

MacVector 17

for Mac OS X

Auto Annotation Tutorial

MacVector, Inc.
Software for Scientists

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Introduction

The auto annotation function was added to MacVector in release 11.0. The idea behind this functionality is that you can maintain a curated folder of carefully annotated sequences and when you receive a new sequence from any source, simply scan it against the folder and it will be automatically annotated with matching features from the curated sequences. As well as adding the matching features, MacVector also assigns feature appearance information to the features so that you can be sure that, for example Ampicillin resistance genes always appear as a green arrow. You also have the option of simply replacing the graphics appearance of any matching features that already exist in the source sequence. This is particularly useful if you download an annotated sequence from GenBank or have a colleague who has sent you a sequence in GenBank or EMBL formats – simply scan the sequence against your curated folder of sequences and all your features of interest will be displayed exactly as you like them.

The algorithm uses sequence similarity to identify matching features and has a certain amount of fuzziness that you can control to handle minor sequencing errors.

Sample Files

This tutorial uses the sample file pBR322Ascii.txt which is found in the following folder:

```
/Applications/MacVector/Tutorial Files/Auto  
Annotation
```

It also uses the curated vectors found in:

```
/Applications/MacVector/Common Vectors
```

Tutorial

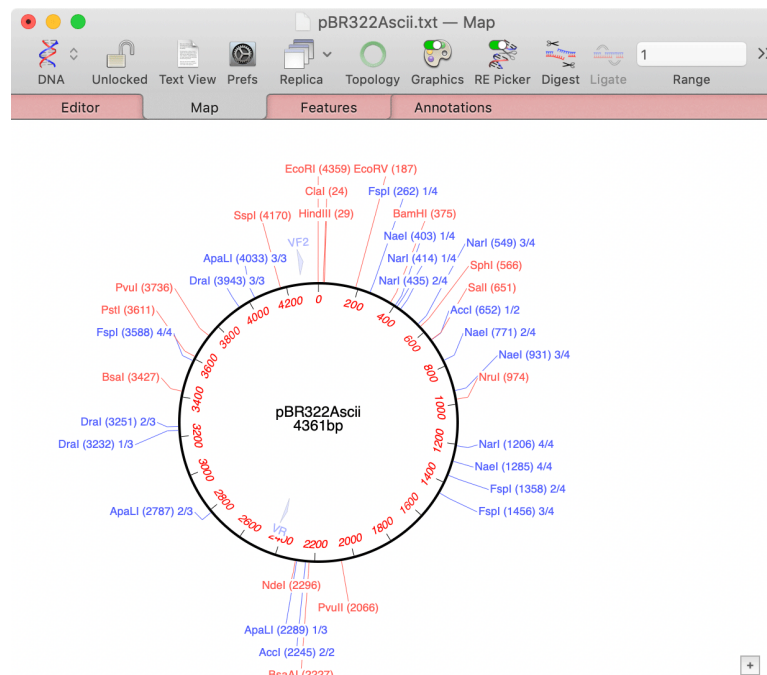
A Simple *E. coli* Vector

MacVector comes with a variety of annotated plasmid vectors that can be found in the `/Applications/MacVector/Common Vectors/` folder. These folders include vectors formatted to match the New England Biolabs, Invitrogen and Promega catalogs. There is also an `Annotated Fragments` folder containing a number of fragments of DNA, each containing a gene, replication origin or other feature found in common cloning vectors. You can use this folder as a first pass to annotate a new DNA sequence.

We'll start by annotating a bare sequence that is actually the sequence of one of the most historically significant vectors, pBR322.

Select **File | Open** and navigate to the /Tutorial Files/AutoAnnotation/ folder. Select the file pBR322Ascii.txt and click **Open**.

The sequence will be imported, but if you look at the **Map** or **Features** tabs, you will see that there are no features assigned to the sequence. Note that for the purposes of this tutorial, the **Scan for Missing Features** and **Scan for Open Reading Frames** options have been temporarily turned off in the **MacVector | Preferences** dialog.



If your **Map** tab does not look like the one above, click on the **Fit to Window** button in the floating **pBR322Ascii.txt – Map** graphics palette. If the graphics palette is not visible, select the **Window | Show Graphics Palette** menu item or click on the **Graphics** toolbar button. If you don't see a circular sequence, click the **Topology** button to tell MacVector that this is a circular plasmid vector.

Now choose **Database | Auto-Annotate Sequence**. Click on the **Choose** button at the top of the sheet and select the /Applications/MacVector/Common Vectors/Annotated Fragments/ folder.

Sequence Folder

AnnotatedFragments Choose...

Search in enclosed folders (recursively)

Feature Characteristics

Only consider visible features Minimum feature length: 10

Discard shorter duplicates Residues around point feature: 30

Allow gaps in CDS features Maximum allowed mismatches: 1 %

Maximum allowed gaps: 0.5 %

Point Feature Characteristics

Include point features

Include point features enclosed by other features

Feature Modifications

Leave existing qualifiers and graphics unchanged

Factory Defaults Cancel OK

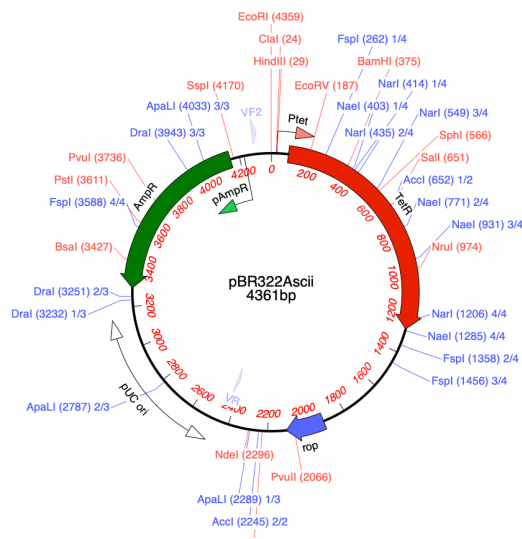
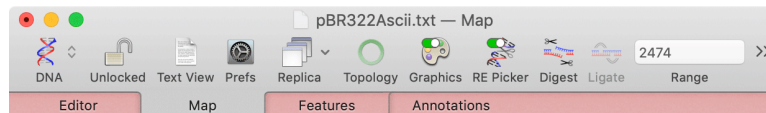
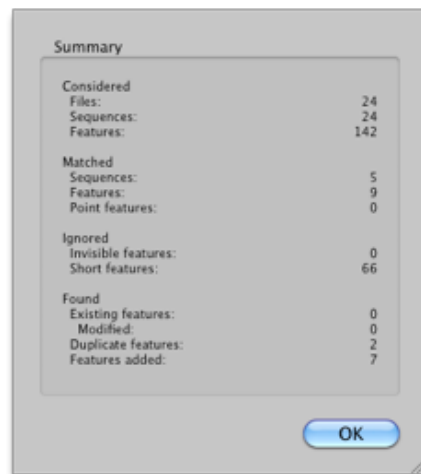
You can leave the rest of the parameters with the default settings.

Note that Sequence Folder is a combo box – it remembers all of the previous places you have searched. This makes it easy to toggle between all your favorite folders with different searches. These history combo boxes are used in numerous places through MacVector to simplify selection of folders and analysis data files like Restriction Enzyme files or comparison matrices. In addition, if you are using Mac OS X 10.5 or later, you can drag and drop folders or files onto the combo box to select that folder or file.

Auto Annotation analyzes are submitted to the Job Manager. Although most jobs will complete in a few seconds for long sequences you can hide the dialog and continue working on other sequences. When the job has completed the MacVector icon in the Dock will bounce once and a red digit will appear to show the number of completed jobs available in the Job Manager that you can view. Click **Window | Job Manager** to display these.

Click on the OK button to run the analysis. Jobs are submitted to the Job Manager and once completed may be viewed by clicking **View**. For long sequences you can click **Close** and track progress using the **Job Manager**.

When the job has completed you will first see a results summary sheet that will indicate what **Auto Annotation** has found, which features it will add, and how many were found but ignored. Dismiss this sheet and you will see that the **Map** has been updated to show several new features, including Tetracycline and Ampicillin resistance genes and the pMB1 origin of replication.



As well as annotating new features you can also use **Auto Annotation** to curate your own lab's collection of vector sequences and ensure they all share the same appearance.

To show this, we will use our annotated pBR322Ascii.txt. However, this time we will use another set of curated vectors that have a different graphical appearance. This time we will use the /MacVector/Common Vectors/NEB/ folder – this contains a selection of vectors available from New England Biolabs, formatted to match the appearance in their catalog.

Keep the previously annotated pBR322Ascii.txt. Choose **Database | Auto-Annotate Sequence**.

Instead of looking for missing features we are now going to look for matching *existing* features. Once found we will replace the

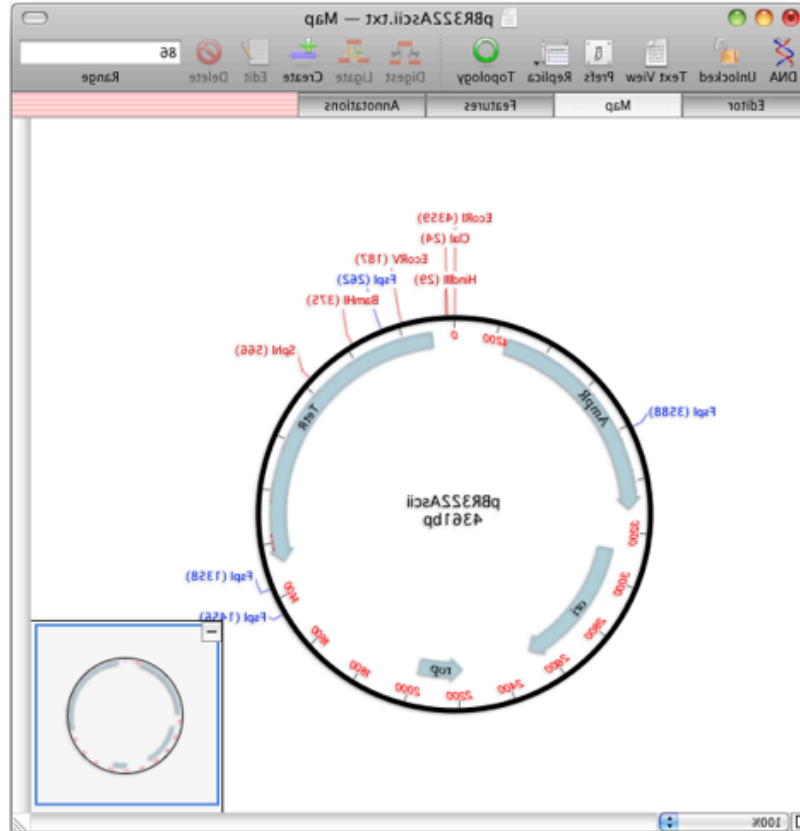
Click on the **Choose** button at the top of the sheet and select the /Applications/ MacVector/Common Vectors/NEB/ folder. Change the **Feature Modifications** option to **Replace only graphics for existing features**. Click **OK**

Symbol feature appearance with the appearance from the curated file's appearance.

The screenshot shows the 'Auto-Annotate Sequence' dialog box in MacVector. The 'Sequence Folder' is set to 'Morcheeba HD:Applications:MacVector 12:Common Vectors:NEB'. The 'Search in enclosed folders (recursively)' checkbox is checked. Under 'Feature Characteristics', 'Discard shorter duplicates' is checked, while 'Only consider visible features' and 'Allow gaps in CDS features' are unchecked. The 'Point Feature Characteristics' section has 'Include point features' and 'Include point features enclosed by other features' unchecked. The 'Feature Modifications' dropdown is set to 'Replace only graphics for existing features'. The dialog has 'Defaults', 'Cancel', and 'OK' buttons at the bottom.

This time, when the algorithm completes, the features take on the typical appearance seen in the NEB catalog. Note that the CDS features have not been duplicated – MacVector realizes the features

already exist and just replaces the graphic symbols. You can also optionally set the algorithm to ignore duplicate features completely, in which case the sequence appearance would have been left unchanged.



You can use the **Auto Annotation** function to scan any folder containing DNA sequences. They don't have to be in MacVector format, although features from GenBank or EMBL files will be given the default appearance for the feature type. There is a certain amount of fuzziness built into the algorithm – it can handle mismatches and even a few gaps and still identify matching features.

Reference Manual

Overview of the Algorithm

The auto annotation algorithm reads each file in the target folder(s) in turn and determines if it encodes a DNA sequence containing annotated features. It then works through each feature in the DNA, copying the sequence corresponding to the feature and comparing that to the target sequence. If a high quality match is found, the feature is copied to the target sequence.

There are several things to note about the algorithm;

- (i) It will iterate through sub-folders within the folder you select, and sub-folders within those folders as well. However, it ignores any aliases or shortcuts to other folders.
- (ii) It will discard duplicate features, which it assumes are those of identical type that start and stop at the same location on the same strand of the target sequence. It does not consider the description/qualifiers associated with a feature when determining duplicates.
- (iii) If the matching feature was found in a MacVector format file, then the graphical appearance symbol information will also be applied to the new feature.

Parameters

The screenshot shows a dialog box titled "Auto Annotation Parameters" with the following sections:

- Sequence Folder:** A text field containing "NEB" and a "Choose" button. Below it is a checked checkbox for "Search in enclosed folders (recursively)".
- Feature Characteristics:** A group of settings including:
 - Checked checkbox: "Discard shorter duplicates"
 - Checked checkbox: "Re-evaluate CDS features after scan"
 - Minimum feature length: 10
 - Residues around point feature: 30
 - Maximum allowed mismatches: 1%
 - Maximum allowed gaps: 0.5%
- Point Feature Characteristics:** Two unchecked checkboxes:
 - "Include point features"
 - "Include point features enclosed by other features"
- Feature Modifications:** A dropdown menu set to "Replace only graphics for existing features".

At the bottom, there is a help icon (?), "Defaults", "Cancel", and "OK" buttons.

Sequence Folder

This parameter is fairly self-explanatory and displays the folder that will be searched for annotated sequences with similarity to the target sequence. Click on the **Choose** button to select a different folder. The algorithm will scan the folder and drill down into all the sub-folders looking for sequence files.

Feature Characteristics

Only consider visible features - by default, MacVector considers all features in the annotated sequence. However, you can restrict the features to just those that are visible if you want to avoid cluttering your sequences with large numbers of hidden features. For example, the standard GenBank pBR322 vector sequence has around 60 features assigned to it, but only four are displayed in most schematic diagrams of the plasmid.

Discard shorter duplicates – normally, if features have different start and/or stop locations, they are considered to be different. However, many vectors have slight differences in the extent of the replication origin or features such as T7 or SP6 promoters. If you were to scan a folder full of vectors, you may find that the same feature becomes annotated several times, with each feature differing from the others by one or two residues at either end, reflecting differences in the annotated vectors. If you select this checkbox, any features that lie entirely within another feature of the same type will be discarded and only the longest feature will be retained.

Allow gaps in CDS features – MacVector allows some fuzziness in the identification of matching features, allowing a limited number of gaps and mismatches in the alignment. However, because CDS features by definition encode proteins, if any gaps are introduced the encoded protein may have frameshifts and may encode a completely different protein than that encoded by the original annotated feature. Accordingly, MacVector usually does not allow gaps in CDS features when comparing annotations. However, if you know your target sequence may have sequencing errors, you might want to allow gaps in CDS features so that they are annotated as expected.

Re-evaluate CDS Features after Scan – if an annotated CDS feature is not a 100% match to the original scanned feature, then some of the annotations may be incorrect. If this checkbox is selected, then MacVector (a) checks for the presence of stop codons in the CDS and may extend or truncate the feature to ensure the CDS is valid and (b) will update the `/translation=`

qualifier to reflect the actual amino acid translation of the predicted CDS product.

Minimum feature length – because the algorithm uses sequence similarity to determine if a feature is present on the target sequence, very short features may be incorrectly annotated. For example, if you had a 4 base pair misc_feature labeling an important *MboI* site, that would get added at every *MboI* (GATC) site on the target – every 256bp on average. You can use the Minimum feature length parameter to prevent short features that might match by random chance from being annotated onto the target.

Residues around point feature – MacVector treats point features as a special case. A “point” feature is one where the start and stop location are the same. These might be SNP locations, a replication start site, or just a particular point of interest. When the algorithm encounters a point feature, it takes a region of N residues centered around that point and uses that to determine if the feature matches the target.

Maximum allowed mismatches – MacVector does allow some fuzziness in the determination of what is a matching feature. This parameter controls the number of mismatches permitted before a feature is considered to be non-matching. The default of 1% means that only 1 residue in 100 can be mismatched – features of 99 residues or less will need to have a perfect match to be added to the target.

Maximum allowed gaps – similar to the mismatches parameter, this limits the number of permissible gaps with the default value of 0.5% meaning just 1 gap per 200 residues is permitted in matching features.

Point Feature Characteristics

Include point features – check this box if you want MacVector to include point features when it performs the scan. If selected, it will use the *Residues around point feature* setting to determine relevant matches.

Include point features enclosed by other features – an alternative way of including point features is to have them added only if a feature that encloses them is added. Suppose you have SNPs annotated within a CDS feature – if the CDS feature gets annotated onto the target, then all the SNPs that lie within that will be annotated as well.

Feature Modifications

This popup menu has three settings that adjust the way the algorithm handles any existing features in the target sequence as follows;

Leave existing qualifiers and graphics unchanged – when this is selected, if the target sequence already has a feature of the same type at the same location as a matching feature, then the matching feature is discarded and the target sequence feature is left unchanged. Select this to make sure that none of your existing features are changed while allowing new features to be added.

Replace qualifiers and graphics for existing features – this will allow any matching features to completely replace the same feature on the target sequence. Features can only be replaced – if there are existing features that have no match to any feature in the scanned folder, they will be retained unchanged. If you want to auto annotate a sequence “from scratch”, you should first delete all existing features before running the auto annotation algorithm.

Replace only graphics for existing features – This setting keeps all of the qualifier/description information for any existing features with a match in the scanned folder, but replaces the graphic appearance information. This is particularly useful if you have downloaded a sequence from Entrez or imported a GenBank or EMBL format file. By choosing this option, you are guaranteed that you will not lose any textual annotation, but the features will take on the graphical appearance you prefer.

Limitations

The primary limitation of the Auto Annotation function in MacVector is that the entire feature from the scanned folder must be present in the target sequence uninterrupted before it will be added. If a feature is truncated, it may not be included in the annotation. If you think this may be happening, try increasing the Maximum Allowed Mismatches setting. For example, if this is set to 10%, then truncated features will be annotated as long as they are at least 90% of the length of the original feature. Similarly, if a feature has been interrupted, e.g. because you inserted a fragment of DNA into a gene, neither part of the feature will be annotated.