MacVector 18.6

for Mac OS X

The online updater for this release is 224 MB in size

You must be running MacVector **15.5.4** or later for this updater to work!

If the updater fails, DOWNLOAD THE FULL INSTALLER HERE!

System Requirements

MacVector 18.6 is a Universal Binary supported on any Intel or Apple Silicon Macintosh running **Mac OS X 10.13** (macOS High Sierra) or higher, up to and including macOS Ventura. There are no other specific hardware requirements for MacVector – if your machine can run OS X 10.13 or above, it can run MacVector. A complete installation of MacVector 18.6 uses approximately 500MB of disk space. Please note this release will NOT run on OS X 10.11 or earlier versions of OS X.

ASSEMBLER NOTE: If you are performing contig assembly using *MacVector with Assembler*, we recommend you have **at least** 2 GB of **FREE** RAM available on your machine. For any serious NGS work using phrap, velvet, SPAdes, Flye or bowtie, you should have at least 8 GB and preferably 16 GB or more for satisfactory performance.

Installation and License Activation

You can choose to install MacVector in one of two ways; if you want to install MacVector for all users of the computer, simply drag the MacVector folder onto the Applications folder. You will be prompted for a system administrator account and password during this copy. If you don't have administrative privileges, or if you want to install it for just your own use, you can install MacVector in the /Applications/ folder in your own personal home directory. To do that, double-click on the **OpenUserApplicationsFolder** icon to open the folder in a separate window, then drag the MacVector folder into that window.

When you first run MacVector, you must enter a valid license owner, serial number and activation code if one does not already exist on your computer. This information is usually sent by e-mail but is also printed on the inside of the CD sleeve if you opted to receive MacVector on physical media. If you previously installed an earlier version of MacVector and have a serial number with a maintenance end date of July 1st 2023 or later, MacVector 18.6 will automatically use your existing license and you will not be required to enter the details again. NOTE: you can optionally activate a license for your own use without requiring Administrative privileges.

Changes for MacVector 18.6

Direct Codon Optimization of CDS Features

There is a new **Analyze** function that will directly optimize codon usage of CDS features. Simply select a CDS feature in the **Map** or **Features** tab of a nucleic acid sequence and choose **Analyze | Optimize Codon Usage for CDS…** The resulting dialog lets you choose the codon usage table (`.bias` file) to use, along with the genetic code and the optimization algorithm. A filter dialog after the algorithm runs lets you choose whether or not to apply the results to the original CDS, or to simply view the proposed changes.

Automatic Assembly of Sub-projects with Phrap

There is a new tab in the phrap parameters dialog that lets you have MacVector automatically break out the input reads into sub-projects to be assembled separately. A simple pattern-matching text box lets you define which characters in the input filenames should be treated as project names, and which should be treated as read names. After assembly, contigs can be exported (to a variety of file formats, including fasta/q) retaining the project name in the contig names. A great time saver if you do a lot of related small sequencing projects using a well-defined naming convention.

Heterozygote Analysis Enhancements

There is a new checkbox to suppress the default normalization that the heterozygote analysis algorithm uses to better identify potential heterozygotes. Sometimes, clear heterozygotes may be missed if the combined peaks are significantly lower than would be expected in that area of the chromatogram. However, turning off normalization can result in an increase in false positives.

When performing a heterozygote analysis on assembled reads (*Align to Reference* or *Contig Assembly*) the output now includes the location of the potential SNP in the consensus/reference sequence.

Direct Support for .tsv and .csv Primer Database Files

The **Analyze | Primer Database Search** function (and the associated **Scan DNA -> Primers** feature) can now use appropriately formatted text .tsv or .csv files such as those that might be exported from Microsoft Excel, without having to import them into MacVector and save in the MacVector `.nsub` format. The data should have 4 columns – <Selected>/<Name>/<Sequence>/<Comment> where <Selected> and <Comment> are optional. If the <Selected> column is present, the values can only be "0" (unselected) or "1" (selected). The sequence should conform to the standard IUPAC code and "tails" on primers should be indicated by lower case. The use of a header row is optional.

Custom Genbank Export

There is now an option to export sequences in a GenBank text format that includes the graphical feature appearance information that is normally only available in MacVector `.nucl` files. GenBank is a simple text format, so you can view the resulting files in a text editor and its easy to modify the graphical information in those files if you need to. You can then import back into MacVector with those graphical changes fully intact. This new "enhanced" GenBank format can completely substitute for a standard MacVector .nucl file if you or your institution really requires a plain text format for submission to a database or other text-based repository.

Miscellaneous Enhancements and Bug Fixes

There have been some fixes to the **Protein Toolbox Analysis** code to help prevent

certain very rare crashes.

The MacVector-specific 'frag' features now include the name of the user who made the change.

There is a new MacVector-specific 'edit' feature that describes edits made to a sequence with the date the change was made and the user who made the change. Currently, this is only created by the **Optimize Codon Usage for CDS** function, but eventually this will be the basis for a comprehensive history function throughout MacVector.

The *Restriction Enzyme Picker* has been updated to display the number of cuts for each enzyme.

Invoking **Select All** in the *Restriction Enzyme Picker* now ONLY selects the *VISIBLE* enzymes in the picker. This makes it much easier to manipulate lists of interesting enzymes.

There is a new <ctrl>-click context sensitive menu item in the *Contig Editor* and *Align to Reference Editor* that lets you manually change the "clipping" (also known as "trimming") positions at the beginning and ends of sequences.

There are enhancements in the *Align to Reference* scoring algorithm to more closely reflect parameters set by the user.

There is a "mouse-over" tooltip in the *Align to Reference* and *Contig Editors* that displays more information about the read and the alignment score.

The window size of each type of window is now remembered each time you close one, so that a subsequent window of the same type will open at that size.

There is now a <ctrl>-click context menu item to control how read names are truncated in the *Align to Reference* and *Contig Editors*.

You can now hold down <option><shift> to temporarily switch from the normal "**Zoom To Sequence**" mode in the **Map** tab to "**Select Sequence**".

Phrap parameters are now remembered between invocations like most other MacVector parameters.

The licensing code has been cleaned up to do a better job or reporting when licenses are in use on the local network.

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 or licensing problems. New sales of MacVector include 12 months of support that also entitles you to any upgrades to MacVector released during the maintenance period.

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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:

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http://www.macvector.com
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