well to what is expected from C70 derivatives⁴. In a simulation, based on ¹³C solution NMR data of the recently prepared C70 dimer⁵, is presented in Figure 1B. There are some obvious variations of the intensities, where as the regions of the signals are similar. This allows us to assume a presence of other structural units than dimers in the sample. The working hypothesis for the structure of the polymeric materials, based on NMR and other spectroscopic data (Raman, IR), is that it is a 1D (chain) polymer.

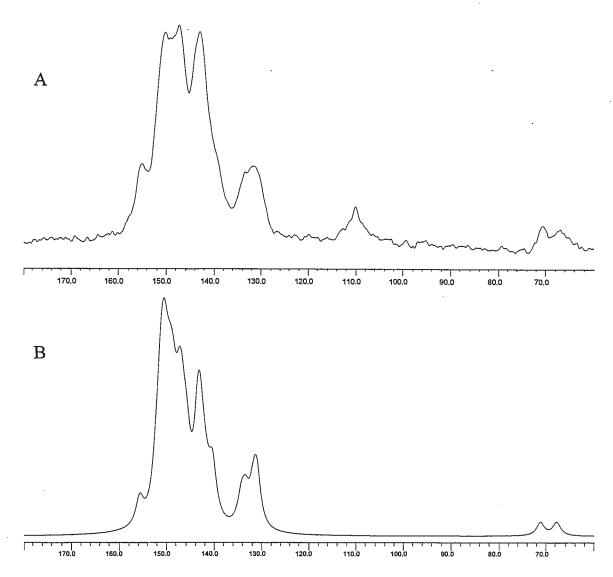


Figure 1. A. Experimental spectrum of P/T treated C70. B. Simulation based on solution NMR data of dimeric C70, a line width of 200 Hz was used.

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P.S. Please credit this contribution to the account of Prof. Ulf Edlund.

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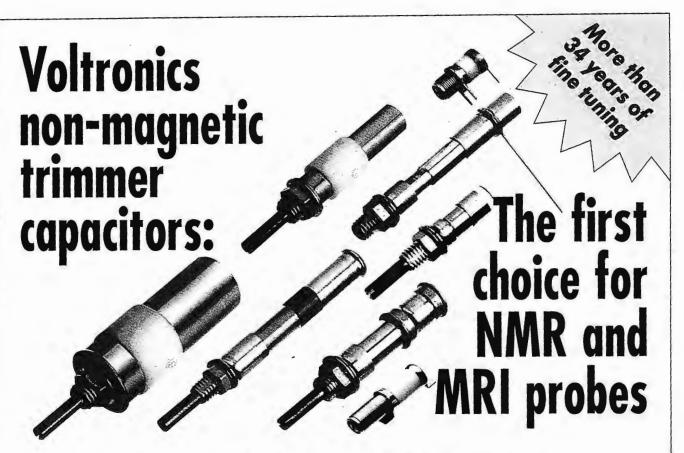
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9		717007	Z41,282-1	50.70	810.30
7	0.0010	0.0005	Z41,284-8	61.20	977.60
8	0.0010	0.0006	Z41,285-6	67.20	1,074.80
	0.0005	0.00025	Z41,286-4	86.90	1,389.50
	0.0005			97.20	1,553.60
7					3,112.00
8	0.0002	0.00015	Z41,289-9	218.00	3,486.70
tubes					
7	0.0030	0.0015	Z41,296-1	\$19.70/ea	\$393.50/25
7	0.0015	0.0005	Z41,298-8	27.20/ea	542.50/25
	7 8 7 8 7 8 7 8 tubes 7 7 7 8 9 7 8 7	7 0.0020 8 0.0020 7 0.0010 8 0.0010 7 0.0005 8 0.0005 tubes 7 - 7 0.0030 7 0.0025 7 0.0020 8 0.0020 9 0.0020 9 0.0020 7 0.0010 8 0.0010 7 0.0005 8 0.0005 8 0.0005 8 0.0005 8 0.00005 8 0.00005 8 0.00005 7 0.0005 8 0.0005 7 0.0005 8 0.0005 7 0.0002	7 0.0020 0.0010 8 0.0020 0.0011 7 0.0010 0.0005 8 0.0010 0.0006 7 0.0005 0.00025 8 0.0005 0.00035 tubes 7 7 0.0030 0.002 7 0.0025 0.002 7 0.0020 0.0010 8 0.0020 0.0011 9 0.0020 0.0012 9 0.0020 0.0012 9 0.0020 0.0012 9 0.0020 0.0015 8 0.0005 0.0005 8 0.0010 0.0005 8 0.0005 0.00025 8 0.0005 0.00025 8 0.0005 0.00025 8 0.0005 0.00035 7 0.0002 0.00015 8 0.0002 0.00015 8 0.0002 0.00015	7 0.0020 0.0010 Z41,290-2 8 0.0020 0.0011 Z41,291-0 7 0.0010 0.0005 Z41,292-9 8 0.0010 0.0006 Z41,293-7 7 0.0005 0.00025 Z41,294-5 8 0.0005 0.00035 Z41,295-3 tubes 7 Z41,277-5 7 0.0030 0.002 Z41,278-3 7 0.0025 0.002 Z41,279-1 7 0.0020 0.0010 Z41,280-5 8 0.0020 0.0011 Z41,281-3 9 0.0020 0.0012 Z41,282-1 7 0.0010 0.0005 Z41,284-8 8 0.0010 0.0005 Z41,284-8 8 0.0010 0.0005 Z41,285-6 7 0.0005 0.00025 Z41,286-4 8 0.0005 0.00015 Z41,288-0 8 0.0002 0.00015 Z41,288-0 8 0.0002 0.00015 Z41,288-0 8 0.0002 0.00015 Z41,288-0 8 0.0002 0.00015 Z41,288-0	7 0.0020 0.0010 241,290-2 \$44.60 8 0.0020 0.0011 241,291-0 50.70 7 0.0010 0.0005 241,292-9 69.50 8 0.0010 0.0006 241,293-7 78.80 7 0.0005 0.00025 241,294-5 113.10 8 0.0005 0.00035 241,295-3 128.50 tubes 7 241,277-5 \$12.40 7 0.0030 0.002 241,278-3 28.70 7 0.0025 0.002 241,279-1 31.40 7 0.0020 0.0010 241,280-5 40.50 8 0.0020 0.0011 241,281-3 45.40 9 0.0020 0.0012 241,282-1 50.70 7 0.0010 0.0005 241,282-1 50.70 7 0.0010 0.0006 241,285-6 67.20 8 0.0010 0.0006 241,285-6 67.20 9 0.0005 0.0005 241,285-6 67.20 7 0.0005 0.0005 241,285-6 67.20 8 0.0005 0.0005 241,285-6 97.20 7 0.0005 0.0005 241,285-9 218.00 8 0.0002 0.00015 241,288-9 218.00 8 tubes 7 0.0002 0.00015 241,289-9 218.00

†TIR=Total Indicator Reading



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Dr. B.L. Shapiro The NMR Newsletter 966 Elsinore Court Palo Alto, CA 94303

december, 14th 1999 (received 12/20/99)

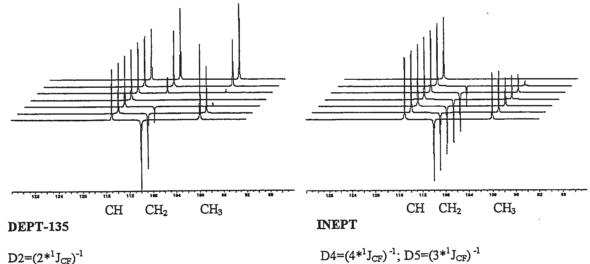
DEPT: What most textbooks do not mention

Testing the ¹⁹F-capabilities of our BRUKER DRX-spectrometers we experimentally compared several pulse sequences dedicated for the detection of multiplicity selective ¹³C spectra, such as DEPT, INEPT (PENDANT) and JMOD (APT). We had to realize that the ²J_{FF} coupling constants of CF₂ and CF₃ groups are close or even larger than the corresponding ¹J_{CF} coupling constants. So the common assumption made for the ¹H-¹³C case (¹J_{CH}>>²J_{HH}) that homonuclear coupling can be neglected is no longer fulfilled for the ¹⁹F - ¹³C case. As a consequence and with the delays adjusted solely to the CF coupling the intensities of CF2 and CF3 signals may heavily be distorted, may even disappear or may be wrong in sign (CF2).

The simplified expressions as mentioned in most textbooks are no longer valid and must be replaced by the full expressions. For the DEPT experiment with 19F broadband decoupling and with P0 and D2 set equal to 135° and $(2^{*1}J_{CF})^{-1}$ respectively they are:

$$\begin{split} &I_{CF3} \sim -1.06 * \sin{(\Pi~^1J_{CF}~D2)^6} \left[\cos{(\Pi~^2J_{FF}~D2)^4} - ~ 2*\cos{(\Pi~^2J_{FF}~D2)^2} * \sin{(\Pi~^2J_{FF}~D2)^2} + \sin{(\Pi~^2J_{FF}~D2)^4} \right] \\ &I_{CF2} \sim -1.00 * \sin{(\Pi~^1J_{CF}~D2)^4} * \cos{(2\Pi~^2J_{FF}~D2)} \\ &I_{CF} \sim -0.71 * \sin{(\Pi~^1J_{CF}~D2)^2} \end{split}$$

According to experimental data and simulations (below) corresponding problems are most severe for DEPT and less severe for INEPT (or PENDANT). Characterizing a series of perfluorated compounds it turned out that JMOD (APT), which is obviously not affected by this "1J_{CF}-2J_{FF}-problem", is the best alternative for this kind of investigations although its well-known higher ¹J_{CF} sensitivity must be taken into account.



¹J_{CF}: 280Hz

 $^{2}J_{\text{WE}}$: 0, 60, 120, 140, 160, 220, 280 Hz (bottom \Rightarrow top)

Yours sincerely Christian Schorn and Peter Bigler

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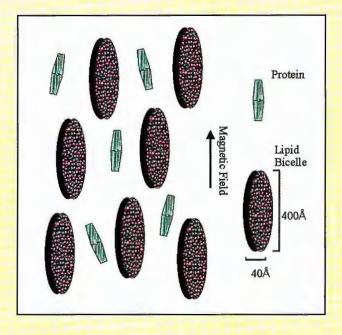
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Offline Processing of Bruker Digitally Filtered NMR Data

January 16th 2000 (received 1/24/2000)

Dear Barry,

The benefits of the oversampling procedure applied to NMR data is well known and certainly one of the most valuable aspects is the increase of the effective dynamic range of a spectrum. However, this requires collecting a FID with a great number of points to provide sufficient digital resolution. The *large* FID is digitally filtered to remove the signal outside the spectral region of interest and decimated to the desired spectral width, the whole procedure taking place on-the-fly by means of high-speed digital signal processors [1]. Unfortunately the procedure may have its own drawbacks. Commercial digital filters are proprietary, so one does not really know what has been done to the data, and some resultant processed spectra can assume a strange form after digital filtering. This seems to be the case with digital filtering employed on Bruker Avance spectrometers (Figure 1).

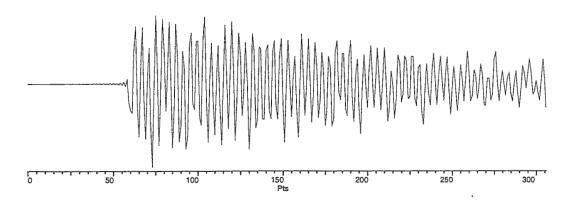
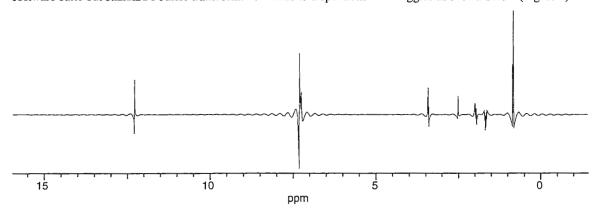


Figure 1. Beginning of typical digitally processed FID obtained on a Bruker DMX spectrometer.

Shown on the Figure 1 is the beginning of a typical digitally processed FID obtained on a Bruker DMX spectrometer. A rising signal starting from zero at the first data point and achieving a maximum at approximately the 60-th point is undoubtedly an artifact of digital filtering. The FID is correctly processed on XWINNMR, a component of the Bruker software suite but standard Fourier transformation leads to a spectrum with wiggles as shown below (Figure 2).





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Figure 2. ¹H NMR spectrum of phenylbutyric acid in DMSO (DMX-400) obtained by straightforward Fourier transformation of digitally processed FID.

The observation that the spectrum shown in Figure 2. can be made to resemble a *normal* spectrum by applying several thousand degrees of linear phase correction gave a key to correct processing of such data. As was shown by W. M. Westler and F. Abildgaard [2] an appropriate number of initial points of the FID should be circularly left shifted before Fourier transformation. The resulting spectrum is almost identical to that processed by XWINNMR (Figure 3A). It is important to perform the circular left shifting after zero-filling and/or apodization to keep the flat baseline. Shown in Figure 3B is the spectrum obtained when exponential multiplication (with LB = 1 Hz) was applied after the circular left shift. Retaining the non-zero points at the end of FID is however a very cumbersome business. Besides this can interact in an unexpected way with some offline processing steps. For example the spectrum shown in Figure 3B would result from the spectrum shown in Figure 3A by inverse Fourier transformation followed by exponential multiplication (with LB = 1 Hz).

