Introduction

MacVector is a desktop sequence analysis program that enables researchers to analyze their DNA and protein sequence data on a Macintosh. It follows the Macintosh Human Interface Guidelines and it is thus a very intuitive and easy-to-use software package. All analyses are integrated within the same package, except for contig assembly. AssemblyLIGN is the contig assembly module for MacVector.

System requirements

MacVector runs on any PowerPC Macintosh and MacOS compatible system that runs Mac OS 8.6 or later, including Mac OS X. MacVector requires CarbonLib 1.4 or later. We recommend the use of OS X version 10.1 or higher as this solves certain problems with USB hardware copy protection devices.

Memory requirements depend on your system software and virtual memory allocation. Under Mac OS 8.6, 9.0, 9.1 or 9.2, MacVector requires a minimum partition of 5000 KB; the suggested partition is 8000 KB if virtual memory is on. This may have to be increased if you are working with many large sequences. Mac OS X does not require a minimum memory partition to be assigned.
Changes for MacVector 7.1.1

Problems Fixed

**OS X 10.1 Specific Problems**
- MSA Options tabbed dialog now works correctly.
- Pasting from external applications now works correctly.
- All dialogs now accommodate the extra space required by the 10.1 System Font.
- Base composition graphical results can be zoomed.

**General Problems**
- Scrolling in text windows is speeded up.
- Error in the Bacterial Genetic Code is fixed.
- Idle loop no longer uses up all spare CPU cycles.
- Handling of the asterisk character (*) in protein alignments is fixed.

Changes for MacVector 7.1

**OS X Compatibility**

MacVector 7.1 now runs natively under OS X. This removes memory limitations, permitting the analysis of longer sequences and the use of a greater number of sequences in multiple sequence alignments. Other running applications will no longer monopolize the processor, so background analyses will run at full speed. The same MacVector executable can also be run under OS 8.6 and all flavors of OS 9, providing complete flexibility under all operating system environments.

**Balloon Help**

Balloon help is not supported under OS X. MacVector 7.1 has replaced balloon help with ToolTips that can be turned on by selecting **Show ToolTips** in the **Help** menu.

**Digitizer Support**

MacVector 7.1 no longer supports the IBI digitizer. This piece of equipment has not been available since 1995 and requires a serial port, missing from all modern Macintosh systems. Several related menu items have been removed and the Mobility Standards folder is no longer installed.
New in MacVector 7.0

Phylogenetic analysis

MacVector can generate and analyze true phylogenetic trees, using a variety of methods, including neighbor joining and bootstrapping. The phylogenetic analysis has a simple user interface, and is integrated with the multiple sequence alignment editor for maximum flexibility - letting you choose which sequences and which positions in the alignment will be included in the analysis. The results are presented in a variety of tree formats. The new Tree Viewer window enables you to analyze phylogenies interactively, and to fine-tune the display for publication-quality output.

Full-featured multiple sequence alignment editor

Originally designed to view and modify the results of ClustalW alignments, the multiple sequence alignment (MSA) editor in MacVector 7.0 has been developed into a general-purpose multiple alignment tool. You can now create empty MSA documents, or import alignments from other applications. You can insert and delete sequences; insert, delete and modify residues; and copy and paste parts of a sequence or blocks of an alignment. The controls for the alignment display are now grouped on a single tabbed dialog box. You can use color to indicate levels of similarity shown at a position, as well as to group residues by their chemical properties. In addition, the MSA editor allows easy access to phylogenetic analyses.

New algorithms for coding preference plots

New algorithms have been added to help you distinguish more clearly between coding and non-coding regions of a nucleotide sequence. These include G+C % composition analysis, three algorithms from Staden, and the Wisconsin Package™ codon preference algorithm. You can select from a menu of Open Reading Frames and coding analyses, and see all the graphical results aligned in a single window. The controls for color and appearance of the display have been improved, and locations of start, stop and rare codons are included. The display is interactive, so that clicking on a start codon or ORF will highlight the corresponding residues in the sequence window.

Gapped BLAST searches

MacVector 7.0 can access NCBI’s enhanced BLAST 2.0 programs, and use gapped alignment with its blastn, blastp, blastx and tblastn programs. Gapped alignment yields results that are more biologically meaningful than those of ungapped alignment.
Transcription based on exons or other features

You can now easily generate a translated protein from a DNA sequence that includes non-coding intron regions. The new Transcription Analysis functionality enables you to use features of a sequence to determine which parts will be transcribed to mRNA. You can generate a transcript by specifying any of the following: a single coding sequence, one or more exons, one or more introns, or one or more RNA features.

Enhanced file input/output

MacVector’s ability to handle data generated by other applications has been extended, with new support for the import and export of EMBL and SWISSPROT feature tables, and for importing and exporting data in NEXUS, PHYLIP, NBRF and GCG-MSF multiple sequence alignment formats.

Enhanced codon bias table generation

MacVector can now generate more accurate codon bias tables from GenBank sequences. A genome type filter has been added, to help ensure that the most appropriate sequences are used to generate the codon bias table.

Modern file navigation user interface

MacVector 7.0 uses Apple’s new ‘Navigation Services’ dialogs when running on Mac OS 8.5 and later. Navigation Services offers resizable file lists, shortcuts for commonly used folders, and the ability to open several files simultaneously.

Enhanced usability

Various enhancements have been made to the usability of MacVector in version 7.0, including an improved Entrez interface with a more informative and adjustable display, more rational setting of the DNA/RNA attribute, and easier resetting of defaults in many dialog boxes. In addition, MacVector 7.0 handles large sequence files better, with the removal of length limits on folder alignments and Pustell matrix analyses.

New KeyServer network licensing software

If you have a network license to run multiple copies of MacVector, the KeyServer controller software that you use has been updated. The version of KeyServer supplied with MacVector 7.0 will run on a wider range of Macintosh configurations than the previous version, and will be compatible with Mac OS X when that is available.
Note that if you use a hardware copy protection device (dongle), the changes in KeyServer do not affect you. Further, if you are upgrading from MacVector 6.5 and you already have a working KeyServer installation, then you do not need to upgrade your KeyServer - your existing installation will continue to work with MacVector 7.0. However, if you have compatibility problems with new hardware and Mac OS versions, you should install the new version.

Further information is provided in the *MacVector Network Information for Administrators* booklet, and the *KeyServer Administrator’s Reference* included with the KeyServer software on the MacVector 7.0 CD-ROM.

**MacVector documentation set**

MacVector is accompanied by a comprehensive documentation set, including both printed and on-line components.

The *Getting Started* booklet and *User Guide* are available as printed books, and as on-line books (PDF format). The PDF books include a hypertext menu and a keyword search facility (*Tools | Find*). You need Adobe® Acrobat® Reader 3.0 or later to view these books and other PDF files. If you do not have Adobe Acrobat Reader installed on your computer, you can install it directly from the MacVector CD-ROM.

The following documents are available in the MacVector documentation set:

**CD-ROM Installation booklet**

The CD-ROM *Installation* booklet contains information about installing MacVector and using a copy protection device.

**Getting Started booklet**

The *Getting Started* booklet contains the tutorials for MacVector 7.1.

**User Guide**

The *MacVector User Guide* describes the MacVector sequence analysis software and how to use it.

**MacVector help**

When MacVector is running, on-line help is available via *Help | MacVector Help*. This provides a comprehensive guide to the MacVector software.
Problems fixed in MacVector 7.0

BLAST and Entrez operations

- If a BLAST search was cancelled, subsequent BLAST searches could sometimes show incorrect results.

- Entrez would fail to display anything for sequences expressed as CONTIGs of other sequences (i.e. sequences in the GenBank CON division.) The Details button will now list the accession number of all the component sequences, although they must be downloaded individually.

- Occasional Medline and Entrez sequences would fail to be retrieved, with no error message.

- Incorrect Entrez search results would be obtained on a two term expression involving NOT when the second term had a wildcard.

- An occasional File not found error as a BLAST search initiated has been fixed.

File import and export

- GenPept protein file import would display an error message when the DBSOURCE and PID annotations were encountered.

- The protein IUPAC code ‘U’ (for selenocysteine) would cause an error if encountered during file import. It is now converted into an ‘X’ and imported without a warning.

- Large (> 10 MB) GenBank files would not import correctly.

- Circular graphic maps pasted into Word 98 would print with excessively thick lines.

- Text files copied from other operating systems could not be opened unless they had correct Finder file type information.

Large files

- Many length limits have been removed. The Align to Folder and Pustell Matrix analyses are now limited only by available memory. The ClustalW analysis is now limited to 940 sequences.

