(37) Haraki, K. S.; Venkataraghavan, R.; McLafferty, F. W. "Prediction of Substructures of Unknown Mass Spectra by the Self-Training Interpretive and Retrieval System". *Anal. Chem.* **1981**, *53*, 386-392.
(38) Sharaf, M.; Stauffer, D. B.; McLafferty, F. W., in preparation.
(39) Mun, I. K.; Venkataraghavan, R.; McLafferty, F. W. "Computer Assignment of Elemental Compositions of Mass Spectral Peaks from Isotopic Abundances". *Anal. Chem.* **1977**, *49*, 1723-1726.
(40) Mun, I. K.; Venkataraghavan, R.; McLafferty, F. W. "Computer Prediction of Molecular Weights from Mass Spectra". *Anal. Chem.* **1981**, *53*, 179-182.
(41) Heller, S. R. "Chemical Information System and Spectral Databases". *J. Chem. Inf. Comput. Sci.* **1985**, *25*, 224-231.

Structure Elucidation System Using Structural Information from Multisources: CHEMICS

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One of the best ways of structure elucidation would be if a system could select the most probable structure from a gigantic file including all the possible structures that are known to exist, or that might exist from a chemical point of view, with the help of structural information, for example, a chemical spectrum. However, it is not possible to store all possible structures in a file. For example, even $C_{23}H_{48}$ has 5 731 580 isomeric structures. To overcome this, the present CHEMICS is designed to store all the substructures (called "components") necessary for building any likely structures. The set of components has been devised so that it is possible to construct any structure by selecting appropriate components from the component set. To store such a set of components in a computer is logically synonymous with storing all the complete structures that could be present. CHEMICS (CHEMICS-6) contains 189 components for the structure elucidation of organic compounds consisting of only C, H, and O atoms. A trial and error method was adopted in the selection of these components, with due regard to the prerequisites that the components should have no substructures overlapping one another and that the presence of the components could be deduced from structural information such as molecular formula and spectral data. Furthermore, 572 components have recently been prepared for CHEMICS-7 to handle samples that contain N, halogen, and S atoms in addition to C, H, and O. In the image space, all components are possible for an unknown compound (the analyst faces an almost infinite set of possible structures when he is without any structural information). CHEMICS-6 and -7 have the following tasks: (1) to eliminate unappropriate components, from the prepared component set, that are inconsistent with the molecular formula and spectral data; (2) to generate complete structural formulas from the retained components; (3) to exclude unlikely structures from those that have been generated; (4) to generate possible stereoisomeric structures, if a candidate structure possesses a stereocenter; (5) to output the most likely candidate structures, ideally the single correct solution. This paper describes the progress story up to the present CHEMICS. As to the details of the current CHEMICS, readers are requested to refer to the article that appeared in *Computer Enhanced Spectroscopy* (**1983**, *1*, 55).

Organic chemists acquainted with chemical information sciences have developed the ongoing system CHEMICS,[1-3] which is a total system of chemists, by chemists, and for chemists. The acronym stands for Combined Handling of Elucidation Methods for Interpretable Chemical Structures.[3] The system has been designed so as to enumerate exhaustively all possible structures consistent with given information for unknowns of moderate-sized structures. This system will work well to give more precise response by combination with a spectral file retrieval system (Appendix 1). CHEMICS has been improved step by step, and there are several versions of CHEMICS (the CHEMICS family) as shown in Figure 1. The value of each version of CHEMICS is not sequential but vectorial (Table I). The present paper will describe the main principles used in CHEMICS development.

Earlier versions of CHEMICS, as will be described later, presented only partial structures derived from spectral data input.[1,4,5] Now the system enumerates all possible structures by means of a set of possible components extracted from the list of whole components that are necessary and sufficient to build any kind of structure (Appendix 2, Figure 2).[6,7] The extraction is carried out by the comparison of the unknown's spectral data and molecular formula with the list followed by checking them by ^1H and ^{13}C NMR spectra again (Appendix 3).

