MacVector 12.0.6

for Mac OS X

System Requirements

MacVector 12 runs on any PowerPC or Intel Macintosh running Mac OS X 10.4 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 10.4 or above, it can run MacVector. A complete installation of MacVector 12 uses approximately 155 MB of disk space.

Installation

The installation procedure has changed slightly for MacVector 12.0. Previously, after installation you were given a grace period of 21 days before you were required to enter a valid serial number and activation code. Due to abuse, we have had to remove this functionality – you must now enter a valid 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 are simply upgrading from an earlier version, MacVector will automatically recognize your existing license.

Changes for MacVector 12.0.6

Bug Fixes

An occasional hang when starting up on Mac OS X 10.4 has been fixed.

A couple of axis-dependent bugs with Pustell matrix analysis ("dot-plots") have been fixed. You should now get essentially identical results if you swap the axes your sequences are placed onto.

Pasting a short sequence into a multiple alignment no longer duplicates a couple of residues if there are gaps at the end of the alignment.

A crash when clicking on the graphics palette when in "Copy Feature Appearance" selection mode has been fixed.

All features are now correctly inserted into a target vector if the ligated fragment overlapped the circular origin of the source molecule.

The Align To Reference algorithm is no longer confused by long stretches of Ns in the Reference sequence.

Changes for MacVector 12.0.5

Bug Fixes

The installer now installs writable codon bias table files and the code has been changed to

ensure the Nucleic Acid Toolbox functionality works even if those files are read only.

The floating graphics palette window now stays hidden when set that way.

Asymmetric restriction enzymes sites now copy correctly from one enzyme list window to another.

Changes for MacVector 12.0.4

Bug Fixes

Find searches using the "literal" flag now correctly finds matches on the reverse strand.

Sequences containing more than 32766 features can now be downloaded and saved from the Entrez database browser.

Incorrect error messages displayed by Primer3 when it actually ran successfully have been removed.

A problem with the LOCUS line when saving new sequences in GenBank format has been fixed.

Staggered restriction sites in the map view now display correctly when on the complementary strand.

The Feature list no longer resets to the top after editing a feature.

The "Forward-delete" button now works as expected in the Trace editor.

The performance of the multiple sequence alignment editor has been improved so that you can now easily edit alignments containing thousands of sequences with no lag.

The Generate Transcript function now correctly handles sequences with non-zero origins.

MacVector is now more tolerant importing GenBank files with malformed LOCUS lines.

Changes for MacVector 12.0.3

Bug Fixes

Some problems with the Align to Folder alignment output incorrectly displaying reverse-complemented matches have been resolved.

A problem where the Primer3 algorithm would fail with the error "Illegal value for INCLUDED_REGION" has been fixed.

The Contig Editor now always provides a vertical scrollbar to prevent the occasional problem where Reads would be scrolled off-screen with no easy way to view them.

The restriction enzyme output window has been reworked to ensure asymmetrical cleavage enzymes are always reported consistently.

A bug where the cDNA Align to Reference algorithm would occasionally freeze with certain base combinations has been fixed.

The Assembly Editor now highlights the editable sequence when you select objects (open reading frames, primers etc) in result windows, allowing you to easily create corresponding features.

Changes for MacVector 12.0.2

Bug Fixes

Find now correctly finds matches at the very end of a sequence.

Find now finds matches that cross the circular origin.

The Align to Reference "Remove Seqs" toolbar icon now becomes enabled when one or more sequences are selected.

Find matches in the Align to Reference editor now stay highlighted.

The Align to Reference editor no longer deselects after a copy operation.

An occasional problem where restriction sites would be duplicated near the origin of circular sequences has been resolved.

Feature data is no longer left on the clipboard when you copy a text sequence from outside of MacVector.

The graphics palette now allows entering of radius values in cms and points.

Sequences with a mixture of upper and lower case residues can now be saved in GenBank, FastA, GCG and EMBL formats without losing the lower case residues.

Changes for MacVector 12.0.1

Bug Fixes

Selecting items in the Symbol Editor treee view now selects them in the Map view.

The subsequence editor now correctly saves newly created subsequences so that they are included in subsequence searches.

Chromatogram files are now saved correctly as SCF files by default.

Align To Reference assemblies are now saved in the correct default format after being edited.

A number of crashes when using Align To Folder to search in folders containing non-

sequence files have been fixed.

Restriction Enzymes and Subsequences are now displayed alphabetically in their respective editor windows.

Changes for MacVector 12

Enhanced Circular Sequence Support

While MacVector has always been able to display and analyze circular sequences, MacVector 12 has added a number of significant enhancements. You can now select across the 12 o'clock origin of circular sequences and features can seamlessly span the origin. The order that you select features or Restriction Enzyme sites is now important – the selection is propagated in the clockwise direction. Most algorithms are now completely circular sequence aware, allowing you to e.g. find open reading frames that cross the origin, or select a region that crosses the origin for analysis.

Enhanced Graphics

The Map graphics has had a huge amount of work;

There is a new collapsible overview pane that displays a full-length miniature version of the sequence so that you can orient yourself when zoomed into a long sequence.

Graphics Palette

The graphics palette has been rewritten with a lot of new functionality;

Selection Modes – a row of buttons lets you choose between the following selection modes;

(a) Zoom – this is the default and the mode used by older versions of MacVector – you can click on features or sites to select them and if you click, hold and drag, the display resets to "zoom in" to the segment you selected.

(b) Feature Selection – clicking and dragging selects all the features or sites that are touched by the selection rectangle.

(c) Sequence Selection – clicking and dragging selects just the sequence touched by the selection rectangle.

(d) Magnify – clicking magnifies the display 2-fold. <option>-clicking reduces the magnification 2-fold.

(e) Slide – this mode lets you drag the current zoomed region to the left or right. You can also use this to rotate circular sequences so that any arbitrary location is set to the 12 o'clock position.

(f) Copy Feature Appearance – this mode is only available if you have one or more features selected. Once selected, if you then click on a different feature, all the selected features will change appearance to match that feature.

Quick Fit Buttons – four buttons let you quickly adjust the display to useful range and scaling;

(a) Zoom to Sequence – adjusts the residues per inch so that the residues are just visible. Does not change the current displayed sequence range.

(b) Fit To Window – adjusts the residues per inch so the entire sequence range can be displayed in the window.

(c) Fit To Page – adjusts the residues per inch so the entire sequence range can fit on the currently selected printable page.

(d) Fit Residues – this resets the displayed range to the entire sequence and adjusts the residues per inch so that residues are just visible.

Navigation Buttons – these let you scroll around in the Map graphic;

(a) Slide Left – if you have a range selected, this nudges the range to the left. Full circular molecules are rotated slightly to the left. The left arrow key also performs this function.

(b) Slide Right - if you have a range selected, this nudges the range to the right. Full circular molecules are rotated slightly to the right. The right arrow key also performs this function.

(c) Home – this centers the current range in the top center of the window and resets rotation of circular molecules.

(d) Zoom In – this zooms in so the displayed range is reduced 2-fold.

(e) Zoom Out - this zooms out so the displayed range is increased 2-fold.

(f) Reset Zoom – this resets the zoom so the entire sequence is displayed and fits it to the window.

To make room for all the new buttons, a number of infrequently used buttons (e.g. shadowing and anti-aliasing control) have been moved to Map View Preferences pane.

Symbol Editor

The symbol editor has been completely rewritten for MacVector 12. There are new symbol types ("Delimited Line", "Full Height Hollow Box", "Simple Line" and "Single Arrow No Drop") and new "meta tags" that can be accessed by clicking on a drop down arrow to the right of the Label edit box.

Sequence Display

You can now display sequences at the residue level in double-stranded form.

When at the residue level, restriction enzyme sites are displayed with the actual cut sites ends displayed on the sequence. If you select a restriction fragment, the highlights clearly show the structure of any staggered ends.

There is now the option to display the actual sequence of certain types of features – in particular, you can show the amino acid sequence of CDS features aligned above or below the DNA sequence. Other features that can be displayed as residues are RNA features and the primer_bind feature type.

Sequence Editor Enhancements

There is now the option to color the sequence in the main Editor tab. This is controlled through the Preferences->Colors pane. Any features that are visible in the Map tab are displayed in color in the Editor when this is enabled.

You can also select a range in the editor, then choose Edit->Transformations->Color: to set that range to a color of your choosing.

The Editor now supports the use of lower case characters. You can mix and match upper and lower case characters to indicate regions of interest and the appropriate case will be used in all printed output. You can change the case of any selected region using the items in the Edit->Transformations menu. Note that the case of the sequence does not have any effect on any of the analysis functions.

The search function has been reworked to simplify searching both strands for a sequence. The search will now correctly find e.g. primer sequences on the minus strand using the default settings.

Restriction Enzyme Enhancements

There is now the option to search for "one out" restriction enzyme sites by selecting a checkbox in the restriction enzyme analysis dialog. These are displayed in a more pastel color shade than normal sites and have an asterisk appended to distinguish them in text lists.

Unique Restriction Enzyme sites in a molecule are now shown in Red.

If you double-click on a Restriction Site, all of the sites of that type (e.g. EcoRI, BamHI etc) will be selected so you can quickly see where all the sites of a particular type lie on the sequence.

If a DNA fragment with "sticky ends" has been copied to the pasteboard using Edit->Digest, then sites in the Map view are highlighted with pastel red and/or green to indicate which end of the fragment they are compatible with.

Miscellaneous Enhancements

The Align to Reference, Trace and Multiple Sequence Alignment Editors have all been rewritten to use Quartz graphics resulting in higher quality displays and printouts and images that are copied to the pasteboard using the OS X standard PDF format.

You can now sort sequences in the Align to Reference editor.

There is a new SNP report tab in the Align to Reference window. This lists all of the potential SNPs that are present in the aligned reads. For chromatogram files, the algorithm considers the area under the curves to determine which SNPs appear "probable" and which SNPs are "possible".

Many analysis results (e.g. Restriction Enzyme, Subsequence, ORF and Primer3) can now be easily converted to permanent features by right-clicking (or <ctrl>-clicking) on the result object and choosing "Create xxx Feature" from the context-sensitive menu (xxx will be substituted by the appropriate feature type).

You can also drag result objects and drop them on the parent window to automatically create a corresponding permanent feature.

The sequence Find dialog has had some redundant controls removed and the algorithm reworked to simplify searches. In particular, the "Reverse" and "Complement" checkboxes have been removed. All searches against "Both Strands" now automatically search for reverse-complemented matches.

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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