Option 1: Search for sequences and then build a phylogenetic tree

1. Identify nucleotide sequences to include in the phylogenetic tree analysis: mouse-over the “Search Data” tab and click “Nucleotide Sequences”. For flu, we recommend you use nucleotide sequences for phylogenetic analysis unless you are analyzing widely divergent sequences.

2. Choose search criteria on the Nucleotide Sequence Search page and click the “Search” button to run your search.

3. Select sequences from the search result page by clicking the checkboxes. Mouse-over the yellow “Run Analysis” button, and click “Generate Phylogenetic Tree”. If you want to include sequences that are not in this search result, select desired sequences and click “Add to Working Set”, then add additional sequences to the same working set. Click the “Workbench” tab, find the working set you saved and click next to it. On the working set details page, mouse-over “Run Analysis” and click “Generate Phylogenetic Tree”.

4. On the Generate Phylogenetic Tree page, choose parameters and click “Build Tree”.

Customize tree tip labels

Options to select and optimize evolutionary models
• Customize tree display, rooting, subtree arrangement, tree tip labels, tree leaf coloring, etc.
• Export a publication quality tree image

IRD is funded by the National Institute of Allergy and Infectious Diseases (NIAID) under Contract No. HHSN266200400041C and is a collaboration between Northrop Grumman Health IT, University of Texas Southwestern Medical Center, Veena Technologies, SAGE Analytica and Los Alamos National Laboratory. Comments, questions, suggestions? Contact us at feedback@virusbrc.org

http://www.fludb.org/
Option 2: Use a working set or upload your own sequences and then build a phylogenetic tree

1. Mouse-over the “Analyze & Visualize” tab and click “Generate Phylogenetic Tree”.
2. On the Generate Phylogenetic Tree page, choose “Quick Tree” to use default parameters or click “Custom Tree” to set your own parameters. For flu, we recommend you use nucleotide sequences for phylogenetic analysis unless you are analyzing widely divergent sequences.
3. You have three options to input your sequences:
   3.1 Upload a FASTA- or Phylip-formatted file.
   3.2 Paste sequences in FASTA or Phylip format.
   3.3 Use a working set from your Workbench. Choose the format of sequences you provided. Then click “Build Tree”.

Customize the look of the tree

1. After the tree analysis is finished, click “View Tree” to load the Tree Viewer window.
2. A tree viewer window will pop up - see screenshot to the left.
3. Many tree customization options exist:
   - Click the node of a reference point to reroot the tree
   - Collapse/expand/display subtree
   - Swap descendants
   - Choose tree decoration options to custom-color tree leaves
   - Resize the tree
   - Change tree type: rectangular, circular, unrooted, etc.
4. Download the tree image/legend from the “File” menu.