AUTHORS' STAND ON THE SYSTEM CONTRACTION

Use of All Available Information from Multisources. CHEMICS makes it a general rule to utilize any relevant information that is available. However, use of much effective information is compelled to be postponed due to two main reasons. One is the limitation of the hardware available for our use. Because of this limitation, only a small part of the given information was utilized in CHEMICS. The limitation was particularly significant at the earlier stage of development, when only a computer with a cpu core of 4K 16-bit words was available. The other is the difference between styles of elucidation of human chemist and CHEMICS. Human chemists treat all things as working hypotheses because chemical knowledge is not always well-defined, so that a determined structure is only one of the possibilities afforded by a complex

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cycle comprising induction, deduction, and abduction processes. In fact, only a few papers of structure revision have been published hitherto. On the other hand, CHEMICS accepts only the chemical knowledge remodeled for computer usage. The remodeling is carried out by transformation of ambiguous knowledge into clearly defined statements.

In the earliest stage, CHEMICS used ^{1}H NMR, IR, MS, and UV data.[1] For more efficient use of UV and MS data, deeper analysis and larger resources were necessary; thus, they were set aside at that time. Instead, ^{13}C NMR data[8] and partial structures that can be arbitrarily entered by an operator have been employed.[9] In CHEMICS, a whole structure is expressed by a combination of partial structures. It is desired that all signals in the spectrum could be assigned to interaction among those partial structures. These molecular mechanistic methods[10] are too difficult from a theoretical point of view to be applied in current CHEMICS. Such methods should be included in the system as important sources of information for handling compounds with more complex structures.

Correctness Assurance of Deductions. CHEMICS assures that structures retained are consistent with the data used.

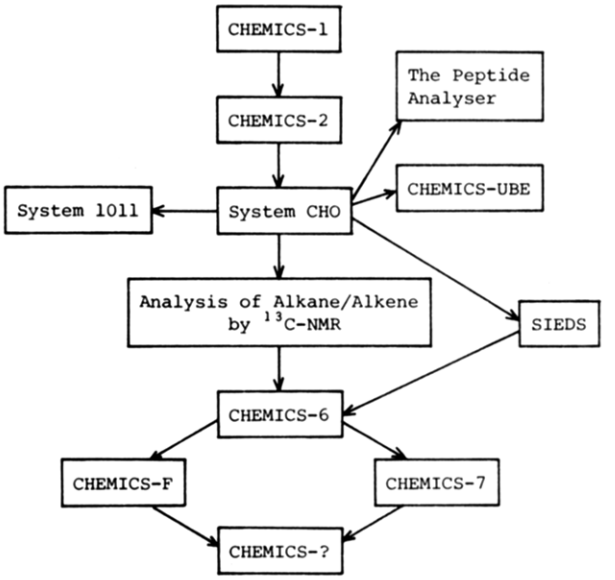

Figure 1. CHEMICS family.

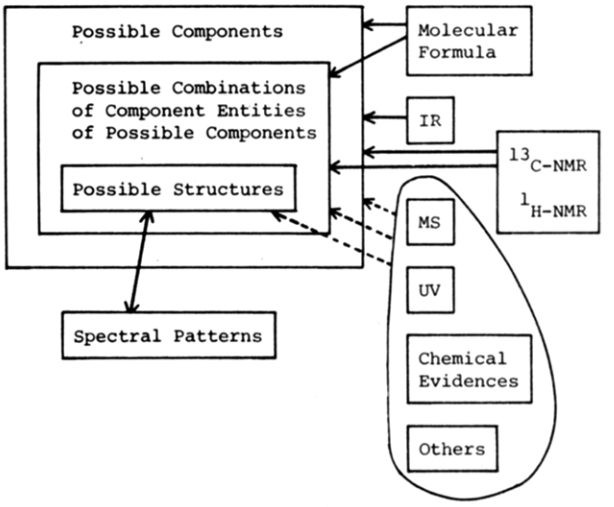

Figure 2. Procedures being used in current CHEMICS.

CHEMICS assures the enumeration of a working hypothesis under the assumption that all the theories, empirical rules, and data used in the system are fully correct. The CHEMICS system will not judge whether these theories and empirical rules are correct. If a contradictory theory were given to the system, the system would answer that there are no relevant structures. Thus, CHEMICS is operated on the basis of "correct" theories alone; therefore, accumulated logical operations will never increase the ambiguity of the deductions.

