



**MacVector: Sequence Analysis Software. Version 4.1.; AssemblyLIGN:
Sequence Assembly Software.**

Review Author[s]:
Axel Meyer

Quarterly Review of Biology, Volume 70, Issue 1 (Mar., 1995), 128-129.

Stable URL:

<http://links.jstor.org/sici?sici=0033-5770%28199503%2970%3A1%3C128%3AMSASV4%3E2.0.CO%3B2-3>

Your use of the JSTOR archive indicates your acceptance of JSTOR's Terms and Conditions of Use, available at <http://www.jstor.org/about/terms.html>. JSTOR's Terms and Conditions of Use provides, in part, that unless you have obtained prior permission, you may not download an entire issue of a journal or multiple copies of articles, and you may use content in the JSTOR archive only for your personal, non-commercial use.

Each copy of any part of a JSTOR transmission must contain the same copyright notice that appears on the screen or printed page of such transmission.

Quarterly Review of Biology is published by The University of Chicago Press. Please contact the publisher for further permissions regarding the use of this work. Publisher contact information may be obtained at <http://www.jstor.org/journals/ucpress.html>.

Quarterly Review of Biology
©1995 The University of Chicago Press

JSTOR and the JSTOR logo are trademarks of JSTOR, and are Registered in the U.S. Patent and Trademark Office. For more information on JSTOR contact jstor-info@umich.edu.

©2003 JSTOR

DYNAMIC ANIMAL MOVEMENT ANALYZER.

By James B. Hoy, Marshall W. Sutherland, and Jason D. Cook. *University of Florida, Gainesville (Florida)*. Shareware [one 3½" disk (asking a \$450.00 contribution to a University of Florida donor account after a 30 day trial period)]. 1993. [Requirements—MAC Centris 660AV, 1MB free memory, QuickTime 1.6.1, any software that uses the DSP chip disabled; DAMA Replay requires a MAC Plus, ½MB free memory.]

This no-frills program uses the input from a video camera to track the movements of an animal on a contrasting background. The camera is trained on an empty "arena," and you instruct the program to record a reference frame. The animal is then introduced, and the program locates the animal by detecting its contrast with the reference frame. Data are recorded for the designated period of time. The output is an ASCII file that gives X-Y coordinates of the animal at up to 7.5 frames/second, plus linear and angular velocity averaged over the last 5 tracked points. This file can also be graphically replayed with lines showing the animal's movements, and saved as a PICT file. Tests were run using an inanimate object moved in front of the camera, and the program worked well when using light-on-dark or dark-on-light contrast.

The program requires an AV Macintosh with QuickTime installed. There are controls for contrast threshold, size of object tracked, number of frames per second, and length of run. The controls are easy to set but the explanation of what some of the controls do is unclear. A more explicit description in the manual would be helpful.

The program lacks the standard Macintosh commands and menus, and if you forget to change the file name from your last run, the file will be overwritten without a warning. You also do not have control over where the files are saved—they are automatically placed in the folder with the main program. Despite these shortcomings, the program performs its basic function well. If you need a record of the movements of an animal in a controlled situation, this program is very useful.

JEFF MAHON, *Zoology, University of Hawaii at Manoa, Honolulu, Hawaii*

MACVECTOR: SEQUENCE ANALYSIS SOFTWARE. *Version 4.1. Life Science Products.*

International Biotechnologies (Eastman Kodak Company), New Haven (Connecticut). \$2495.00 (four 3½" disks). 1993. [Requirements—MAC: (except Macintosh Plus and earlier models), System Software V. 6.0.7 or higher, 1MB RAM with Finder System 6, 2MB RAM with MultiFinder or System 7. *AssemblyLIGN* software and Eve Key included. *Entrez: Sequences* database compact disc sold separately.]

ASSEMBLYLIGN: SEQUENCE ASSEMBLY SOFTWARE.

International Biotechnologies (Eastman Kodak Company), New Haven (Connecticut). Two 3½" disks; included with *MacVector*, but available separately for \$795.00. 1993. [Requirements—MAC: SE or later models, System Software V. 6.0.3 or higher, 1MB RAM hard disk with 2MB free disk space, color monitor. Eve Key included.] With a plethora of useful and powerful features for DNA and protein analyses, *MacVector* is one of the leaders in sequence analysis software for personal computers. DNA sequences are continuing to accumulate at a breathtaking pace, emphasizing the need for programs like this. Many researchers prefer to conduct analyses—such as searches for open reading frames, hydrophilicity plots, and restriction enzyme analyses—that do not require main-frame computers. Like other competing programs (e.g., *GeneWorks*, from *IntelliGenetics*), this program was written for the Macintosh for users who might feel more at ease with molecular biology than with computers.

Data entry and data analysis in *MacVector* are supported by two optional pieces of hardware, the IBI gel reader and a compact disc (CD-ROM) player. The Version 4.1 release of *MacVector* includes several new and extremely useful features that were not available on earlier versions: *Entrez: Sequences*, a powerful on ramp to searches in data banks (*Entrez: Sequences* was developed at the National Center for Biotechnology Information, NCBI), a PCR (polymerase chain reaction) primer analysis module, and more sophisticated capabilities for base compositional analyses.

