MacSpec and ConvertIt

Tilman Brodmeier and Ernö Pretsch*

Department of Organic Chemistry, Swiss Federal Institute of Technology (ETH), CH-8092 Zürich, Switzerland

Received June 30, 1993

GENERAL DESCRIPTION OF THE FEATURES

In the past decades, much effort has been invested into the development of computer programs for the automatic interpretation of molecular spectra. The success of these contributions is limited, and it is restricted to academic examples. This is at least partly due to the fact that spectrum interpretation relies on heuristic rules. On the other hand there is a great number of calculable steps (logical combinations, bookkeeping, etc.) for which computer programs would be ideally suited as a support. Astonishingly little work has been done to develop tools to perform such calculations. MacSpec[1] is one of the first commercially available tools for personal computers for such calculations needed during the interpretation of mass spectra. It runs on Mac Plus or higher with 1 MB RAM; a hard disk is strongly recommended.

In the following a list of the most important calculations is given, which can be performed by MacSpec:

- A suspected *structure* can be entered using drawing tools. The masses and isotope peak pattern can be calculated of any fragment selected by a drawing tool (lasso). Patterns resulting from overlapping peaks due to fragments of different elemental composition can be constructed.
- On the basis of the *molecular formula* (or other element constraints), possible elemental compositions for a selected mass can be calculated. This can be done for the whole spectrum, if it is entered.
- On the basis of an *elemental composition*, the isotope pattern can be calculated. Isotopic enrichments can be accounted for.
- On the basis of an *isotopic pattern* and the ranges of the number of allowed elements, the elemental composition of a fragment can be determined.
- On the basis of the *entered spectrum*, metastable peaks may be assigned.

Previously several programs were published (but they are not commercially available) performing similar calculations.[2-7]

In several of these programs[3,5,7] it is possible to calculate all signals which would be obtained directly by breaking individual bonds (with or without H-rearrangements). These possible fragment ions of a proposed molecule can be correlated with the experimental spectrum. Such a feature is not included in MacSpec so that the generation of fragments and the assignment have to be done manually.

TEST EXPERIENCES

We installed MacSpec on a Powerbook 170 and on a Mac IIfx. The installation is simply done by copying the program to the hard disk.

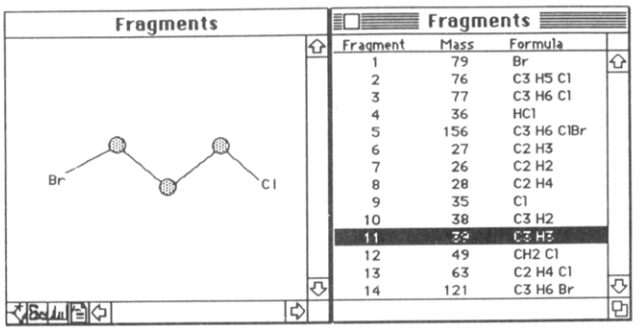

Figure 1. Drawn molecule and fragment list.

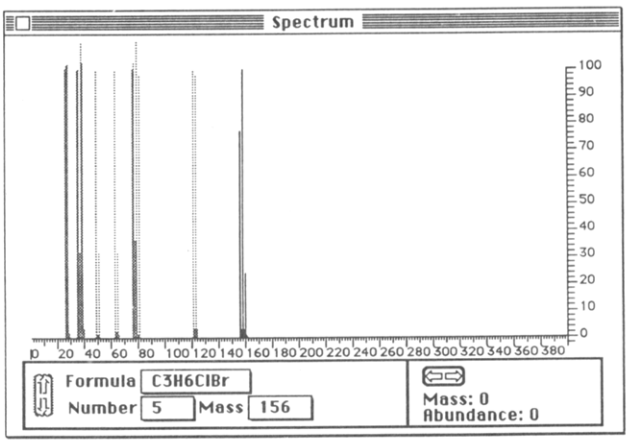

Figure 2. Simulated mass spectrum.

After starting MacSpec, the user is automatically in the structure entry mode. The structure editor is easy to use. It offers the most basic features but naturally cannot offer all the features and comfort included in established structure drawing programs like ChemIntosh or ChemDraw.

Once the user has completed his drawing, he can enter the fragment mode: with a lasso he can cut out pieces of the molecule and thus capture the atoms which are supposed to build up a fragment. The fragments defined with this tool are listed together with their elemental compositions (Figure 1), and the corresponding spectrum can be plotted in another window (Figure 2). Fragments can be "inverted" (i.e. the charge can be left on either of both parts of the molecule). Single or multiple (up to 4) hydrogen rearrangements can be accounted for. A limitation is that altogether only 20 fragments can be defined this way.

In the display of the spectrum generated with this tool, all fragments initially appear with 100% relative intensity. The intensities of their isotope peaks are calculated on the basis of the elemental composition. The user can manually set the intensities of the peaks, and the isotope peak intensities will be automatically adjusted.

The program shows a table with mass differences between the user-defined fragments. If a mass difference corresponds to the mass of a fragment, it will be highlighted. Clicking on it brings up the display shown in Figure 3. Since only the

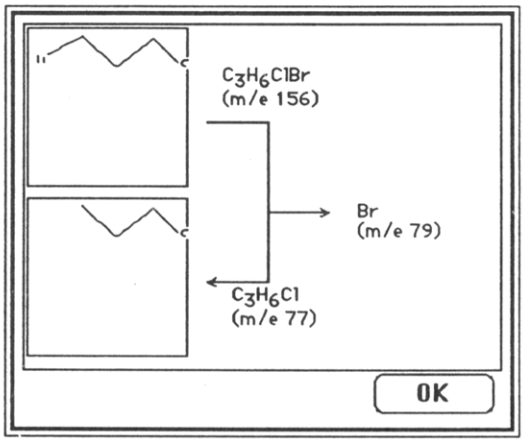

Figure 3. Proposed fragmentation pathway for user-defined fragments.

