

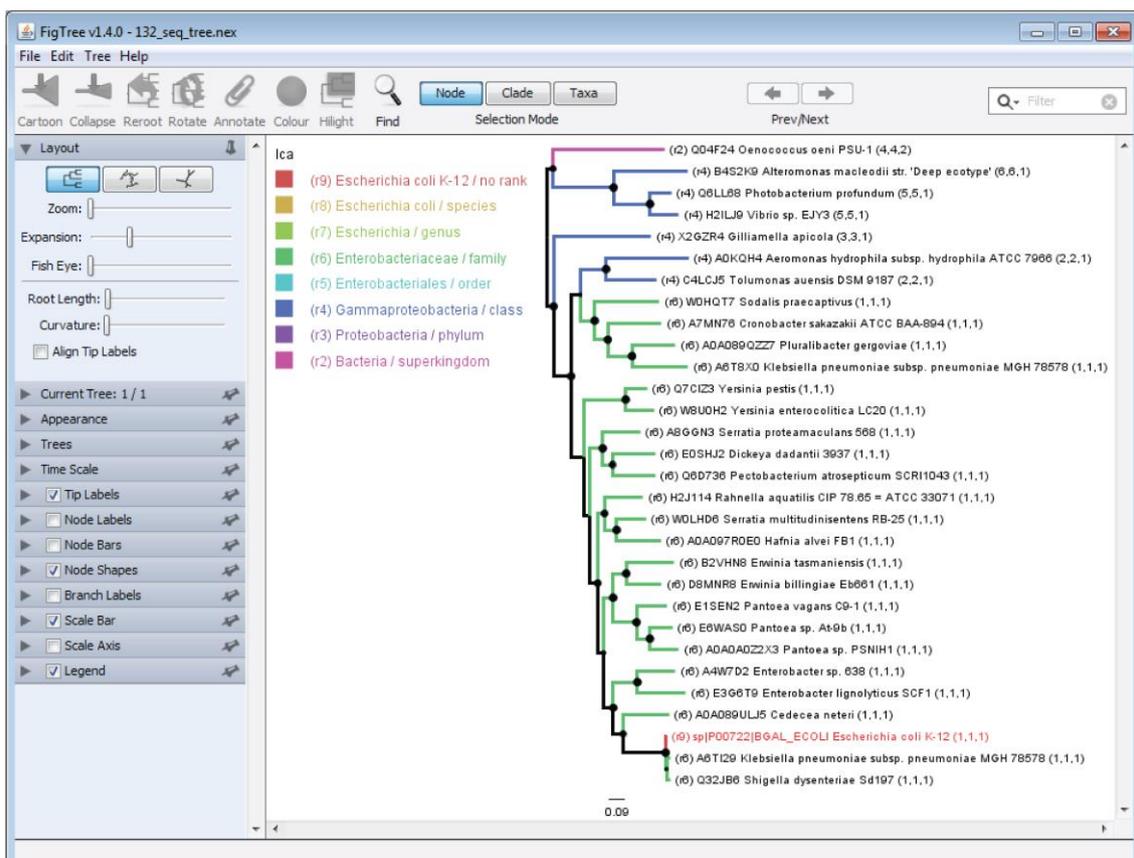
# TaxOnTree

Including taxonomic information into your tree

## Opening your tree in FigTree

After running TaxOnTree from web ([maxixe.icb.ufmg.br/tot/tot.html](http://maxixe.icb.ufmg.br/tot/tot.html)) or from source code ([sourceforge.net/projects/taxontree/?source=directory](http://sourceforge.net/projects/taxontree/?source=directory)), TaxOnTree will generate a Nexus file structured to use some of FigTree resources. FigTree is a free graphical viewer of phylogenetic trees developed by Andrew Rambaut group. In its website ([tree.bio.ed.ac.uk/software/figtree/](http://tree.bio.ed.ac.uk/software/figtree/)) there are versions for Mac, Unix and Windows. So, once with your Nexus file in hand, just download FigTree and open the Nexus file in it. In this manual, I will use one of tree sample available in TaxOnTree website.

After opening the Nexus file in FigTree, you will see your phylogenetic tree with the branches colored according to the LCA (Lowest Common Ancestor) between the query species and the other species in the tree like in the Figure 1.



