MacVector 18.7.4

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 18.7 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 Sonoma. 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 18.7 uses approximately 500MB of disk space. Please note this release will NOT run on OS X 10.12 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*, *bowtie* or *minimap2*, 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 June 1st 2024 or later, MacVector 18.7 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 18.7.4

Bug fixes

A problem with MacVector's logging system has been resolved. This would sometimes cause the log file to become bloated, and also result in slow startup times while the old log file was backed up.

Scrolling of large multiple sequence alignment data has been dramatically speeded up.

Existing BAM files are no longer discarded when repeatedly saving Assembly Projects after different analyses.

A rare crash in **Align to Folder** has been fixed.

Some display glitches in the **Click Cloning** window have been fixed.

Changes for MacVector 18.7.3

Bug fixes

A bug where MacVector would hang when calculating the pI of certain protein sequences has been resolved.

Changes for MacVector 18.7.2

Bug fixes

Using pre-filtering with fastq files in minimap2 now works as expected.

The checkbox to turn on/off Restriction Enzyme sites in the Scan DNA preference pane now works as expected.

Changes for MacVector 18.7.1

macOS Support

This release now supports all macOS releases from macOS 10.13 (High Sierra) through macOS 14.5 (Sonoma) and has also been tested on beta releases of the upcoming macOS Sequoia operating system.

Bug fixes

Unique and non-unique restriction sites now correctly get updated to the appropriate color when inserting or deleting sequence data.

The *minimap2* consensus calculation now includes quality information.

The *minimap2* input parameters dialog now provides more intuitive enablement/disablement of parameters when the preset parameters menu is used.

The **History** tab now reports '`source`' features as well as '`frag`' and '`edit`'.

Changes for MacVector 18.7

Long-Read NGS Reference Alignments using minimap2

If you have the Assembler module, you can now assemble noisy long-read data from Pacific Biosciences or Oxford Nanopore using the popular *minimap2* algorithm. This is similar to *bowtie* but can handle long reads whereas *bowtie* is optimized for short (<500nt) reads. To use *minimap2*, create a new **Assembly Project**, then click on the **Add**

Ref toolbar button to add one or more reference sequences. Then click on the **Add Reads** toolbar button and select one or more NGS data files. While not essential, it is usually also a good idea to double-click on the *Status* column of each read to let MacVector know exactly what type of data you are analyzing. Finally click on the **Assemble** toolbar button and select **minimap2** from the menu. The simplest option is to choose one of the presets in the resulting dialog that will tune the assembly parameters for your specific type of data. Note that *minimap2* is actually very good at assembling short read data and in some circumstances may out-perform *bowtie*.

Translate All CDS Features

There is a new **Analyze | Translate All CDS Features…** menu item that lets you batch translate all CDS features in the active sequence. You might typically use this with an entire annotated bacterial genome, though it works just as well with eukaryotic sequences. There are options to display (and then copy or save) all of the translated proteins in fasta format, or to create a codon usage table ("`.bias`") from the results.

Translate All CDS Features in Folder

There is a new **Database | Translate All CDS Features in Folder** menu option that is similar to **Translate All CDS Features** except that it takes a source folder and then loads every sequence file in the folder and translates each CDS feature that it finds, accumulating the results and offering the same result options as **Translate All CDS Features**. A codon usage viewer window is always created and displayed when you select this option (see below).

Codon Usage Enhancements

MacVector now includes a simple viewer for codon usage "`.bias`" files. This displays the data in a standard text format with one row of data per codon, identical to codon usage output windows used in other MacVector translation functions. **New From Clipboard** will create a new `.bias` viewing window if text on the clipboard adheres to this format, or to the popular "GCG" format available on codon usage websites such as CUTG (http://www.kazusa.or.jp/codon/).

The viewer has a toolbar button for the **Translate All CDS Features in F**older function described above. You can invoke this multiple times and each new set of results will be added to the existing codon usage data. You can use this to slowly build up the codon usage information from a large sequence data set in multiple folder locations on your computer.

History Tab

There is a new tab in nucleic acid single sequence windows called **History**. This tab lists several MacVector-specific features relating to the editing history of the sequences such as '`frag`' and '`edit`'. These features now contain additional information such as the date of the operation, the name of the user who performed it and additional sequence information. In the future, all MacVector sequence modifications will write out this information allowing the full history of any construct to be determined and even allowing a simple reversion of the construct to how it existed on a specific date.

Change in Default Restriction Enzyme File Location

By default, MacVector now stores restriction enzyme files in `~/Library/Application Support/MacVector/Restriction Enzymes/`. Because this location is within the current user's home folder, it will always be writeable, even if the user does not have *Administrator* access to the machine. Note that if you have already copied restriction

enzyme files to a different location, then you will not be affected by this change. And your original files will be unaffected

When MacVector starts for the first time, it will create and populate this directory with the latest set of restrictions enzymes shipped with MacVector. It will then look in the old `/Applications/MacVector/Restriction Enzymes/` folder and if any files in there have a newer time stamp than the default enzymes, then those files will be copied to the new location, ensuring no user edits to the data files are lost.

Miscellaneous Enhancements and Bug Fixes

The **Align to Reference SNPs** tab now also displays the percentage of each residue present in each heterozygote SNP.

The **Align to Reference** consensus calling threshold default has been raised to 70% so that heterozygous SNPs are more consistently reported on the consensus line.

A crash when repeating heterozygote analysis has been fixed.

Copied fasta text data is now more reproducibly parsed as single sequence data by **New From Clipboard**.

The protein pI calculations have been modified to also report the pI ignoring `Trp` and `Cys` residues. This brings the results more in agreement with the popular ExPASY website.

A bug where the “blocking” for protein sequences was taking the DNA values has been fixed.

Exporting sequence data in the *Sequin* .tbl format now correctly writes out the correct sequence for the minus strand of segmented features.

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:

`http://www.macvector.com`