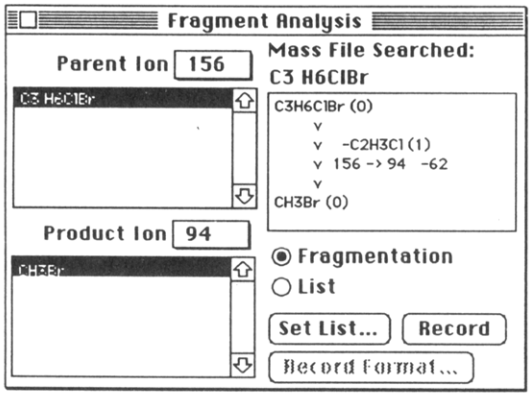

Figure 4. Typical results of a fragment analysis.

masses are checked and not the elemental compositions, senseless results may be produced by this tool.

Another possible usage of MacSpec is based on the measured spectrum and a molecular formula. On the basis of the molecular formula, a "mass file" can be calculated. This file contains the elemental compositions of all possible combinations of the elements occurring in the molecular formula. On the basis of this file, all possible elemental compositions of every signal will be calculated. Since the mass file contains all chemically rational combinations (but no structural information), the mass files can become quite large and their calculation very time consuming. For example, the calculation of the mass file for $C_{14}N_3O_3Br_3Cl_5H_{25}$ (M_r = 695) takes about 20 min on a Powerbook 170 and the corresponding file needs about 3 MB of storage.

Once the user has entered a spectrum, he can select a parent ion and a possible product ion. For both ions the possible elemental compositions will be displayed. Upon selection of individual elemental compositions, the program checks if the two may correspond to a fragmentation. If this is the case, the corresponding transition will be shown (right-hand window in Figure 4). A variety of fragment search methods can be selected by using a great number of settings. The user must carefully select the limits in order to get a managable list of possible solutions. The selection of the right search parameters will need a bit of experience.

There are two basically different search options. The first scans all signals of the observed spectrum for possible elemental compositions, so one can determine fragmentations as shown in Figure 4. In the second case the calculated isotope patterns of each elemental composition are also matched to the spectrum. In the latter case the tolerance of the intensities can be varied. If variable tolerance is used, the search analysis will be limited to 20 hits.

The second search option is especially useful if the molecule contains elements with significant isotope intensities, such as Br, Cl, Si, and S. It is important to point out that "noisy" mass spectra containing a significant background are not easy to analyze this way.

Another very useful tool is provided for the interpretation of metastable peaks. All signal pairs of the experimental spectrum are checked for the entered mass of a metastable ion.

LIMITATIONS

One major drawback of MacSpec is that it is not easy to use. The novice user is confronted with such a larger number of windows and dialog boxes with options to set that one can rapidly get lost. Unhappily there is no on-line help or Balloon Help, which could provide fast information. The layout of several windows and dialog boxes is disappointing. In some windows the relevant features are stuffed in a corner, leaving about 50% of the window white! Buttons in dialog boxes are placed very close, losing semantic relevance and overview. It is unfortunate that some features have to be activated by mouse clicks in combination with the option or shift key, thereby being hidden from the novice user.

The manual that comes with the program is very extensive and gives a guide to MacSpec showing its features solving a couple of examples. Most examples are extremely simple cases (e.g., calculation of various compositions for m/z 28 and performing isotope cluster analysis on them). A kind of quick reference could be helpful.

ConvertIt[8] is the tool for the conversion of raw spectrometer data (MS-DOS, ASCII) to the MacSpec format. Without ConvertIt the observed spectra have to be typed in manually. In our view, the features of ConvertIt should be included in MacSpec. The extra fee of $60 for such a simple conversion program does not seem justified.

CONCLUSIONS

MacSpec certainly implements many useful ideas with a lot of nice computational features. The major point of critics is the limited user friendliness. The occasional user will miss a feature like on-line help, which could inform about available tools. The user interface, the graphical layout, and some bugs should be subject of revision for later versions.

The theoretical limitations (64 atoms for a molecule, a maximum of 4 stable isotopes with user-definable enrichment percentages or 4 user-defined groups, and the allowed maximum molecular mass of 800 amu) do not seem as severe as the practical limitations mentioned for some calculations with larger molecules. It seems that the program is mainly suitable as a teaching aid. There will be some problems when real-life spectra with masses above 200 are to be interpreted.

REFERENCES AND NOTES

(1) MacSpec is written by Dr. Paul A. Zucker and published by Spire Software, P.O. Box 1002, Maplewood, NJ 07040. Phone (201)762-0505. The list price is $295.00 (academic price $250.00).
(2) Varmuza, K. *Fresenius Z. Anal. Chem.* **1985**, *322*, 170–174.
(3) Kubinyi, H. In: *Software-Entwicklung in der Chemie 2*, Gasteiger, J., Ed.; Springer Verlag: Berlin, 1988; pp 167–179.
(4) Fürst, A.; Clerc, J. T.; Pretsch, E. *Chemom. Intell. Lab. Syst.* **1989**, *5*, 329–334.
(5) Siegel, M. M.; Gill, G. *Anal. Chim. Acta.* **1990**, *237*, 459–472.
(6) Heuerding, S.; Clerc, J. T. *Chemom. Intell. Lab. Syst.*, in press.
(7) Brodmeier, T.; Gloor, A.; Cadisch, M.; Bürgin, R.; Pretsch, E. *Anal. Chim. Acta* **1993**, *277*, 297–304.
(8) See note 1. The list price is $60.00.