**Figure 1:** Screenshot of FigTree having a Nexus file generated by TaxOnTree just opened.

## Leaves nomenclature used by TaxOnTree

Firstly you will see that there is a single leaf in **red**. This leaf represents your query sequence.

Taking a leaf name from the sample tree, we have the following pattern:

**(r6) Q32JB6 Shigella dysenteriae Sd197 (1,1,1)**

- **(r6)** → “r” means “nodes from the root”. In this case, the Lowest Common Ancestor between *Escherichia coli* and *Shigella dysenteriae* is 6 nodes from the root considering the lineage of *E. coli* from NCBI taxonomy. The higher this number, more recent is the LCA between two species. The maximum number is one showed in the query leaf (in this case, 9). This number is the same displayed in the color legend.
- **Q32JB6** → Protein accession number.
- **Shigella dysenteriae Sd197** → species or strain that the protein belongs.
- **(1,1,1)** → A taxonomic rank code for family, order and class respectively. Species that belong to the same family will present the same taxonomic code for family and so on. The query sequence will always have the code (1,1,1).

## Coloring branches by a taxonomic rank

You can also color the tree according to some taxonomic rank. Take the following steps:

- 1) In the FigTree side menu bar, go to Appearance;
- 2) By clicking on “Colour by”, it will display various taxonomic ranks as options for coloring the branches. Here I chose “12-family” (Figure 2). You can setup the branch colors by clicking in Colours;
- 3) Branch color will change immediately, now you have to change the color legend. Go to Legend in the FigTree side menu bar and in Attribute, set the same taxonomic rank that you selected to color the tree (Figure 3).

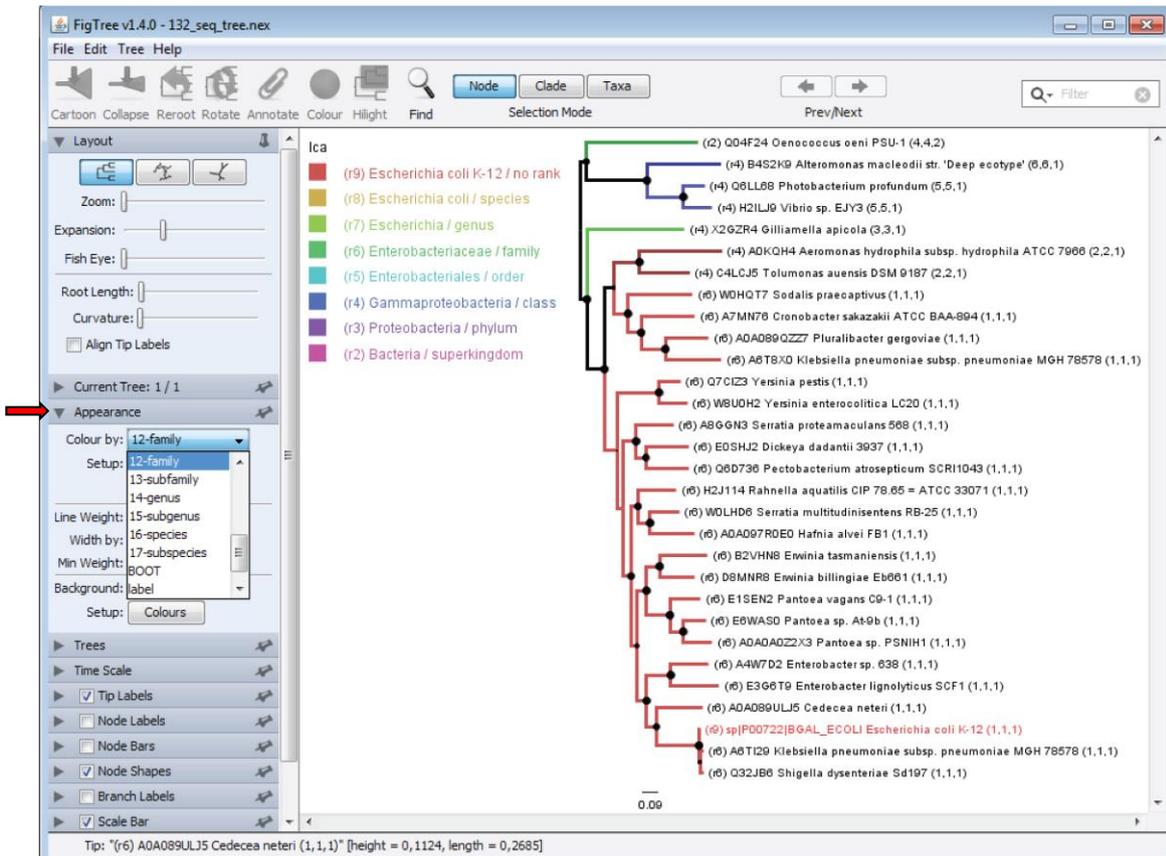


Figure 2: Coloring the branches according to some taxonomic rank.

