Tree Display Survey

Tree Display Survey, General

1. Which professional category best describes you? Please select only one.

◯ Life Science Researcher   ◯ Bioinformatics Professional

◯ Geneticist   ◯ Computer Scientist / Software Developer

◯ Genetic Counselor   ◯ Educator

◯ Clinical Testing Laboratory Staff   ◯ Student

◯ Physician   ◯ Librarian / Information Specialist

◯ Other Healthcare Professional   ◯ Patient / Family of Patient

◯ Other (please specify)

[   ]

2. Pick one category that best describes your organization

◯ College or University

◯ Commercial or Industry

◯ Hospital / Clinical / Medical Practice

◯ Non-Profit Organization

◯ Government

◯ Other (please specify)

[   ]

3. What is your primary reason for visiting the page today?

[   ]

4. Please outline the workflow that you use with the data you are seeking today at NCBI, including other NCBI and non-NCBI resources used.

[   ]

5. Did you plan to use the tree display in your visit to this page today?

○ Yes

○ No

Tree Display Survey, Current page

6. How easy was it to use the tree display to accomplish your planned task(s)?

○ Very easy

○ Easy

○ Somewhat easy

○ Neither easy nor difficult

○ Somewhat difficult

○ Difficult

○ Very difficult

7. Given the primary purpose of your visit to this page, what features of a tree display do you find most important, regardless of whether you used this feature today? Please check all that apply.

☐ node labels

☐ search tree

☐ filter tree (by various data attributes)

☐ sort tree (by various data attributes)

☐ highlight nodes/branches

☐ compress/expand nodes/branches

☐ tree navigation (e.g. pan, zoom)

☐ change tree layout (e.g. circular, rectangular)

☐ an overview of tree displayed at all zoom levels

☐ publication quality image generation

☐ download data in commonly used tree formats

☐ upload and display other trees for comparison to the one provided by NCBI

☐ upload and display approximate location of new (user-supplied) data in the tree

☐ get a list of terminal nodes for a selected internal node

☐ Other (please specify)

[   ]

8. Which of the following tree-related features that are under development would you find useful (check all that apply)?

- [ ] View kingdom-wide trees for GenBank bacterial, fungal and/or protist assemblies

- [ ] Download kingdom-wide trees for GenBank bacterial, fungal and/or protist assemblies

- [ ] View trees for prokaryotic 16S rRNA sequences, fungal ITS (Intergenic Transcribe Spacer) rRNA sequences, and/or fungal 28S rRNA sequences

- [ ] Download trees for prokaryotic 16S rRNA sequences, fungal ITS (Intergenic Transcribe Spacer) rRNA sequences, and/or fungal 28S rRNA sequences

- [ ] Other (please specify)

9. Would you like more information on the algorithm used to generate the tree on this page?

- ( ) Yes

- ( ) No

If yes, please tell us what information you would like.

Tree Display Survey, Databases (a)

10. Which of the following tree-related features that are under development would you find useful (check all that apply)?

☐ View kingdom-wide trees for GenBank bacterial, fungal and/or protist assemblies

☐ Download kingdom-wide trees for GenBank bacterial, fungal and/or protist assemblies

☐ View trees for prokaryotic 16S rRNA sequences, fungal ITS (Internal Transcribed Spacer) rRNA sequences, and/or fungal 28S rRNA sequences

☐ Download trees for prokaryotic 16S rRNA sequences, fungal ITS (Internal Transcribed Spacer) rRNA sequences, and/or fungal 28S rRNA sequences

☐ Other (please specify)

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[                                    ]
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11. Do you use tree displays offered in any of these other NCBI resources? (check all that apply)

☐ BLAST results

☐ COBALT results

☐ SmartBLAST

☐ NCBI Virus

☐ Pathogen Detection Isolates Browser

☐ Genome Workbench

☐ Entrez Genome

☐ None

☐ Other (please specify)

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[                                    ]
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12. Pick the scale of the dataset you typically visualize in your analyses

◯ 10

◯ 100

◯ 1000

◯ >1000

13. Please describe further how you use the tree display in the resource(s) you selected. Please select all that apply.

☐ to identify a dataset to build your own tree for the same data

☐ to identify a dataset for comparison to an unsubmitted sequence by BLAST

☐ to identify a dataset for comparison to an unsubmitted sequence through phylogenetic tree building

☐ to identify one or more genome assemblies or annotations for use in some other sequence analysis (not for tree building or comparison to an unsubmitted sequence)

☐ to examine relationships/identify patterns/exceptions within genome assemblies/sequences for an organism

☐ to download image of tree (e.g. PDF file)

☐ to download tree data (e.g. Newick file)

☐ Other (please specify)

[   ]

Tree Building Frequency

14. How often do you build trees?

◯ Never

◯ Sometimes

◯ Often

Tree Display Survey, tree building

15. When building a tree, what is more important to you?

◯ Speed of rendering is more important than accuracy

◯ Accuracy of the tree is more important than speed

◯ Speed and accuracy are equally important

16. What type of tree building algorithms are you interested in? (check all that apply)

☐ Distance matrix based (e.g. neighbor joining, least squares, minimum evolution)

☐ Maximum likelihood

☐ Parsimony

☐ Bayesian

☐ Other (please specify)

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17. What other tools do you use to build your phylogenetic trees and what do you like or not like about them?

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18. When visualizing a phylogenetic tree that you have built, what tool features are most important? Please check all that apply.

☐ Support for custom annotation of nodes and branches

☐ Download/export tree data in popular formats

☐ Navigation options

☐ Share tree online

☐ Create publication quality image

☐ Visualize supporting alignments in context of tree display

☐ Support for different tree layout options (e.g. unrooted trees, unscaled branch lengths)

☐ Other (please specify)

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Tree Display Survey, more feedback

19. How likely is it that you would recommend NCBI's Tree Displays to a friend or colleague?

Not at all likely   Extremely likely

0	1	2	3	4	5	6	7	8	9	10

20. Is there anything else you'd like to tell us?

Tree Display Survey, write to us

Please write to us at suggest@ncbi.nlm.nih.gov if you would like to provide additional feedback on NCBI's tree displays.