MacVector 12.6

for Mac OS X

System Requirements

MacVector 12.6 runs on any PowerPC or Intel Macintosh running **Mac OS X 10.5** or higher. It is a Universal Binary, meaning that it runs natively on both PowerPC and Intel based Macintosh computers. There are no specific hardware requirements for MacVector – if your machine can run OS X 10.5 or above, it can run MacVector. A complete installation of MacVector 12.6 uses approximately 165 MB of disk space.

Installation and License Activation

Install MacVector 12.6 by double-clicking on the MacVector 12.6.pkg installer application. You will be prompted for a system administrator account and password during installation. Once installation is complete, you must enter a valid license owner, serial number and activation code the first time you run MacVector. This information is usually sent by e-mail and is also printed on the inside of the CD sleeve. If you previously installed MacVector 12.5 and have a serial number with a maintenance end date of May 1st 2012 or later, MacVector 12.6 will automatically use your existing license and you will not be required to enter the details again.

Changes for MacVector 12.6

Quicktest Primer Interface

There is a brand new interactive primer design interface that lets you quickly view the properties of any primer, see instantly where it binds on any open sequence window and even nudge the primer on a sequence to find the optimal primer characterstics. You can edit the primer to introduce mismatches and see the impact of the mismatches on translations crossing the binding site and even add tails containing restriction site. Finally, you can run Primer3 from the Quicktest dialog to find a matching primer suitable for PCR and copy a DNA sequence containing the predicted PCR product, complete with any mismatches or tails introduced by the primers. The new functionality is invoked from the **Analyze |Primers | Quicktest Primer** menu item. For more details, please read the new "Primer Design Tutorial.pdf" document in the /MacVector 12.6/Documentation/ folder.

Feature Import

You can now import features from GFF, GFF3, GTF and BED files. To use this, open the parental sequence and choose **File | Import Features**. Perfectly duplicated features will be discarded, so you can use this to repeatedly import features from an external source where the features in the source file may be updated from time to time without having to start over from scratch. This feature allows you to import annotation directly from many

Genome Browsers such as the UCSC Genome Browser.

Phrap *de novo* Assembly of NGS data

The add-on Assembler module has been enhanced to allow phrap assemblies of file-based (i.e. FastQ) formatted sequences. Please see the Assembler Release Notes for more details.

Miscellaneous Enhancements

The Map graphics layout and drawing performance have been speeded up. In particular, MacVector can now display all of the features from a typical bacterial chromosome almost instantaneously and lets you zoom in and out from interesting regions extremely quickly.

You can now edit the LOCUS name in DNA sequences.

If you option-click on a Read sequence in the Align to Reference Editor, the corresponding trace chromatogram will slide into view in the lower multiple-trace pane. This is particularly useful if you have hundreds of aligned clonal variants and want to quickly inspect the chromatogram to validate mutations.

Sorting an Align to Reference assembly now ensures assembled Reads always float to the top.

All Tm calculations now use the updated thermodynamic nearest neighbor parameters of Santa Lucia (1998) and also take into account divalent cation concentration and dNTP concentrations as described by von Ahsen et al (2001).

You can now save all open sequences into a single GenBank file – simply open all the sequences of interest, choose **File | Save As**, then choose **GenBank** from the format menu and set the **Window** parameter to "All open sequences".

The **Analyze | Translation** output now has an additional option to provide more flexibility in the annotated sequence display so that you can force the display of a defined region within the context of the entire sequence.

The label that is displayed for each feature on sequence Maps is now much smarter to help cut down on the amount of text that is displayed by picking out and displaying selected qualifiers for certain common feature types.

The contents of the multiple sequence alignment Editor tab are now copied to the clipboard as a graphical image when nothing is selected and you choose **Edit | Copy**.

The Map results of **Analyze | Subsequence** searches now automatically show hits on the plus strand above the sequence and hits on the minus strand below the sequence.

Import of plain DNA sequences (ASCII or FastA) with lots of N's is now handled better so users are not prompted to select the type of sequence.

The maximum size of a primer that can be searched for or tested in all of the primer design functions has been increased to 80, except for Primer3 which has an internal limit of 35.

The Auto-Annotation function can now handle finding features that are less than 20nt in length.

The Pustell Matrix analysis functions have now been moved under an **Analyze | Create Dot Plot** sub menu. The DNA:DNA matrix now has a maximum ktup value of 12 – use this to rapidly generate dot plots comparing whole bacterial genomes (analysis time is cut to seconds rather than hours).

Non-sequence characters are now stripped out of text pasted into the Find and Test PCR and Sequencing primer dialog boxes.

You can now run T-Coffee on long alignments (e.g. 10,000 residues or more) without it running out of memory.

New sequences can be imported with full annotation by the copy and paste of GenBank, EMBL and FastA documents.

Support information

For assistance with MacVector, please contact your local MacVector, Inc office. You will need a current MacVector maintenance contract to be eligible for technical support other than for basic installation problems. New sales of MacVector include 12 months of support that also entitles you to any upgrades to MacVector released during the maintenance period.

USA

Toll Free: (866) 338 0222

Telephone: (919) 303 7450

Fax: (919) 303 7449

E-mail: support@macvector.com

Europe

Telephone: + 44 (0)1223 410552

Fax: +44 (0)1223 709429

E-mail: support@macvector.com

Worldwide

Telephone: + 1 919 303 7450

E-mail: support@macvector.com

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:

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http://www.macvector.com
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