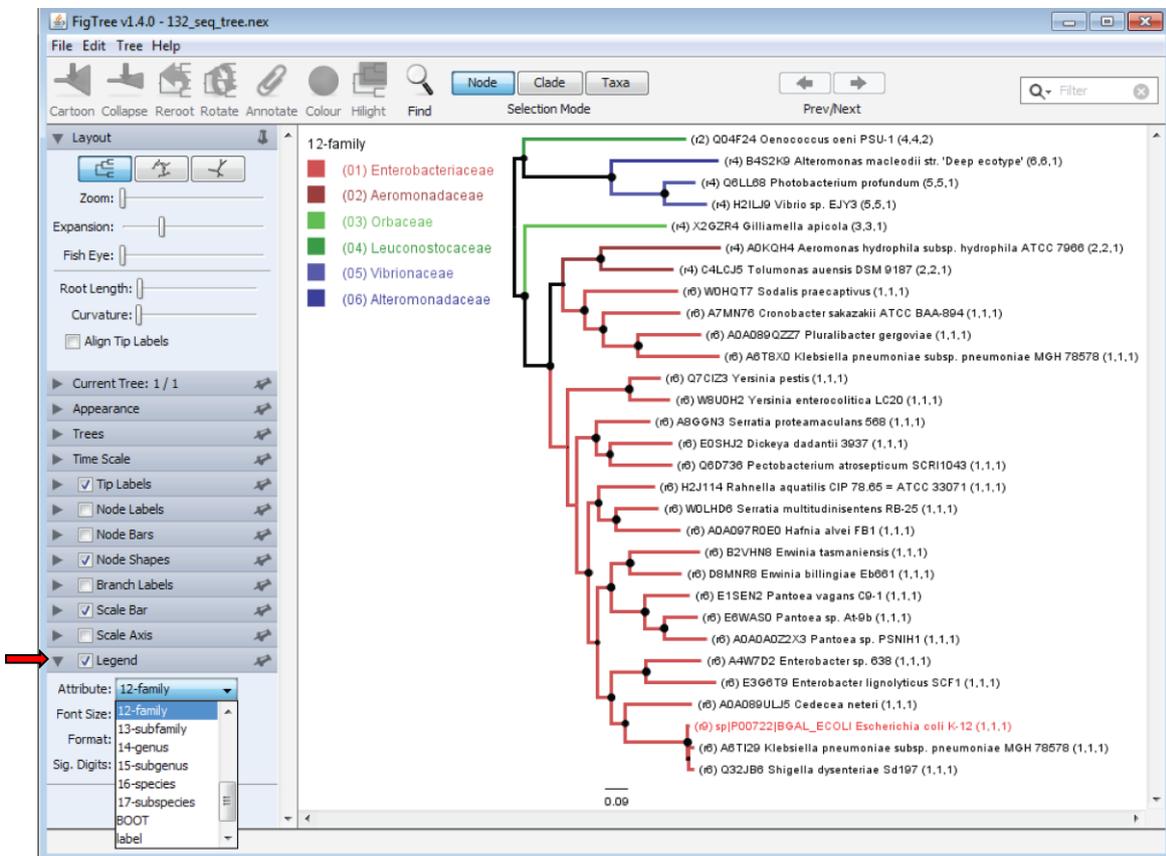


Figure 3: Changing the color legend according to the branch color.

## Contact

This is a provisional instruction to use TaxOnTree. If you are having some trouble or have suggestions to improve our work, please contact us by the following email address:

[tetsufmbio@gmail.com](mailto:tetsufmbio@gmail.com) (Tetsu Sakamoto)

[miguel@icb.ufmg.br](mailto:miguel@icb.ufmg.br) (J. Miguel Ortega)

Laboratório de Biodados

Instituto de Ciências Biológicas

Universidade Federal de Minas Gerais

Minas Gerais – BRAZIL

2015