(57) Each substructure determined in the algorithm has its own decision function.
(58) The only exception known is the recognition of vinyl polymers and copolymers, described in reference 41.
(59) Provided the empirical formula is known explicitly or from MS.
(60) This research project is realized under the auspices of the Polish Academy of Sciences, as part of the problem MR-I-32, "New Analytical Methods".

Computer Systems for Laboratory Networks and High-Performance NMR

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Modern computer technology is significantly enhancing the associated tasks of spectroscopic data acquisition and data reduction and analysis. Distributed data processing techniques, particularly laboratory computer networking, are rapidly changing the scientist's ability to optimize results from complex experiments. Optimization of nuclear magnetic resonance spectroscopy (NMR) and magnetic resonance imaging (MRI) experimental results requires use of powerful, large-memory (virtual memory preferred) computers with integrated (and supported) high-speed links to magnetic resonance instrumentation. Laboratory architectures with larger computers, in order to extend data reduction capabilities, have facilitated the transition to NMR laboratory computer networking. Examples of a polymer microstructure analysis and in vivo ^{31}P metabolic analysis are given. This paper also discusses laboratory data processing trends anticipated over the next 5-10 years. Full networking of NMR laboratories is just now becoming a reality.

INTRODUCTION

Nuclear magnetic resonance (NMR) spectroscopy and (recently) magnetic resonance imaging (MRI) have shown remarkable development as powerful and increasingly influential analytical techniques.[1-3] In the early 1960s, NMR spectroscopy first received wide application to solution chemical structure elucidation; by 1985, NMR is ubiquitous in applications to solution and solid-state studies of small molecules, biological and synthetic polymers, molecular complexes, and even complex biosystems such as living cells.[1] Current NMR methods examine nuclei across the periodic table with increasingly complex multipulse experiments that can be designed to probe specific features of these structures. In magnetic resonance imaging, complex radio-frequency pulse sequences combine with pulsed magnetic field gradients to spatially encode resonance frequency information. Magnetic resonance images promise revolutionary change in diagnostic medicine.[3]

All of these modern NMR and MRI experiments are totally dependent on current computer techniques. In the 1960s, NMR spectrometers could add simple "computer" signal averagers; by the early 1970s, most research NMR instrumentation operated in pulse Fourier-transform mode, necessitating dedicated, if not fully integrated, minicomputer systems to control pulse generation and data acquisition, both at time resolutions of 1-100 μs. During the 1970s, commercial NMR spectrometers integrated their dedicated computers until by 1980 the computer was the central subsystem of most NMR instruments. A recent trend has been to utilize multiple computers in NMR instrumentation, distributing the tasks of pulse generation, data acquisition, monitoring instrument functions, and providing user interaction. In 1985, research NMR spectrometers utilize fast 20-32-bit word length mini-computers for central functions, with coordinated 8- or 16-bit microprocessors dedicated to spectrometer control and oversight tasks. Newly developing magnetic resonance imaging instrumentation, designed for clinical use, extends these trends with near state of the art computer and graphics technology.

Despite the advances in application of computer methods over the past 25 years, current NMR instrumentation has lagged in utilization of one of the most important developments in computer architecture: *networking*. Part of the reason for this is understandable. Until the mid 1980s, "universal" computer hardware interconnections were limited to slow protocols such as the RS-232 serial link. NMR data files, especially 2-dimensional data sets, can be extremely large—several megabytes or even much larger. NMR data transfers are thus very inefficient by these slow links.

Ethernet,[4] which is the current "standard" for local area networking, offers very high speed (10 million bits/s), but the Ethernet collision detection base-band design is not nearly ideal for large laboratory networks that can transfer very large files from several spectrometers. Unfortunately, implementation of useful NMR laboratory computer networks is currently restricted by the lack of widely implemented alternatives to Ethernet. Thus, heterogeneous configurations of spectrometers and other network nodes (fileservers for data storage, laboratory concentrators for off-line processing, mainframes if desired, etc.) mandate use of Ethernet, except when an alternative structure is provided by manufacturers—and currently this would limit networking to interconnecting instruments of individual manufacturers, without fully supported links to other computers.

There are several computer network activities especially relevant to NMR laboratories: (1) removal of primary data reduction from spectrometer computers to increase overall laboratory efficiency; (2) provision for archival data storage; (3) use of larger laboratory superminicomputers or mainframe computers to run sophisticated computational software for data reduction, simulations, etc.; (4) development of interinstrument and interlaboratory data sharing, necessitating a common implementation of data formats or "translators" for each format present on the network; (5) eventual integration of NMR data processing into *comprehensive* Laboratory Information Management Systems (LIMS).

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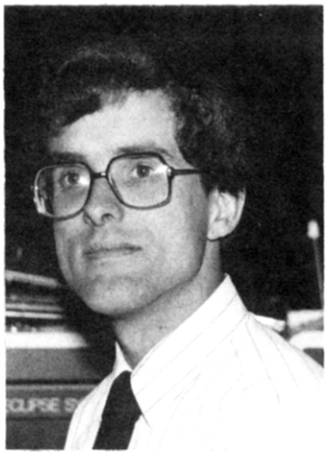

John H. Begemann (Ph.D. in chemistry, Northwestern University, 1983) is a Senior Scientific Programmer directing the on-going programming efforts of the Syracuse University NMR and Data Processing Laboratory. These efforts encompass several projects including optimization of data reduction in NMR, as well as establishment of intercomputer communications in analytical laboratories. Dr. Begemann has been at the Syracuse University laboratory for 2 years; during the last year he has been head of software development.

Implementation of capabilities as described immediately above would significantly enhance NMR research capabilities. Use of current network technology based on Ethernet will start this process; broad-band network implementations will presumably be widespread by the early 1990s.

NMR LABORATORY COMPUTER NETWORKING

Figure 1 depicts two typical (but hypothetical) NMR laboratory computer networks of 1985. In the first network

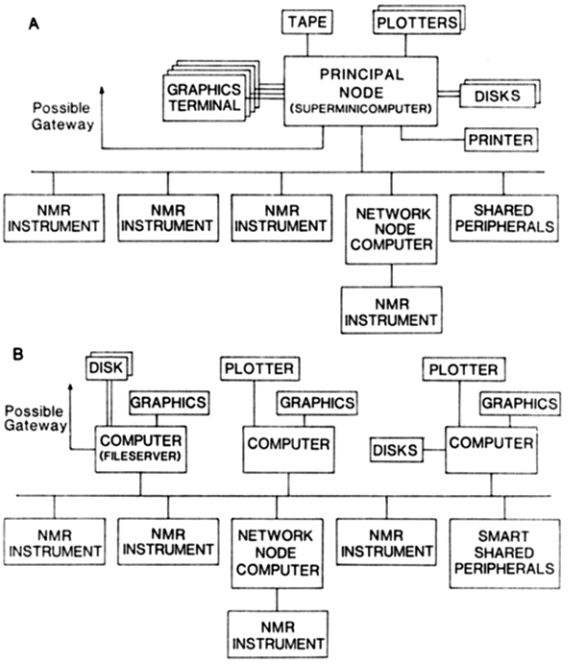

Figure 1. NMR laboratory network based on a principal node that provides most network resources. In this architecture, most NMR instruments are connected directly to the network, while other NMR instruments may require small network node computer interfaces to the network. (B) Distributed model for NMR laboratory computer network. In this case, several smaller computers can be used for network and data reduction tasks. Disks, graphics systems, and plotters are generally attached to individual computer nodes. NMR instruments that cannot be directly attached to the network go through network node computers as in (A), but here, the network node computer is likely to also be a data reduction computer. A distributed architecture does not prevent use of shared peripherals as indicated in (B).

architecture (Figure 1A), a centralized node performs essentially all high-level data processing functions, acts as file server, operates peripherals, etc. In the second example (Figure 1B), there is no central node; processing and data storage are distributed in the network. The processing node of the centralized network typically is a superminicomputer such as a Digital Equipment VAX (or PRIME, Perkin-Elmer, Data General MV, etc.) running a multiuser multiprogramming operating system; in the decentralized network, smaller laboratory computers or (super) microcomputers are typically used. In both network approaches, some NMR instruments may be connected to computers acting as network interfaces (or in network 1B, additionally as full processing stations). This may be necessary if an NMR manufacturer has not implemented network hardware/software in its instrument.

Early centralized laboratory networks have included implementations at the General Electric Corporate Research and Development Laboratory in Schenectady[5] (although FT NMR was not included) and our own system started at Florida State University[6] but now evolved somewhat differently at Syracuse University. Decentralized NMR networks are being developed at the Universities of Wisconsin and South Carolina, based on IBM CS/9000 nodes (although in at least one case, a central VAX node will be added).

It should be pointed out that current NMR laboratory computer networks do not support all networking activities. At this point in time, data flow is largely restricted to offloading spectrometers, data reduction, plotting, etc., and data storage. Reverse-direction data flow and generalized interprocessor communications are yet to be implemented. There are at least two obstacles to complete networking of NMR laboratories. The most significant problem is nonuniformity of data formats, file headers, and even languages. In fact, at

least one of the manufacturers does not exercise proper control over *changes* in file-header structure from one release to another *of the same program.* A second obstacle to full computer networking results from the fact that the individual manufacturers are not uniformly choosing any specific Ethernet network protocol (nor are they apparently planning support of gateways to provide internetwork communications).

It is, of course, necessary to be concerned about the network protocol since the Ethernet standard defines only the first two of seven network software layers (ISO model, Figure 2). At this point in time, at least three network protocols may be implemented by different groups including proprietary protocols such as DECNET, XNS, and the TCP/IP system, widely implemented for UNIX operating systems (and embedded within Berkeley UNIX-BSD 4.2).

The most significant current networking task in NMR laboratories is off-loading data reduction from the spectrometer computer. Manufacturers of commercial NMR instrumentation currently provide satellite processing in one of several modes, generally using similar computers as in the spectrometer but without data acquisition hardware. Packages provided by the NMR instrument companies may be limited to use with instruments of that manufacturer (Table I). Even though NMR laboratory computer networks are as yet rudimentary, distributed processing serves critical needs for high-performance NMR. There are two main factors: one economic and the other scientific/technical: (1) A state of the art NMR instrument costs $300 000–$600 000 or more and its throughput is generally limited by data reduction, plotting, and other processes not directly linked with data collection. Even with multitasking instrument computers, this bottleneck can be severe. (2) The second factor comes from the fact that computer hardware and software available on commercial NMR instruments are not sophisticated enough to provide higher level data processing capabilities. Recent integration of array (or vector) processors has greatly enhanced spectrometer data processing in 2D FT NMR, where the sheer quantity of data is limiting. However, augmentation of a simple micro- or minicomputer with a vector processor does not alleviate two other limitations of these computers: limited address space and, more important, limited computation power for high-level "intelligent" algorithms, including 32-bit and extended-precision floating point formats for statistical and other computations.

Current 32-bit superminicomputers are appropriate for such computations. Use of these systems (Digital Equipment VAX, Data General MV, PRIME, etc.) is further enhanced by their collective characteristics: (1) Power to execute >1 million instructions per second in fixed point *or* floating point formats; support of fast double-precision floating point calculations. (2) Efficient virtual addressing to 512 megabytes or larger (up to 4 gigabytes). (3) Input/output (I/O) bandwidth to allow a large number (typically 32–128) of fast serial ports with significant, simultaneous parallel I/O (disks, graphics, and other peripherals). (4) Use of high level multiuser multiprogramming operating systems with powerful software development environments.

Points 3 and 4 are often overlooked in evaluation of computers for scientific laboratories. A high (preferably ≫10 megabytes/s) I/O bandwidth is necessary to support the level and mix of activities expected of a principal laboratory network node. Modern superminicomputer operating systems provide software development environments (compilers, editors, high-level debuggers, program control utilities, etc.) that greatly improve productivity in programming, making palatable development of large and complex software systems.

It is axiomatic that tomorrow's personal computers (PC's) will be able to do >1 million floating point calculations (MFlops) per second. (Of course, tomorrow's superminicomputer will probably have an average speed of 5–10 MFlops). Whether inexpensive PC's will develop the necessary I/O structure to operate as versatile central network processing nodes is questionable, but they certainly will become efficient personal processing nodes in distributed networks (Figure 1B).

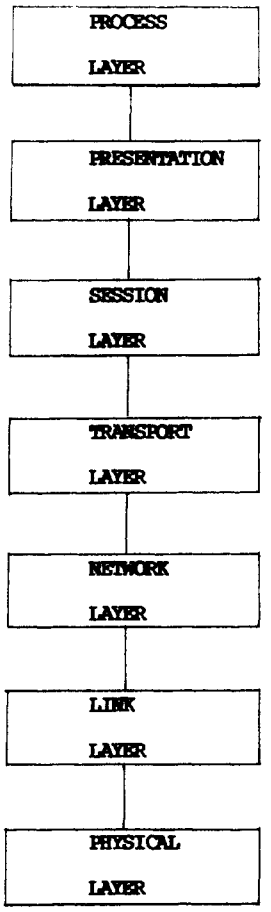

Figure 2. ISO model for computer networks.

A third type of computer system, the engineering/scientific work station (e.g., Apollo, Sun, etc.), bridges the gap between personal computer and superminicomputer. High-end work stations have supermini computational power but are not configured with I/O for many simultaneous users. The work stations do include integrated high-resolution graphics systems and network environment utilities; many are based on UNIX or UNIX-like operating systems.

Optimal exploitation of an NMR computer network requires advances in data processing capability along with throughput and communications and availability of (archival) data. The next section discusses advances in data reduction software that can provide NMR laboratory networks with added tools with which to pry information from the experimental data.

SOFTWARE FOR REDUCTION OF NMR AND OTHER SPECTROSCOPIC DATA

In the 1960s, FT NMR data reduction typically encompassed performing a magnitude fast Fourier transform (on-line phase-sensitive calculations were not implemented at that time) and plotting the results. The standard tools of modern NMR instrumentation data reduction have developed over the last 15 years (Table II). Current NMR data reduction is far faster than was possible even a few years ago, and there have been significant advances in the degree of sophistication of certain algorithms (e.g., phasing, apodizations), but all present instrument data reduction software remains basically *interactive*, with the spectroscopist making processing decisions

Table I. Commercial Off-Line NMR Data Reduction Systems

NMR instrument manufacturers	primary instrument (cpu)	offered satellites	NMR instrument program language	software links to various NMR instruments	data reduction software	comments
Bruker	Aspect-3000 (24 bit)	peripherals only (option 1) 24-bit Aspect 1000 (option 2)	Assembly, Pascal	no	same	option 2 can include various plotters
GE NMR (Nicolet)	Nicolet 1280 (20 bit)	Nicolet 1280 (option 1) VAX or μ-VAX (option 2)	Assembly	no	some NMR1, NMR2	option 2 under comarketing agree with New Methods Research, Inc.
IBM Instruments	Aspect-2000, -3000	CS/9000	Assembly, Pascal	some	Pascal Program	can be networked by RS-232 links
JEOL	JEOL & DEC PDP-11	DEC PDP-11	Pascal	no	same	
VARIAN	Advance 4000 (Motorola 68 000 based 16/32 bit)	Advance 4000	Pascal	some	same	
Mattson instruments		Starlab-100 (Motorola 68 000)		some	2D NMR (D. Hare)	
New Methods Research, Inc., and Syracuse University[a]		DEC VAX DG MV Apollo Sun others		yes	NMR1, NMR2 (Fortran 77) environments	wide variety of supported hardware

[a] The NIH Biotechnology Research Resource for Multi-Nuclei NMR and Data Processing, Syracuse University.

Table II. Evolution of the NMR Data Reduction Process

timeframe	hardware	added capabilities
1970s	Varian 620i, Nicolet 1080, Bruker BNC, Texas Instruments 900 series	standard interactive phasing, etc.; tape, floppy, and hard disk storage of spectra; simple base-line corrections; peak pickers; analog plotters, and then dumb digital plotters
1980s (early)	Nicolet 1180, Bruker-Aspect 2000	foreground–background processing and data acquisition; color raster graphics; improved base-line corrections; automatic phasing (often but not universally reliable); satellite processing; 2D FT NMR processing; multitasked processing
1985	Varian Advance, Nicolet 1280, Bruker-Aspect 3000, JEOL GX series (LSI 11)	integrated arrays processors for 2D FT and other functions; improved display algorithms; smart plotters; macroinstructions

based on what he or she sees at a graphics terminal. Examples of noninteractive algorithms that have been used (although not yet on commercial spectrometers) include extensions of Pearson's base-line flattening,[7] DISPA analysis and automatic phasing using DISPA,[8] deconvolution of overlapping lines by automatic curve fitting,[9] signal to noise and resolution improvement using the maximum entropy method (MEM),[10] etc.

In 1977, our group began development of a spectroscopic data reduction system that utilized sophisticated, statistically based algorithms to impart a measure of intelligence to the software and to prevent results from unintentionally reflecting user bias.

(A) An Approach to Intelligent NMR Data Processing: The NMR1/NMR2 Project.[7] Design considerations can vary for a high-level software system to optimize data reduction in Fourier-transform spectroscopy. In our situation, we initially set the goals listed in Table IIIA, which also lists design considerations and constraints that resulted from the designation of those goals.[7] Table IIIC lists goals that were added over the period 1983–1984 to further develop the software and to direct the project toward development of the first family of expert systems for *characterization of the quantitative information resulting from NMR and other spectroscopic/imaging experiments*.

The magnitude of work involved in the NMR1/NMR2 project has been significantly increased by the need to produce portable code that supports a variety of peripherals as well as central processing unit environments. By the close of 1984, approximately 30 man years had been expended, including code development and maintenance. In early 1985, seven professionals and nine student programmers (largely computer science students) were working on NMR1 or NMR2 and their projected extensions.

A primary motivation for development of these software systems was to develop improved methods for quantitating spectral features in difficult chemical and biomedical NMR spectroscopy. An example of the former application is accurate peak area measurement for spectra having a very large dynamic range (with peaks having areas over a ratio of 10^3 to 10^4 in a single spectrum). An example of a biological application is quantitation of high-energy phosphates in an in vivo metabolic NMR spectrum (in vivo spectra are usually characterized by low signal to noise—short time acquisitions are typical—and poorly defined base lines and line shapes.

Two examples of NMR1 processing sessions are described immediately below. In each case, the NMR spectra were recorded on a Bruker WM-360 wide-bore FT NMR spectrometer. Data were transferred in one case to a Data General MV/8000 and, in the other case, to a digital Equipment VAX 11/750 via RS-232 link using a transfer/file-header decoding program developed for NMR1.

(1) Polymer Tacticity Analysis from ^{13}C NMR. ^{13}C NMR

Table III. Design Goals and Design Considerations for the NMR1/NMR2 Data Reduction Software Systems

(A) Early Goals

(1) complete separation of the data acquisition and data reduction processes
(2) allow multiple users simultaneous access on one computer
(3) provide as much hardware independence as possible
(4) design a software system that does not require extensive user interaction in processing data
(5) use of algorithms for spectral conditioning and analysis that utilize statistically-based decisions, avoiding unintentional introduction of operator bias
(6) design of a program architecture that is easily extended and adapted for new capabilities
(7) a design that is highly flexible for expert users and highly prompting for novice users; extensive user help

(B) Design Considerations and Constraints

(1) use of computers with large address space and multiuser operating system
(2) all code is written in FORTRAN 77 (largely structured)
(3) program design is top-down and modular
(4) the programs provide support for 15 graphics devices (adding more all the time!), but this necessitates compromises in usage of graphics features, such as cursors and input devices (restricted to keyboards in most implementations of NMR1/NMR2)
(5) the sheer size of the programs mandate a virtual memory operating system
(6) floating point implementation for highest dynamic range and for statistical treatments requires efficient floating point execution, eliminating use of some hardware

(C) Added Goals (1983–1984)

(1) extend statistical methods to independently evaluate intermediate results
(2) automated tracking of spectral features with full statistical analysis of changes in peak intensity, position, etc. (relaxation analysis, kinetics, etc.)
(3) develop on-line parser/interpreter to insert user-selected equations, and relationships (e.g., for evaluation of complex kinetics)
(4) design versatile program command language with ability to develop complex, totally automated analysis protocols that support conditional branching, etc.
(5) develop custom analysis modules for automated polymer analysis (tacticity, degree of polymerization, etc.) and other specific applications; include user-specific database where appropriate
(6) extend individual user customization capabilities, adding parameters, flags, and user-interface characteristics to personality profiles that are kept between sessions
(7) provide initial software interfaces for future development of postprocessor Expert Systems
(8) develop initial logic programming applications (e.g., 2D FT NMR peak picker, including logical differential of "real" peaks from experimental artifacts and noise)
(9) install as modules user-friendly versions of existing spectroscopic software packages (e.g., LAOCOON5, DAVINS, DNMR5)
(10) develop maximum entropy method (MEM) algorithms for simultaneous signal-to-noise and resolution enhancement, phasing, automatic spectral conditioning, ab initio deconvolutions, etc.
(11) develop and optimize capability for 3D and 4D (chemical shift–volume imaging) NMR

spectra have significant application to evaluation of the tacticity of synthetic polymers.[11] ^{13}C shieldings in vinyl polymers, for example, are sensitive to remote stereochemistry such that *pentad*, and often *heptad*, structures (stereochemical configurations over three bonds from the observed carbon in each direction) are distinguished. At high magnetic fields *heptad* peaks can even shown *nonad* fine structure. While microtacticity is well reflected in ^{13}C spectra, significant overlap of *triad* and especially *pentad* or *heptad* bands makes quantitation difficult. Typical NMR tacticity studies are undertaken with initial evaluation (manual quantitation) and assignment of bands and subsequent entry of results into computational routines on mainframe computers. NMR1 can perform polymer tacticity analysis in a totally automatic mode once

