

C C A T T 0 1 0 0 0  
G A G G A 0 1 1 0 1  
G A A T T 0 0 1 1 0  
A C A A G 0 0 1 0 0  
T A C C A 0 0 1 1 0  
T T A C A 0 1 0 0 0  
A C C T C 0 0 0 1 0  
A A G G A 0 0 0 0 0  
G A T G A 0 1 1 0 0  
T A G A T 0 0 1 0 0  
G A T G A 1 0 1 0 0  
T G T A G 1 0 0 0 0  
T A G T A 0 0 0 0 0  
G A T A T 1 0 0 0 0  
G A G T G 1 0 0 0 0  
A G A T T 1 0 0 0 0  
G A G T A 1 0 0 0 0  
T G A T G 1 0 0 0 0  
A T T A G 1 0 0 0 0  
T A G A T 1 0 0 0 0  
G A G A 1 0 0 0 0  
G T A 1 0 0 0 0  
G A T 1 0 0 0 0  
T A G 1 0 0 0 0  
A G 1 0 0 0 0  
G A 1 0 0 0 0  
A 1 0 0 0 0  
T 1 0 0 0 0

# Tutorial

## Tutorial: Phylogenetic Trees

February 17, 2014



## Tutorial: Phylogenetic Trees

You can make a phylogenetic tree from an existing alignment. (See how to create an alignment in the tutorial: "Align protein sequences").

We use the 'ATPase protein alignment' located in 'Protein orthologs' in the Example data. To create a phylogenetic tree:

**click the 'ATPase protein alignment' in the Navigation Area | Toolbox | Alignments and Trees (📁) | Create Tree (🌳):**

A dialog opens where you can confirm your selection of the alignment. Click **Next** to move to the next step in the dialog where you can choose between the neighbor joining and the UPGMA algorithms for making trees. You also have the option of including a bootstrap analysis of the result. Leave the parameters at their default, and click **Finish** to start the calculation, which can be seen in the **Toolbox** under the **Processes** tab. After a short while a tree appears in the **View Area** (figure 1).

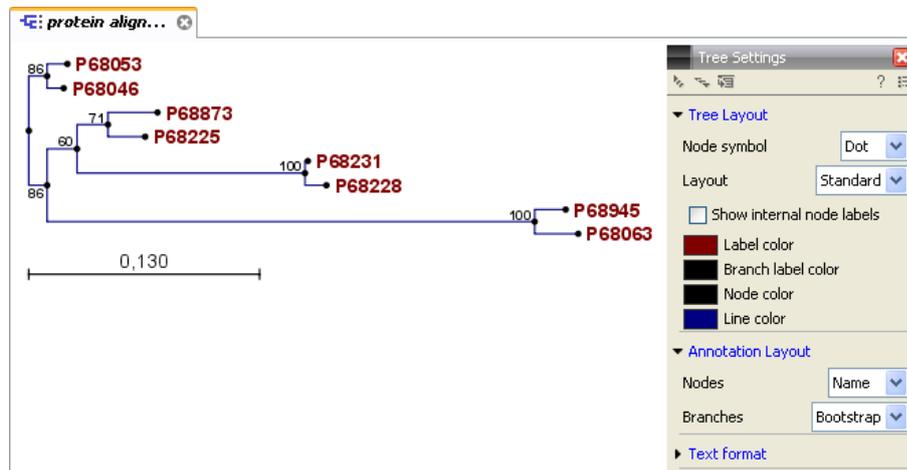


Figure 1: After choosing which algorithm should be used, the tree appears in the View Area. The Side panel in the right side of the view allows you to adjust the way the tree is displayed.

### Tree layout

Using the **Side Panel** (in the right side of the view), you can change the way the tree is displayed.

Click **Tree Layout** and open the **Layout** drop down menu. Here you can choose between standard and topology layout. The topology layout can help to give an overview of the tree if some of the branches are very short.

When the sequences include the appropriate annotation, it is possible to choose between the accession number and the species names at the leaves of the tree. Sequences downloaded from GenBank, for example, have this information. The **Labels** preferences allows these different node annotations as well as different annotation on the branches.

The branch annotation includes the bootstrap value, if this was selected when the tree was calculated. It is also possible to annotate the branches with their lengths.