- Popup menus containing the list of features for a sequence would only show 200 features in MacVector 6.5. Feature-rich sequences would overflow this limit. The popup menu has been changed to group features of each type into submenus, allowing many more features to be accessed via the menu.
Many improvements have been made in the handling of large files, including better progress and error reporting, improved cancelling ability, and increased robustness to out-of-memory conditions.

**Miscellaneous**

- Mac OS Stationery files are now handled correctly. Opening a Stationery file opens a new, untitled copy of the file.
- Ambiguity symbols in DNA alignments would be lost during a ClustalW alignment and all ambiguities converted to ‘N’. Ambiguities are now correctly retained.

**Known Problems**

The following list shows the problems found with this version of MacVector:

**BLAST and Entrez operations**

- BLAST searches can be very slow when the NCBI servers are busy. You may find it helpful to do your searches outside of North American business hours where possible.
- Sometimes the very first BLAST or Entrez search of a session can require two attempts to connect to the NCBI servers. If you get a connection error message, retry the command.

**Sequence files**

- Features tables containing more than 8000 features cannot be edited beyond the 8000th feature.
- Annotations containing more than 256 characters will be truncated to 256 characters if edited (a warning is given on the editor dialog box).
- Spurious annotations can sometimes appear in the textual alignment output window of the Align to Folder analysis.
- The proposed new IUPAC protein code ‘U’ for selenocysteine cannot be typed in MacVector sequences.
- The sequence editor window has a limit of 65535 lines of residues. When working with large sequences (> 4 MB), you may need to resize the sequence window to make it as wide as possible, in order to be able to view all the residues. Residue information is never discarded - even if the sequence editor window does not display it, it is safely maintained, and used by MacVector’s analysis functions.
File Import/Export

- File reading and writing is slow to Novell servers. If you use a Novell server and experience speed problems, we recommend that you always copy files to your local hard disk, using the Finder, before working with the sequence.

Miscellaneous

- Editing circular maps in third-party graphics applications can be difficult. There is an extensive FAQ (Frequently Asked Questions) section on the MacVector Website http://www.accelrys.com/ dealing with this issue.

- If you are running MacVector on a PowerBook and using a recognized hardware Eve key (“dongle”), the key will sometimes not be recognized if the PowerBook goes to sleep and then wakes up. You could use the PowerBook’s Energy Saver Control Panel to prevent it from going to sleep. Alternatively, remove and reinsert the key.

Troubleshooting

In general

Where possible, restart your Macintosh with system extensions off and try repeating your actions. (To turn system extensions off, hold down the Shift key while starting up until you see the message “Extensions Disabled” displayed.) It may not always be possible to do this, particularly if you need to access network services that require certain extensions to operate, but minimizing the number of non-Apple extensions that are loaded in your system can help to isolate conflicts.

BLAST and Entrez services

If BLAST or Entrez searches fail, first check that your Internet connection is working properly by testing whether you can access Internet Web sites using your Web browser.

If your Web browser does work correctly but BLAST and Entrez searches do not work, it is possible that your site has an Internet firewall installed for security, and that this is preventing MacVector’s Internet connection from working. Full information on configuring NCBI clients and firewalls is in the file NCBI Firewall Info in the Documentation folder.

Note that versions of MacVector prior to 6.5.3 can no longer perform BLAST searches, because the new NCBI servers require a different connection: use MacVector 7.1.
If you have previously performed successful BLAST or *Entrez* searches with MacVector 6.5.3 or higher, and you are therefore sure that there is not a firewall problem, please bear in mind that the success of these services relies on the availability of the NCBI Internet servers. If your network, or the Internet connection your network uses, or the NCBI’s Internet connection, or their server machine(s) have any problems, you may be temporarily unable to perform BLAST or *Entrez* searches. Also, the time of day can affect the speed of your search, depending on how much other data is “on the Internet” at the time.

Because of the transient nature of the above problems, you will often find that if you try your search again at a later time - either an hour later or the next morning - it works.

**Support information**

For assistance with MacVector, please contact your local Accelrys office.

**USA**

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When contacting Customer Support with a technical problem, please be prepared to give your product serial number as well as a detailed description of your problem and any error messages you encounter.

Visit the MacVector Web site for details of any available updates, and any relevant information that could not be added to these release notes in time for publication:
