

Tree Display Survey

OMB Control Number: 0925-0648

Expiration Date: 05/31/2021

Public reporting burden for this collection of information is estimated to average 7 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a current valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden, to NIH, Project clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-0648). Do not return the completed form to this address.

Tree Display Survey, General

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

- Life Science Researcher
- Geneticist
- Genetic Counselor
- Clinical Testing Laboratory Staff
- Physician
- