MacVector 15.0.2

for Mac OS X

The online updater for this release is 54.8 MB in size

System Requirements

MacVector 15 runs on any Intel Macintosh running the **64-bit** version of **Mac OS X 10.6** or higher. There are no other specific hardware requirements for MacVector – if your machine can run the 64-bit version of OS X 10.6 or above, it can run MacVector. A complete installation of MacVector 15 uses approximately 175 MB of disk space. If you are running Mac OS X 10.6, please be sure to read the section below on **OS X 10.6 Limitations**.

ASSEMBLER NOTE: If you are performing contig assembly using MacVector with Assembler, we recommend you have **at least** 1 GB of RAM installed on your machine. For any serious NGS work using phrap, velvet 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.

Once installation is complete, you must run MacVector and 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 May 1st 2016 or later, MacVector 15 will automatically use your existing license and you will not be required to enter the details again. NOTE: one important change for MacVector 14.0 and later is that you can now activate a license for your own use without requiring Administrative privileges.

Changes for MacVector 15.0.2

Enhancements

The range popup menu now displays the same text that is used as the label in the **Map** tab.

Copied sequences containing CDS features now preserve the original frame via adding a /codon_start qualifier.

The mono-spaced text output now uses the same label text as the **Map** tab.

There are new "thin" versions of the **Hollow Box** and **Hollow Arrow** graphics symbols.

The **Multiple Sequence Alignment Editor** tab now supports **File->Export Tab Contents As…**

You can now use the **Edit | Transformations | Maker lower case/Make upper case** menu items in the Subsequence/Primer editor.

Bug Fixes

Sometimes the **SNP** tab in the **Align To Reference** window would show "no text". This has been fixed and the **SNP** text data has been enhanced to include additional information.

The selected Genetic Code is now honored in all views containing translations.

Changes for MacVector 15.0.1

CRISPR Indel Detection

There is a new preset in the **Align To Reference** alignment dialog that optimizes the parameters for use in CRISPR indel detection at the cost of slower performance. These settings are tuned to allow for insertions of up to 10 nt in length and deletions of any length. In addition, the alignment algorithm has been adjusted to generate much cleaner alignments across the indel locus.

Bug Fixes

An intermittent problem that affected a subset of users in many different ways running OS X 10.10 ("Yosemite") has been resolved. These included inability to open certain file types and even crashes on startup.

Fasta files can now be correctly imported via the file system or by the **File->New From Clipboard** interface.

The ability to enter ambiguous residues in the **Align To Reference/Contig Editor** has been restored.

Changes for MacVector 15.0

InterProScan

You can now scan proteins for functional domains using the popular online InterProScan collection of algorithms. This is accessed from the **Database** menu. You can easily permanently add the found domains as features by clicking on the little plus icons next to the graphic representing each domain.

Multiple Sequence Alignment Enhancements

There is a new **Mode** toolbar button in the **Editor** tab of both protein and DNA multiple alignments. For proteins, this lets you assign the last sequence as a "reference" so that the displays key off that sequence when showing similarities. This allows you to view proteins in a similar way to the DNA **Align To Reference** interface.

The second new capability is that you can now view and align DNA sequences via their virtual translations. You can choose to display both the DNA sequences and their amino acid translations at the same time (or even just the amino acid translations). When amino acids are displayed, you can use ClustalW, Muscle or T-Coffee to align the amino acid translations – the alignments are then reflected in the underlying DNA sequences.

Everything is updated dynamically as you edit so that you can delete DNA residues and immediately see the impact of the change on the amino acid alignments.

Miscellaneous Enhancements

The **Database | Auto-annotate Sequence** function now supports Applescripting. There is an example script in the `/Applications/MacVector/Applescripts` folder. You can create a **misc_feature** by right-clicking on any restriction site to have a permanent record of any RE site associated with the sequence.

There have been a number of tweaks to the **Map** view to clean up the display e.g. better positioning of graphics to avoid even minor overlap between them at high resolution and better handling of labels to reduce the amount of text displayed.

A new option to control the size of font in lists and tables.

You can now undo CluatalW/Muscale/T-Coffee alignments.

You can now choose the /regulatory_class of a **Regulatory** elements from a popup menu. The **Regulatory** type replaced the old **-10**, **-35**, **enhancer** etc types in the last couple of years in the Genbank standard.

Termination codons ("*") are now retained after alignment by ClustalW/Muscle/T-Coffee rather than getting converted to X.

The **Primer Database** editor now directly supports entering "tails" as lower case residues.

MacVector 15 Limitations on Mac OS X 10.6

In order to take advantage of many of the built-in enhancements in more recent releases of OS X, if you run MacVector 15 on OS X 10.6, you will find there are certain limitations;

(i)   The mouse pointer does not change in a context-sensitive way when moving over different interface graphical items.

(ii)   Tool tips within the editors do not display.

(iii)   The Feature tab list only display the first qualifier for each feature (but if you double-click to open the editor, you will see that all of the qualifiers are present).

(iv)   The Primer Database selection popup scrolling menus are not available – you should instead open the actual .nsub file and copy the primer sequence from there.

(v)   The Sparkle automatic online updater is non-functional.

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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.

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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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