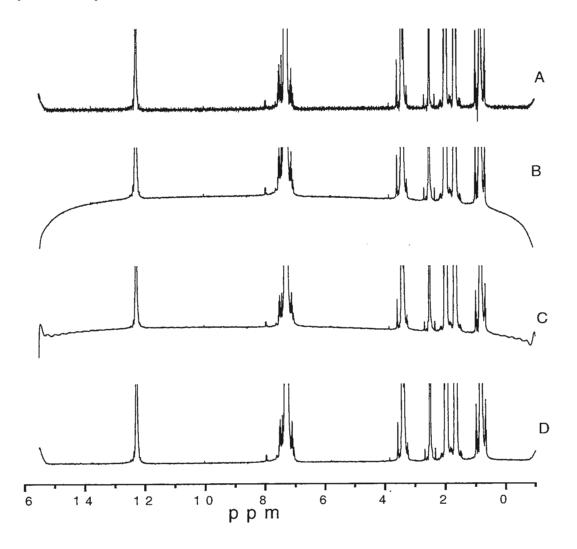


Figure 3. ¹H NMR spectrum of phenylbutyric acid in DMSO (DMX-400). A - Fourier transformed by XWINMR, B - exponential multiplication (with LB = 1 Hz) was done after circular left shift of initial points, C- exponential multiplication was done after 'digital to analog' conversion by XWINNMR, D - exponential multiplication was done after digital FID conversion by our technique

Our challenge was to think of a conversion of some kind that would allow us to treat afterwards digitally filtered data like 'normal' data. Bruker's own conversion routine "convdta" is applicable only to acquisition data [3] and sometimes significantly distorts baseline (Figure 3C) and appears to be unsuitable.



Advanced Chemistry Development

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We would like to describe our empirical treatment that was found to eliminate all resulting nuisances generated by digital filtering. The basic steps for the digitally filtered FID are the following:

- 1) zero-filling,
- 2) circular left shift of appropriate number of points,
- 3) Fourier transformation,
- 4) phasing
- 5) extracting real part and its inverse Fourier transformation,
- 6) truncating the obtained FID

The resultant FID can be processed further without any complications. The first step of the procedure is necessary to keep the number of spectral points while step 2 is that proposed by W. M. Westler and F. Abildgaard [2].

Shown in Figure 3D is the Fourier transformed result of exponential multiplication (with LB = 1 Hz) of such "converted" data. Please note that a flat baseline is retained as displayed in Figure 3A. The quality of the baseline after this conversion is dependent on phasing quality. The best baseline is achieved when the purely adsorptive part is taken as real (Figure 3D) and the worst one - when the purely dispersive part is taken as real (result is very similar to Figure 3B). The protocol for conversion of Bruker-processed 1R files is very similar and has the advantage that the result does not depend on the effectiveness of the phasing routine.

More and more institutions and laboratories are utilizing third party tools for access and processing of NMR data. We believe that a thorough examination of the quality of data generated away from the spectrometer using these tools is necessary to take into account different approaches taken by the vendors.

Yours sincerely,

C. Touothere.
Sergey Golotvin

Advanced Chemistry Development

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January 10, 2000 (received 1/11/2000)

Professor B. L. Shapiro The NMR Newsletter 966 Elsinore Court Palo Alto CA 94303-3410 USA

Renewable Resources

Dear Barry,

Since the first deployement of a supercon (200) NMR in Hungary in 1980 we collect the evaporating He gas at low pressure in a 1 m³ bell floating on an oil bath and then we regularly compress the gas in cylinders. Now, we have a 360 and a 500 magnet connected to the same recovery system. It turned out, that the 500 is sensitive to both the change in atmospheric pressure (the wheather in Central Europe is often changeable...) and the recovery process (lock level is unstable). So, when sensitive measurements were carried out we did not use the recovery system. Now, we installed an electronic absolute pressure stabilizer for the magnet He cryostat. The excess gas is fed to the same bell. The weight of the bell is a cause of an extra 20 mbar pressure in addition to the atmospheric pressure. However, the total excess pressure over the atmospheric pressure is generally less than 40 mbar, which is less than the third of the total excess pressure during a regular helium refill procedure, which shouldn't harm the magnet. The investment costs USD 2000,- and we enjoy a more stable instrument and better milage.

Yours truly,

Gyula Batta

Address all Newsletter correspondence to:

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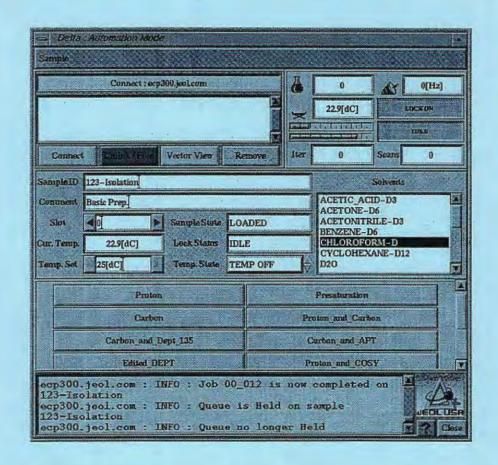
Royal Society of Chemistry: 15th International Meeting on NMR Spectroscopy, Durham, England, week of July 8-13, 2001; Contact: Mrs. Paula Whelan, The Royal Society of Chemistry, Burlington House, London W1V 0BN, England; +44 0171 440 3316; Email: conferences@rsc.org\

Additional listings of meetings, etc., are invited.

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