Informational Homologues (Appendix 4).[2,11] Spectral data, chemical data in general, are said to be "shadows" of the original structure of a chemical substance. Deduction of a structure from its shadows is always shadowed with some ambiguity. Generally, the minimum amount of information is required to discriminate objects with a certain ambiguity, i.e., entropy. Conversely, any given amount of information has an intrinsic maximal ability of discrimination. The members in a group discriminated by a certain information are called "informational homologues" for the information. There will be two approaches for determining informational homologues: "netting" and "angling" (Appendix 5). The usual structure determination is forced to use a picking up method (angling) because the boundary of searching area is not specified (Appendix 6). Thus, it happens upon occasion in this approach that the results are subject to structure correction (Appendix 7). In other words, unsuccessful results were caused

Table I. Areas CHEMICS Covers

version	C	H	O	index of hydrogen deficiency	N	other elements	notes (source of information)
CHEMICS-1	14	∞	1	3	0	0	^{1}H NMR, MS, IR, UV
CHEMICS-2	∞	∞	∞	0	0	0	^{1}H NMR, IR
System CHO	∞	∞	∞	0	0	0	components first adopted
System 1011	10	∞	1	1	0	0	^{1}H NMR, MS, IR, UV
SIEDS	∞	∞	∞	∞	∞	∞	structure constructed by inputted substructures
CHEMICS-6	∞	∞	∞	∞	0	0	^{13}C NMR newly added; also, substructures by operator
CHEMICS-F	∞	∞	∞	∞	0	0	spectral file search used complementarily
CHEMICS-UBE	∞	∞	∞	∞	0	0	modified for industry use
CHEMICS-7	∞	∞	∞	∞	∞	S, halogens	^{1}H and ^{13}C NMR
CHEMICS-?	?	?	?	?	?	?	?

by the fact that a single hypothesis (a working structure) had been found but another more plausible hypothesis had not been noticed. On the contrary, CHEMICS makes an exhaustive survey, leaving no unchecked omissions (netting) on the basis of the assumptions that all the theories used in the system are correct. Thus, if the CHEMICS approach had been taken, such uncorrect results as mentioned above may have been avoided.

THE HISTORY OF CHEMICS

CHEMICS-1[1] **(The Origin of CHEMICS-1).** The first CHEMICS system only presented likely partial structures by using ^{1}H NMR, IR, MS, UV, and molecular formula. Immediately after the paper was read at the Pittsburgh Conference on Analytical Chemistry and Applied Spectroscopy, 1968, *Chemical and Engineering News* announced it very sensationally. As for the others, only a few papers[12] on the automated structure analysis using MS alone were published, mainly C. Djerassi et al. at the same period. The only total system, in some sense, in those days was the one proposed by M. E. Munk,[13] in which an organic chemist determined a necessary and sufficient set of partial structures of an alkaloid and a computer composed all the possible structures by proper combination of them.

CHEMICS-2.[4,5] A series of open-end lists (a kind of knowledge data base) were prepared, which involved components with their necessary conditions such as the numbers of atoms, the range of spectral signal positions, etc. Those components either overlapped or not. When the data of an unknown sample are given, the system searches the lists for the possible components by checking their agreement with the data.

System CHO.[7] Evaluation of CHEMICS-2 from users' point of view proved that the system could not make users feel that they obtained definite and conclusive information. The system would not make positive approval of the presence of displayed results and would tell nothing about undisplayed ones. Therefore, the system was improved to give definite meaning to both displayed and undisplayed results. Namely, CHEMICS was meant to decisively deny the possibility of the presence of undisplayed structures and to positively assert that relevant structures are to be found only among displayed structures. Display of more than one structure was meant to suggest that sufficient information has not been prepared for precise structure analysis. In order to realize the concept just described, preparation was made of a necessary and sufficient set of fundamental partial structures (called components) by which any kind of structure can be constructed. A 182-component set was previously stored in a computer and waited for the coming of unknown data.

The introduction of ^{13}C NMR to the system, which had become familiar with organic chemists, was examined to determine whether the data are useful for the selection of the above components. The first application of ^{13}C NMR data was initiated by the analysis of alkanes and alkenes.[8] Because mass spectral data analysis requires rather large memories, it was decided to replace them by ^{13}C NMR. The entry of appropriate substructures by users or prediction of the signal numbers of ^{13}C NMR for each candidate structure was also discussed at this period.

System 1011.[14] Extension of the survey range rapidly tends to decrease the depth of the analysis. Therefore, a trial was made to narrow the range for deepening the analysis. System 1011 handles compounds with 10 or fewer carbons, 1 oxygen, and 1 index of hydrogen deficiency. The number of structures generated was quite satisfactory for all the compounds within this limitation.

SIEDS (Structural Isomers Enumeration and Display System).[9] This is an interactive system that receives only the partial structures specified by a user in accordance with his chemical knowledge. Then, the system displays possible structural formulas on a CRT. The system of Munk[13] requires a user to prepare a complete set of necessary and sufficient partial structures, while SIEDS only requires him to input molecular formulas and arbitrary partial structures. A user of SIEDS composes arbitrary partial structures by use of the basic component set, which the system has prepared, and specifies the range of numbers (maximum, minimum) of the partial structures. The latter function is quite unique.

CHEMICS-6.[15] As described above, many kinds of approaches had been examined, and the stationary system, CHEMICS-6, for the elucidation of the compounds with C, H, and O was established. For description of more precise analysis of ^{13}C NMR, the component of carbon connecting to other than neither hydrogen nor methyl was further subdivided (Appendixes 2 and 3).

CHEMICS-F (Appendix 1).[6,15] A function to compare standard data of different kinds of spectra (IR, NMR, MS) with the data of the unknown was added to utilize the information from the unknown's spectral data thoroughly. One of the problems is how to prepare such multispectral files including a huge number of structures with their standard spectra.

CHEMICS-7.[16] CHEMICS-6 was extended to CHEMICS-7 to handle compounds containing N, S, and halogens in addition to C, H, and O.

CHEMICS-UBE.[17] CHEMICS was designed for a nonproprietary use of certain chemical company. In accordance with their interests, several restrictions, for instance, prohibition of generating structures that are not necessary to consider (e.g., cyclopropanes), were added.

A Peptide Analysis.[18] From the results of CI mass measurements and ordinary amino acid analysis, amino acid sequences were elucidated for both cyclic and acyclic polypeptides with the algorithm of structure generation in CHEMICS.

An Unhappy Accident.[19] An accident happened on the discussion of the property of the characteristic polynomial, as will be described in the comment of Appendix 8. The content

was uncorrectly changed by someone else, and it was published as ours.

DISCUSSION

As already mentioned above, there are two approaches to collect informational homologues: netting and angling. Using the former approach, CHEMICS can make an exhaustive survey leaving no omissions unchecked, on the assurance that the principles for detecting the informational homologues can be correctly and comprehensively applied. The usual method for structure elucidation (Appendix 6) with undetermined detection limits is forced to take the latter approach, and as a natural result, the retrieved structure is frequently subject to structure correction (Appendix 7). In fact, as shown in Appendix 7, there were cases in which wrong results were published from the deduction on the basis of a single working hypothesis, without regard to a more plausible alternative. However, such incorrect results should have been prevented by adoption of the CHEMICS approach.

There is some criticism that CHEMICS returns so many structures.[21] This criticism comes from two different points of view. One is misunderstanding that such a large number of answers was caused by insufficient analysis; in spite that the number is in itself. Another view is quite reasonable, which criticizes insufficient information used in the analysis. The ideal solution to this criticism may be to prepare as much useful and necessary information as possible, but it is not so easy to establish a balance between the volume of really necessary information and the limited resources (computer) available to us. The prerequisites for instruments with highest performance and comprehensive and complete data analysis would decrease the usability of the system.

Two doubts have been posed about chemical shift values used in CHEMICS.[22] One is the doubt about the accuracy of the values, and the other is the one about their weak discriminating power caused by frequent overlapping of chemical shift ranges of different components. The former view points out that there is a considerable difference in chemical shift values between CHEMICS and other systems. CHEMICS requires a chemical shift table that provides the required information. The requirement can be met only by a table prepared from collections of all chemical shifts of all known compounds. It seems that the critics have not noticed that the correlation table of chemical shift and component, a summary of chemical shift data for "normal" conditions, is only a working criterion for analyzing spectral data in CHEMICS (Appendix 3). For improvement of the discriminating power as to the second criticism, the critics have made two proposals: preparation of more detailed partial structures and setting an optimum range derived from the information theory. More detailed partial structures would increase the complexity of the analysis uselessly, since CHEMICS has set a variety of components, well balanced with the current level of the analysis description. The set of components depends on the level of the analysis and can be changed freely at the user's request. CHEMICS intends to use the information reasonably and effectively; for this purpose, only the essence of a different kind of spectral information is positively used rather than the results from exhaustive analysis of a single spectrum, as suggested from the unabbreviated name of CHEMICS. Therefore, if a difficulty is predicted in use of a certain kind of analysis or efficiency of discriminating the components has reached a limit, CHEMICS will look for another simpler and more effective analysis.

The spectral matching method by retrieving gigantic files of chemical spectra is one of the best ways for structure determination. However, there are some obstacles in this approach from a practical point of view because of the almost infinite number of theoretically possible compounds. The molecular mechanistic method is also another good tool for investigation of molecular structure. The CHEMICS system will be improved by introducing the points of excellence of those methods. CHEMICS-F[15,16] was the first attempt; this complementary system in which comparison of predicted structures (candidates) with the structures in the file is carried out by using spectral data will become the strongest weapon for elucidation. Further development of CHEMICS will proceed in this direction.

APPENDIX 1

Spectrum matching has been used as a practical method of structure identification since the days before the invention of the computer. Even now, large systems of this kind are being constructed. This system is most effective when it has stored the spectral data of the compounds that are identical with a sample. The problems in constructing this system are accumulation, standardization, and evaluation of the difference in the measuring conditions of a huge number of spectral data to be registered in a file. Since the number of members in the system is always (and forever) limited, there still remains a possibility of a wrong answer, even if the system displays the same structure as that of a registered compound by spectrum matching within the error range. Combined use of different kinds of spectral data may decrease the possibility[23] but does not always provide the perfect solution. The final solution requires the deductive reasoning of an expert chemist. The major part of such a reasoning process can be computerized under the supervision of a chemist, and CHEMICS has the capability to take charge of such a computerized reasoning process.

APPENDIX 2

In CHEMICS, a chemical compound is expressed by a structural formula described with a combination of a necessary and sufficient set of components.[24] A set of components may be arbitrarily selected. For example, the chemical elements may be chosen as the smallest components. If the size of the components is smaller, their management is easier, but the efficiency of structure description is lower. On the contrary, the large-sized component will make direct description of analytical results much easier, but the number of necessary components will become too large to manage. Therefore, the level and number of components should be optimumly determined with due consideration of the resources available, the purpose of CHEMICS use, and the performance of the current CHEMICS version.

APPENDIX 3

The correlation table of chemical shifts of NMR is compiled on the basis of the data of the most common chemical compounds. The table is applicable for CHEMICS analysis on the condition that the description of the local environment of a compound molecule can represent that of the environment of the whole molecule for the chemical compound in its normal state. However, for compounds in abnormal states such as a molecule in which a substituent is compulsorily placed on a benzene ring by steric requirements, the above condition is not satisfied, and their values are found to be considerably deviated from those listed in the above-mentioned table. To solve this problem, the following methods have been proposed, although none of them seems to provide a complete solution: (i) To automatically judge whether a sample in question is in "normal" or "abnormal" state and to use another correlation table (or other procedures) if the sample is abnormal. (ii) To remodel the correlation table so as it is possible to handle every compound in the same normal manner. (ii-1) To widen the

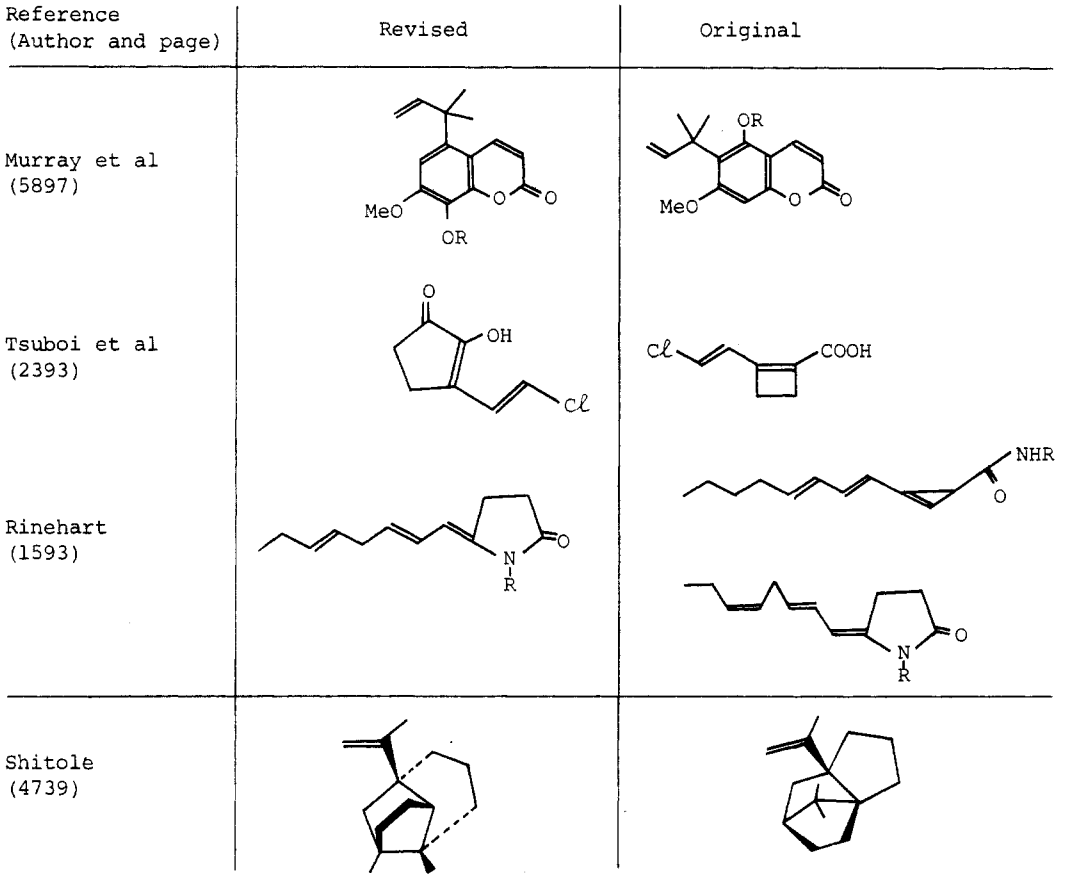

Figure 3. Structure revisions that appeared in *Tetrahedron Letters* (**1983**, *24*).

width of the chemical shift range as much as applicable for any kind of compounds (=no use of chemical shift values in the analysis). (ii-2) To prepare a set of components that can precisely describe all the molecular states including steric configurations and some others. (iii) To predict the partial structure (if possible full structure) of a sample directly from its spectral data (The partial structures determined by user are already utilized as macrocomponents.). (iv) To predict the spectra of all the structures required to be examined and to match them with the spectrum of the sample (This has been partly substantiated in the latest version of CHEMICS.). It can be said that the current CHEMICS system has adopted method i as the practical and the second best alternative in which all samples are regarded as in normal state. For effective use of this method, the followings will be required. The normal states that CHEMICS specifies should reflect the actual normal states as closely as possible. The specified normal states should be readily and clearly displayed to users; then, they may alter the conditions describing standard normal states easily and tentatively. Logical operations at a later step of the process must be made accurately and rapidly.

APPENDIX 4

Once information was given, the possible structures (E) that are known to exist and that might exist from the chemical point of view are classified into two groups (i and ii), and each of the groups is further divided into two subgroups (i-1, i-2; ii-1, ii-2): (i) what can be conjectured from the information (true informational homologues, R); (i-1) structure of sample compound itself (source of the information); (i-2) structures of the compounds other than the sample compound; (ii) what cannot be conjectured from the information; (ii-1) what takes much time and/or many procedures to reach the final conclusion; (ii-2) what are easier to prove inconsistency with the information. The above classification of the whole structures (E) may be exemplified by the use of a compound, neopentane. First, its molecular formula, C_5H_{12}, is given as information; structures (R) of *n*-pentane, isopentane, and neopentane are discriminated from set of the whole structures (E). Neopentane belongs to i-1, and *n*-pentane and isopentane belong to i-2. Three of them are informational homologues about the molecular formula. Actually, neopentane cannot be distinguished from the other two pentanes by this information alone.

All structures other than those three belong to group ii. From the standpoint of an analysis system, in general, discrimination between ii-1 and ii-2 is relatively easy, and the boundary of i and ii is sometimes rather difficult to locate. This difficulty results from the increment of complexity of the information given. Thus, i and ii-1 are occasionally regarded as apparent informational homologues in the system used. The amount of ii-1 depends on the performance of the system, and of course, it is preferable that this be as less as possible.

APPENDIX 5

Let a relevant set of informational homologues corresponding to a given information be R and smaller and larger sets of provisional informational homologues be S and L, respectively. Then, the following relationships will be possible for them: 0 (null or empty set) $\leq S \leq R \leq L \leq E$ (entire set). For finding R, an approach from the L side (initial value = E) is the scoop-up method, and an approach from the S side (initial value = 0) is the pick-up method. The former approach will leave no omission if the work for analysis is discontinued. However, this method cannot be strictly applied to those problems with obscure limits of discrimination (almost all the problems we encounter). L is in sight from the current CHEMICS system, which adopts the scoop-up method. However, since it is only known that R is contained in L, it is unavoidable that the limiting value of L instead of R is sometimes called an informational homologue.

APPENDIX 6

An example of structure analysis in which typical features of the analysis are condensed. The following is a summary of the processes taken by Maruyama et al.[25] for structure determination of gingkolides, components in gingko trees: (i) Comprehensive and complementary analysis of chemical and spectral observations for the natural product clarified the presence of partial structures, I, II, and III_a or III_b, and determined the structure of it. (ii) Adoption of a novel method for structure analysis of organic compounds (nuclear Overhauser effect) lead to the detection of a new partial structure, *tert*-butyl attached to the distorted ring. (iii) Before reaching the final conclusion, the uncorrect working structure had been presented at an international symposium.[26]

APPENDIX 7

Structure revisions are not rare even at present. The revisions include those to other stereoisomers, and structural isomers. For natural products, the number of double bonds is sometimes revised, which is accompanied by a change of molecular formulas. Figure 3 shows recent examples of revisions to other structural isomers.

APPENDIX 8

Our comment printed in the *Journal of Chemical Information and Computer Sciences* (**1976**, *16*, 49) is cited below. In connection with the theme, the concepts Atom Connection Matrix (ACM) and its Characteristic Polynomial (ACMCP) have been discussed. The ACM is a connection matrix whose diagonal elements are not numeral values but the attributes of atoms. There was a proposition that ACMCP uniquely presents the topology of a molecule. "Our" article on the proposition (*J. Chem. Doc.* **1973**, *13*, 225) was vigorously attacked by W. Herndon (ibid, **1974**, *14*, 150). He is quite correct because "our" article is logically funny considering the way "we" announced a conclusion without any proof, regardless of his proof that the proposition is false. Accidently, "our" conclusion was that the proposition is true. Fortunately, the conclusion on the proposition does not have influence on this paper.

After Spialter's conjecture and Balaban and Hosoya's proofs, we wrote an article, "Does not the Characteristic Polynomial Uniquely Determine the Topology of Molecule?", to this journal, in which we indicated that Balaban and Hosoya's proofs were not correct because their "ACMCP" was a special one as a result of a certain modification and that no example denying the conjecture, that the proposition is true, had up to that time been found (i.e., it was not clear at that time whether the proposition was true or not). To our surprise, we received a galley proof, "The Characteristic Polynomial Uniquely Represents the Topology of a Molecule". We then claimed that our original title and content had to be maintained. We found, however, only "our" article in the same form as the galley, whose author is unknown, in the journal.