Entrez: Sequences allows easy access to the nine databases that are distributed, now monthly, by the NCBI. The databases are distributed on CD-ROM disks at a very reasonable subscription rate directly from NCBI; *Entrez: Sequences* is available free of charge from the NCBI. *Entrez: Sequences* is powerful and flexible, and searches can be conducted with *MacVector's* "browser" through various filters, Boolean searches, and keywords—including indexed words (e.g., authors, organisms), definitions, and document ID. The efficiency of searches can be varied through the use of wild card (* and ?) characters. The inclusion of *Entrez: Sequences* into the *MacVector* environment adds much to the utility of the program.

Because of the ever-increasing application of PCR, PCR primer prediction is now a standard feature in this kind of software. *MacVector's* PCR primer prediction is typical in that it can search for primers, taking into consideration G + C content, T_m, secondary structure, amplification product size, additional binding sites, and primer dimers. It can even predict how the T_m of the primers is going to be affected by different formamide and salt concentrations, and allows one to simulate reaction conditions by varying, among other features, the

initial primer concentration. Primer compatibility can be further tested by screening for self duplexes, hairpins, and 3'-end versus 3'-end screens for self-3' dimers. These features will extend the utility of MacVector from the analysis to the planning stage of experiments.

New codon bias analysis and nucleotide frequencies features are important improvements from earlier versions of MacVector, and are going to facilitate work on the molecular evolution of genes. Workers in the growing field of molecular evolution will like to see many more new features in future releases of MacVector, such as NEXUS file format compatibility, transition-transversion counts between sequences, and multiple hit corrections for pairwise sequence comparisons.

An important new cousin of MacVector is AssemblyLIGN, the sequence assembly module of IBI. It allows one to easily assemble sequences from manually or (probably more commonly these days) automatically determined sequences into contigs. Contigs can then be exported to MacVector for further analysis. A useful color bar editor allows one to identify patterns, ambiguities, gaps, and differences between sequences from different strands or clones. This module really should be part of the standard program, but still can be purchased separately.

The optional IBI gel reader allows one to enter data from sequencing gels without the use of a keyboard. In my lab, the gel reader has been reduced to an expensive light box, since it is rather cumbersome and we found that the primitive typing in of data is actually faster and more accurate than data entry with the IBI gel reader. MacVector can read sequences back (in a cute male or female voice), a feature much used in proofing sequences. The manual (really a reference, since the program is easy and invites play) is much improved over the manual for Version 3.5.

Although we have several other similar programs in my lab, MacVector is the one that we use the most.

AXEL MEYER, *Ecology & Evolution, State University of New York, Stony Brook, New York*

THRINAXODON: DIGITAL ATLAS OF THE SKULL.

By Timothy Rowe, William Carlson, and William Bortoff; Foreword by Everett C. Olson. University of Texas Press, Austin (Texas). \$90.00 (one compact disc). 1994. [Requirements—IBM PC: DOS 3.2 or higher, MSCDEX (Microsoft Compact Disc Extensions) 2.0 or higher, 4MB RAM, minimum 6MB disk space and 550K free executable memory, VGA color monitor, mouse or other pointing device.]

Over much of the history of synapsid paleontology, studies of nonmammalian therapsids have concentrated on evolutionary and/or adaptive trends whose

expression culminated in characteristics of Mammalia. More recently, however, greater attention has been focused upon phylogenetic relationships among the nonmammalian therapsids themselves. In this latter endeavor, the senior author and motivational force behind this CD-ROM has been a significant contributor. Whether one is interested in nonmammalian synapsids as "mammal-like reptiles" or as a diverse group of non-sauropsid amniotes in their own right, one taxon in particular is of considerable significance: the Triassic species, *Thrinaxodon liorhinus*. *Thrinaxodon* is of importance because, while many Permo-Triassic forms (including those that are more closely related to mammals) are very poorly known, this 225 million-year-old is represented by a number of well-preserved and complete skulls. *Thrinaxodon* is also of importance because, despite disagreement over the interrelationships among the advanced cynodonts, most workers are agreed that thrinaxodontids represent the sisters of eucynodonts; that is, *Thrinaxodon* represents a reasonable ancestral morph from which eucynodonts (including mammals) could have evolved. It is presumably for these reasons that Rowe and his colleagues decided to focus upon the skull of this particular Triassic therapsid in the compilation of a comprehensive atlas of serial sections derived from computerized tomography (CT).

Computerized Tomography is an important, non-destructive method by which to visualize the internal structures of fossil skulls. It is possible to obtain CT scans exceedingly quickly compared to the time required to visualize a bit of osteological anatomy through conventional preparation of the specimen from the surrounding matrix. Because the technique is non-destructive, it can be applied to virtually any specimen without fear of damage. Thus there can be little doubt that CT technology will play a very crucial role in the study of anatomy and evolutionary morphology. But visualization from CT digital images is one thing—mensuration is quite another. Thankfully, Rowe and his colleagues have not attempted to give measurements for the CT sections, and nor should the user attempt to reconstruct small dimensions (e.g., the thickness of an individual bone or the size of a tooth) from these images. They will not be accurate.

This CD-ROM provides professional paleontologists and students with an easily accessible and, to some extent, interactive format by which to review the detailed anatomy of the skull of *Thrinaxodon liorhinus*. The CT sections, of which there are 767, were recorded in coronal, sagittal and horizontal (erroneously referred to as "transverse") planes. Each section is 200 μ m thick. These can be viewed individually (with or without anatomical labels) or in animated sequence. If one is interested in a particular area of the skull, it is possible to find the rele-