18.5–3 CAMM: A MOLECULAR MODELLING PACKAGE USING REAL-TIME COMPUTER GRAPHICS.

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CAMM (Computer Assisted Molecular Modelling) is a program package designed to display and manipulate molecular structures on several computer graphics systems linked to a PDP 11/60 minicomputer. In the conception of CAMM, emphasis has been placed on the following points: very high degree of interactivity; real-time manipulation of 3D structures; color representation of stick only, ball and stick, and space filling models; hard-copy facility; user friendly interaction with the program. These requirements led us to develop a self-contained package made of three complementary programs, each of them running independently on a different computer graphics system in our laboratory and taking advantage of their individual potentialities.

1. The CAMMVG program displays a structure on a 3D calligraphic system, Vector General 3400, using all its real-time interactive facilities to translate and rotate objects with an instantaneous response. This allows the rapid and easy selection of an optimum molecular orientation for display on the other systems.

2. With the CAMMCG program, it is possible to use the color raster AED 512 system to produce ball and stick or space filling models (with or without atom labelling). Pseudo 3D images are generated using special algorithms such as sphere shading, perspective setting and hidden line or surface removal. Several options are incorporated for interactively modifying the picture. Further, one may produce color slides or photographs of very high quality.

3. CAMMPL offers practically the same possibilities as CAMMCG, but it uses a 4-color Hewlett Packard 7221A plotter as output, and allows pseudo hard-copies of the raster display to be produced.

4. Communication between the different modules of CAMM is fully automatic making the package easily accessible to unexperienced users. The programs are written in FORTRAN and, apart from the graphic modules of CAMMVG, should be readily adaptable to other host-computers or graphic systems.

18.5–4 STRUCTURE-ACTIVITY RELATIONSHIP OF HUMAN CARBONIC ANHYDRASE C AND SULFONAMIDE DRUGS : A MOLECULAR MECHANICS APPROACH. By E.F.Meyer jr, Dept. of Biochemistry, Texas A & M University, College Station, Texas, and A.Vedani, Dept. of Organic Chemistry, Federal Institute of Technology (ETH), Zurich, Switzerland.

The isoenzymes of carbonic anhydrase reversibly catalyze the decomposition of carbonic acid into carbon dioxide and water. The specific inhibition of carbonic anhydrases by aromatic and heterocyclic sulfonamides finds clinical application in the treatment of glaucoma, epilepsy and acute mountain sickness.
The high inhibitory power of certain sulfonamides may only be explained by participation of coordinated water molecules in the enzyme - inhibitor complex or by interaction with amino acid side-chains located more than 10Å from the active site (Vedani & Meyer, J.Pharm.Sci. (1984), in press). Molecular mechanics calculations have been performed with the programs AMBER (Weiner & Kollman, J.Comp.Chem. (1981) 2, 287) and YETI (Vedani, unpublished). YETI is a program that stands conceptually between visual fitting and more elaborate force-field programs. It minimizes the conformational energy by adjusting selected torsion angles of the protein and the substrate combined with rotation and translation of the substrate and solvent molecules . The protein backbone is kept rigid throughout the refinement. This allows for efficient scanning of conformational space. Results on the refinement of Acetazolamide (2-acetamido-1,3,4-thiadiazole-5-sulfonamide), Metazolamide (2-acetimido-3-methyl - 1,3,4 - thiadiazole-5-sulfonamide) and 2-nitro-thiophene-5-sulfonamide will be presented.

18.5–5 MOLECULAR SIGNATURE : NEW DEVELOPMENTS AND USE WITH "MANOSK", A SOFT WARE WRITTEN FOR AN INTERACTIVE COLOR DISPLAY. By E. Surcouf and M.C. Vaney, Laboratoire de Minéralogie-Cristallographie, Université Paris VI, Tour 16, 4 place Jussieu, 75230 Paris Cedex 05, France.

The concept of "molecular signature" was previously proposed (E. Surcouf and J.P. Mornon, C.R. Acad. Sc. Paris, (1982), E 295, 923) to get a better knowledge of the recognition mechanisms between molecules and to predict their associations. Developments have been undertaken to get fast calculations and visualizations. A new software, Manosk, has been written for this purpose. This program runs in - a CII-HB Mini 6/53 computer associated with an array processor FPS 100. It allows manipulations of signatures on a PS 300 Evans & Sutherland color graphic display.