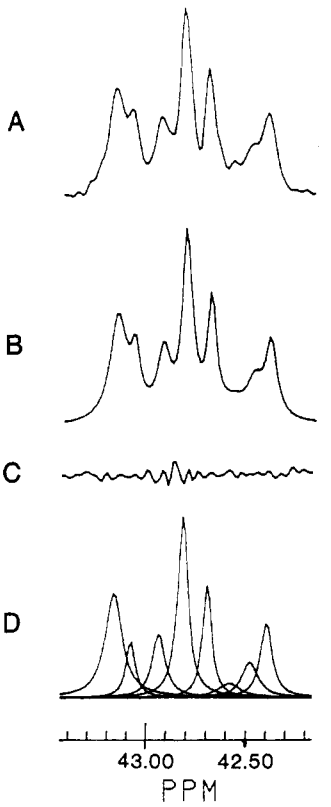

Figure 3. (A) Expanded view of the vinyl CH carbon region of a polyacrylamide sample. (B) Modeled spectrum using NMR1 automatic curve fitting. (C) Difference spectrum between experimental and modeled spectra. (D) Individual spectral components of curve fit calculation.

relevant peak assignments are made and placed in the user database.

We can follow a tacticity analysis through spectral figures. The spectrum of the vinyl carbon region of a polyacrylamide sample is shown in Figure 3A. The vinyl C-H carbon region used in this case for tacticity determination is shown along with a separated spectrum of the individual pentad peaks (Figure 3D), as "deconvoluted" automatically by the NMR1 Levenberg–Marquardt nonlinear curve fitting algorithm. The program then assigns the quantitated peaks by using a previously determined database for polyacrylamides. A typical result is shown in Figure 4.

In this case, the peak at 42.84 ppm was not resolved by the program (but this does not prevent continuation of the analysis). The program next calculates the polymer's exact tacticity (including probabilities, number average sequence length, simulations) by using previously determined models and parameters.

All of the above can be achieved in a few minutes on a small VAX or equivalent computer without any user intervention, or even presence. Much of this time is devoted to curve fitting of the C-H carbon spectrum, quantifying eight pentad structures of 10 possible pentads.

(2) In Vivo ^{31}P NMR Spectra. An analogous automated sequence can be applied to characterize metabolic ^{31}P NMR spectra.[12] In this case, the user database consists of spectral assignments for various tissues (or human red blood cells, for example). In vivo spectra, in particular, suffer from limited signal to noise and ill-defined line-shapes over a poorly defined base line.

NMR1, with signal conditioning and peak analysis including quantitation using statistical curve fitting, is ideally suited for in vivo spectra obtained with surface coils or from chemical shift imaging (thus far, largely limited to ^{1}H chemical shift

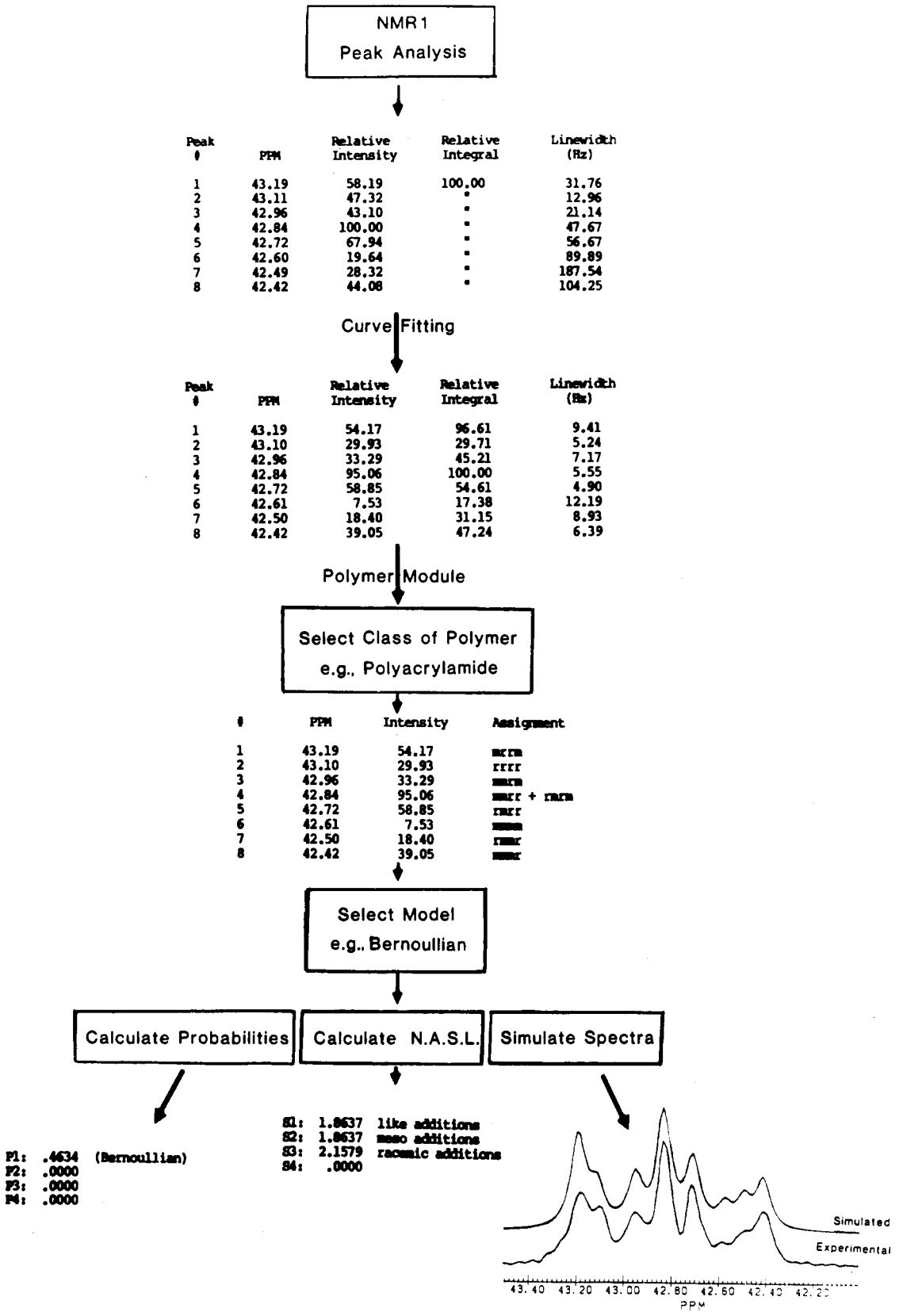

Figure 4. Evolution of a polymer analysis in NMR1 (same polymer sample as in Figure 3).

imaging). The NMR1 ^{31}P analysis module automatically determines high-energy phosphate to inorganic phosphate ratios, tissue pH, etc., after identifying and quantifying all spectral peaks (identification from database entries).

(B) NMR2, a Software System for Reduction of 2D FT NMR and MRI. NMR2 is a newer package derived from NMR1, designed to process two- (or higher) dimensional data. Implementation on 32-bit computer architectures allows very large matrices to be processed: typically up to 32 million floating point data elements (130+ megabytes).

Aside from standard 2D FT NMR data reduction capabilities, future incorporation of logic programming into NMR2 is expected to add (1) pattern recognition features including rejection of artifact peaks, (2) evaluation of quantiative analyses, (3) automatic connectivity determination, etc. Extension of NMR2 algorithms to three- and four-dimensional

data arrays will support future medical applications of NMR, including volume (3D) and volume plus spectrum at each volume element or voxel (4D) imaging. These extensions will truly tax data processing capabilities. Even the advent of faster cpu's and array processors addresses just part of the problem. A moderate resolution 4D image [128 × 128 × 32 (slices) × 512 (point spectrum)] generates a data set with a quarter billion data elements (1 gigabyte for floating point data)!

(C) Maximum Entropy Method. A recent concept, the Maximum Entropy Method (MEM), shows significant promise for both 1D and multidimensional NMR spectroscopy and magnetic resonance imaging. MEM utilizes a mathematic method that extrapolates data from the first portion of an FID, where *S:N* is highest, and retains all possible line-shape information, avoiding line broadening and side lobes (which arise from FID truncation when FFT calculations are performed). The maximum entropy method has been shown to increase apparent NMR *S:N* by 1 order of magnitude while simultaneously optimizing spectral resolution. MEM does pay a penalty in computational requirements since the process requires both more computer memory and more cpu time (up to 1 order of magnitude more memory addressed and up to 2 orders of magnitude more cpu cycles). The potential for MEM is outstanding, particularly differentiating real signals in 2D FT NMR and suppressing artifacts in MRI. Implementation of MEM is clearly facilitated in NMR laboratory networks based on powerful processing modes.

HARDWARE TRENDS

There are a number of current digital hardware trends that will greatly enhence opportunities for networking in NMR laboratories. Of course, actual implementation of these future networks will necessitate a measure of cooperative software development by NMR manufacturers. The paragraphs below detail some of these trends.

(A) Personal Computers with Significant Computational Power, Extended Address Space, and Networking Hardware/Software. Yesterday's personal computer (PC) was based on an 8-bit cpu with 64K program address space, low-resolution graphics, RS-232 communications, and speed of 100K instructions per second (far less for floating point calculations). Today's PC is typically a 16- or 32/16-bit cpu with 1–16 megabytes address space, medium-resolution graphics, optional Ethernet communications, and speed of 300–500K instructions per second (although usually much lower for floating point calculations). By the end of 1986, scientific PC's with the following characteristics should appear: 32-bit cpu with 512 megabyte to 4 gigabyte virtual memory, 1K × 1K (or 768) resolution high-speed color graphics, integrated Ethernet communications (probably TCP/IP running under UNIX), and 1–4 million instructions per second speed. *Memory will cost ~$800 per megabyte.*

Such personal computers and scientific workstations will be able to replace current superminicomputers in distributed network architectures, although it is likely that limitations on users, disk, and other peripheral I/O will prevent such systems from acting as central nodes in large laboratory networks.

(B) Network Hardware and Implementations. The future of computer networking hardware resides in broad-band technology, based in large measure on CATV components and methods. Broad-band networks today have effective bandwidths as high as 350 MHz, with significantly higher frequencies promised. Broad-band networks containing several copies of Ethernet or other base-band networks are also being implemented.

The near-term success of NMR laboratory computer networks depends on common and complete implementation of Ethernet including gateways between Ethernet systems (TCP/IP and DECNET, for example). Some new hardware is appearing with ROM-based implementation of TCP/IP or other network protocols; implementation in silicon may follow this development.

Current estimates of the maximum *throughput* of Ethernet networks range from 3 to 5 million bits per second (Mbs); some reports place limits considerably lower.[13] NMR manufacturers may not even be able to fully utilize the Ethernet bandwidth with current instrumentation. Ethernet-based networks have liberal total length restrictions, and interbuilding connections are allowed. In cases where the network physical size is very large, network repeaters must be installed.

(C) Array Processors. Two of the exciting areas in magnetic resonance—2D FT NMR and imaging, including chemical shift imaging—require Fourier transform and other processing of large multidimensional arrays. Volume imaging (or planar chemical shift imaging) and volume chemical shift imaging require three-dimensional and four-dimensional FT processing, respectively. The size of these tasks can easily be underestimated. Current and future 2D FT analytical NMR can utilize arrays of 2K × 8K, or larger (2K × 8K corresponds to 16 777 216 data elements). For the case sited, 10 240 Fourier transforms are required, as well as weighting, transpose, conditioning, plotting, analysis, etc. In medical applications of NMR, future data arrays could have 512 × 512 × 32 (slices) × 1024 (spectral dimension) = nearly 10^{10} data elements! Such an NMR data array would not be practical for analysis on today's computers.

Array processors can improve performance times for FFT computation by factors of 1000 or more, but enhancement of other data reduction calculations may be far more modest. Also, sheer computational speed is not sufficient; an array processor for NMR either needs a very large local memory or needs a very high bandwidth to host memory. Current array processors range from single board systems (e.g., SKYMNK) to fully packaged subsystems (e.g., ANALOGIC AP400 and 500, CSPI MAPs, Floating Point Systems 5000 series, STAR Technologies ST100, etc). Current speeds range from 1 to more than 20 MFlops (the latter corresponding to <2 ms for a 1024 complex point FFT or a 512 × 512 2D FFT in well under 1 s). It should be pointed out that NMR instruments having integrated array processors are now widely available, with software development reflected in the price charged by manufacturers for this option.

(D) Non von Neumann Computers. Array processors are a special class of non von Neumann machine. The ultimate NMR instrumentation of the 1990s may require fully non-traditional computer hardware, combining aspects of database mechines[14] and architectures used in artificial intelligence applications. Those NMR instruments will also have significantly enhanced traditional computational power, probably equivalent to a current small mainframe.

(E) NMR System Computers in 1995. Along with the computer characteristics discussed immediately above, one should note the probability that a 1995 state-of-the-art NMR system will probably have far more than 10 integrated computers communicating at high speed on an internal computer network. Users will be able to control spectrometer functions by voice control among other inputs. Color graphics (3D?) will have at least 2 million pixels. New pulse sequences will be designed by the computer, on request from the user; the spectrometer will instruct itself to perform additional experiments, if indicated by initial results. And experimental results will include automated compound identification or, in the case of magnetic resonance imaging, automated diagnosis of human disease.

It is an exciting time we live in!

ACKNOWLEDGMENT

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