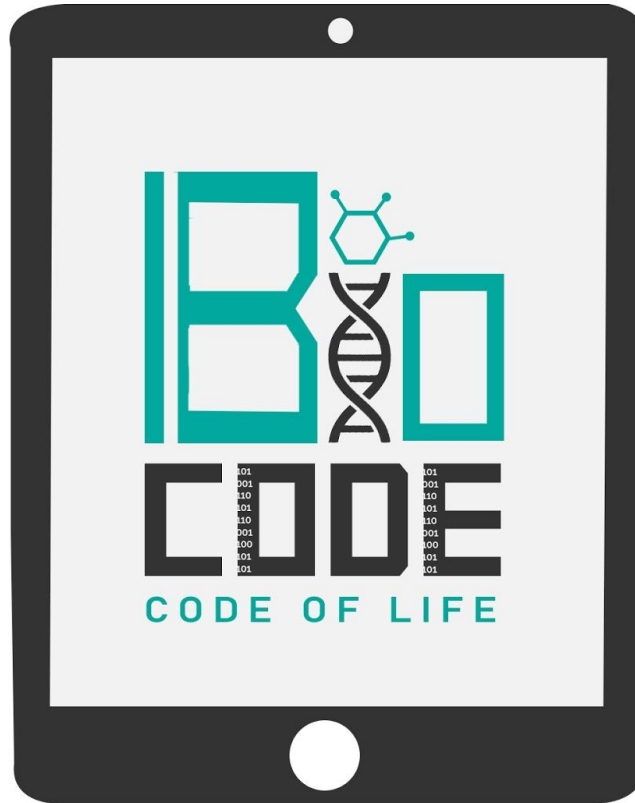


## Prerequ



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### isites:

1. Data from any phylogenetic tree building tool, e.g., MEGA, BEAST, etc.
2. Code Editor installed on your PC.
3. Java installed on your PC.

[Use the link <https://www.java.com/ES/download/> to download Java on your PC.]

## Prerequisite Terminologies:

In order to have a thorough understanding of our main topic, you should have the basic concept of the following terminologies:

1. **Multiple Sequence Alignment (MSA).**
2. **Phylogenetic terminologies.**
3. **Newick format.**

## Introduction:

FigTree is a stand-alone program, designed as a graphical viewer of phylogenetic trees. FigTree used as a program for producing publication-ready figures. Using FigTree, you can add various customizations to your phylogenetic tree to make it visually interactive.

### Purpose:

The main purpose of creating a phylogram/cladogram via the FigTree tool is to create a high-resolution picture of the phylogenetic tree that you can publish in your Research article or Blog. You can make several changes to your phylogenetic tree that you've created using any phylogenetic tree building tool (e.g., MEGA, BEAST, etc.), to make it visually interactive, because these phylogenetic tree building tools don't provide you much annotation and customization of the data.

### Steps:

- Install Java on your PC before moving on, because FigTree is built upon Java 9.

#### ★ Download FigTree on your PC:

- Click on the link below to download FigTree on your PC:  
<https://github.com/rambaut/figtree/releases>
- **For Mac OS-** click on the file with *.dmg* extension.
- **For Windows-** click on the file with *.zip* extension.
- **For Linux-** click on the file with *.tgz* extension.

[It also provides the link to download the *source code* file of FigTree, if you're a developer.]

- If you're a Windows user, download the file with *.zip* extension.

[It'll download your file in a *zip* folder. To extract that particular file you must have WinRAR or WinZip preinstalled on your PC].

- After extracting the files, open the FigTree file with *.exe* extension, which shows it's an executable file and hence, it doesn't require installation.

[It'll open up the whole window of the FigTree tool on your screen].

- Convert the phylogenetic tree you have created using any Phylogenetic tree building tool (e.g., MEGA or BEAST) into Newick format.

[You can input the whole phylogenetic tree into FigTree but we would recommend you use Newick format.]

**Note:** To have a better understanding of Newick format and how to convert a phylogenetic tree into Newick format using MEGA, watch our videos on MEGA and iTOL.

- Go to '**File**' and then click on '**Open**' and then select the file having your phylogenetic tree data in the Newick format, to input your data in the FigTree tool.

[It'll display you the phylogenetic tree generated out of the Newick format, to give you the graphical representation of your tree.]

- Take the cursor of your mouse on any node of the tree, it'll provide you the information about the node, i.e., the length of the entire node, and how far on the time scale that particular node came a far from the root node.
- By clicking on a particular node, you can make various types of customizations to that particular node, e.g., coloring, rotating, rerooting, etc.

[All these options are available on the Menu bar of the FigTree tool].

- Following are some parameters you should apply to your phylogenetic tree make it visually interactive:

<b>Layout:</b>
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To make a circular tree out of your data:	Click on the icon representing the circular tree.
To align all the nodes at the tip of each branch:	Click on <b>'Align tip labels'</b> .
To color the whole tree:	Click on <b>'Appearance'</b> then select <b>'Label'</b> and then color. [It'll color all the tree branches based on the color gradient you selected.] You can also change Line width, Line weight, and Color gradient by selecting the appropriate parameters.
Rooting the Tree:  To order the nodes:  To convert Phylogram and Cladogram:	Click on <b>'Trees'</b> Click on <b>'Root Tree'</b> and then select suitable rooting for your tree. Click on <b>'Order nodes'</b> and then select the suitable ordering method (ascending or descending). Click on <b>'Transform branches'</b> and then select the suitable parameter. [FigTree displays a Phylogram by default, so you can convert it into a cladogram.]
To edit tip labels:	Click on <b>'Tip Label'</b> and select suitable parameters for <b>'Display'</b> , <b>'Color by'</b> , <b>'Font Size'</b> , etc.
To display how many time a node has evolved: (An important factor that must be added in your tree to make it publication ready.)	Click on <b>'Node Labels'</b> and then <b>'Branch Times'</b> . [It'll add numbers to show how many times a node has been evolved.]
To add scaling to your tree:	Click on <b>'Scale Bar'</b> and then <b>'Automatic Scale'</b>
To show how many scaling is being displayed on your tree:	Click on <b>'Scale Axis'</b> .

To display with sort of editing you've done onto your tree:	Click on ' <b>Legends</b> ' and choose suitable parameters.
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**Note:** If you have quite large labels in your dataset, remove extra information from the labels using a code editor.

- To save your tree, go to '**File**' then click on '**Export SVG...**' or any other format.

[We would recommend saving your file in SVG or PDF format, it will not distort your picture of the tree when you zoom in or zoom out.]

### **Summary:**

In this tutorial video of the FigTree tool, we learned to create a publication quality figure out of our phylogenetic tree data. We came to know which parameters should be applied onto our dataset to make it visually interactive, more informative and annotated.