REFERENCES AND NOTES

(1) Sasaki, S.; Abe, H.; Ouki, T.; Sakamoto, M.; Ochiai, S. *Anal. Chem.* **1968**, *40*, 2220.
(2) Sasaki, S.; Abe, H.; Kudo, Y.; Ochiai, S.; Ishida, Y. *Kagaku no Ryoiki* **1972**, *26*, 981, in Japanese.
(3) Kudo, Y.; Sasaki, S. *J. Chem. Inf. Comput. Sci.* **1976**, *16*, 43.
(4) Sasaki, S.; Kudo, Y.; Abe, H. *Kagaku no Ryoiki* **1968**, *23*, 1070, in Japanese.
(5) Sasaki, S. *Yukigosei Kyokaishi* **1969**, *27*, 652.
(6) Sasaki, S.; Abe, H.; Hirota, Y.; Ishida, Y.; Kudo, Y.; Ochiai, S.; Saito, K.; Yamasaki, T. *J. Chem. Inf. Comput. Sci.* **1978**, *18*, 211.
(7) Sasaki, S.; Kudo, Y.; Ochiai, S.; Abe, H. *Mikrochim. Acta* **1971**, 726.
(8) Sasaki, S.; Ochiai, S.; Hirota, Y.; Kudo, Y. *Bunseki Kagaku* **1972**, *21*, 916. Ochiai, S.; Hirota, Y.; Kudo, S.; Sasaki, S. *Bunseki Kagaku* **1973**, *22*, 399, in Japanese.
(9) Kudo, Y.; Hirota, Y.; Aoki, S.; Takada, Y.; Taji, T.; Fujioka, I.; Higashino, K.; Fujishima, M.; Sasaki, S. *J. Chem. Inf. Comput. Sci.* **1976**, *16*, 50.
(10) Serov, V. V.; Elyashberg, M. E.; Gribov, L. A. *J. Mol. Struct.* **1976**, *31*, 381.
(11) Kudo, Y. *Kagaku no Ryoiki, Zokan* **1972**, *98*, 115.
(12) Lederberg, J.; Sutherland, G. L.; Buchanan, B. G.; Feigenbaum, E. A.; Robertson, A. V.; Duffield, A. M.; Djerassi, C. *J. Am. Chem. Soc.* **1969**, *91*, 2973. Duffield, A. M.; Rovertson, A. V.; Djerassi, C.; Buchanan, B. G.; Sutherland, G. L.; Lederberg, J. *J. Am. Chem. Soc.* **1969**, *91*, 2977. Schroll, G.; Duffield, A. M.; Djerassi, C.; Buchanan, B. G.; Sutherland, G. L.; Feigenbaum, E. A.; Lederberg, J. *J. Am. Chem. Soc.* **1969**, *91*, 7440. Petterson, B.; Ryhage, R. *Ark. Kemi* **1967**, *26*, 293. Biemann, K.; Cone, C.; Webster, B. R.; Arsenault, G. P. *J. Am. Chem. Soc.* **1966**, *88*, 5593, Venkataraghavan, R.; McLafferty, F. W.; Vanlear, G. E. *Org. Mass Spectrom.* **1969**, *2*, 1. Crawford, L. R.; Morrison, J. D. *Anal. Chem.* **1971**, *43*, 1793.
(13) Antosz, F. J.; Nelson, D. B.; Herald, D. L.; Munk, M. E. *J. Am. Chem. Soc.* **1970**, *92*, 4933.
(14) Sasaki, S.; Kudo, Y.; Ochiai, S.; Fujioka, I. *Bunseki Kagaku* **1973**, *22*, 25, in Japanese.
(15) Yamasaki, T.; Abe, H.; Kudo, Y.; Sasaki, S. *ACS Symp. Ser.* **1977**, *No. 54*, 108.
(16) Abe, H.; Fujiwara, I.; Nishimura, T.; Okuyama, T.; Kida, T.; Sasaki, S. *Comput. Enhanced Spectrosc.* **1983**, *1*, 55.
(17) Oshima, T.; Ishida, Y.; Saito, K.; Sasaki, S. *Anal. Chim. Acta* **1980**, *122*, 95.
(18) Yotsui, Y.; Nomura, H.; Sano, M.; Kudo, Y.; Sasaki, S. *Bull. Chem. Soc. Jpn.* **1978**, *51*, 1909; *Bunseki Kagaku* **1979**, *28*, 721, in Japanese.
(19) See reference 16 reference 3.
(20) Kudo, Y.; Yamasaki, T.; Sasaki, S. *J. Chem. Doc.* **1973**, *13*, 225.
(21) Szalontai, G.; Recsey, Zs.; Csapo, Z. *Acta Chim. Acad. Sci. Hung.* **1982**, *111*, 239. Szalontai, G.; Csapo, Z.; Recsey, Zs. *Acta Chim. Acad. Sci. Hung.* **1982**, *111*, 249.
(22) Veszpremi, T.; Cronka, G. *J. Chem. Inf. Comput. Sci.* **1980**, *20*, 234.
(23) Kwiatkowski, J.; Riepe, W. *Anal. Chim. Acta* **1982**, *135*, 285, 292, 383. Zupan, J.; Penca, M.; Hadzi, D.; Marsel, J. *Anal. Chem.* **1977**, *49*, 2141.
(24) Kudo, Y.; Sasaki, S. *J. Chem. Doc.* **1974**, *14*, 200.
(25) Maruyama, M.; Terahara, A.; Itagaki, Y.; Nakadaira, Y.; Woods, M. C.; Takagi, Y.; Miura, I.; Nakanishi, K. *Tetrahedron Lett.* **1967**, 299, 303, 309, 315, 321.
(26) Nakanishi, K. *Kagaku to Seibutsu* **1968**, *6*, 628.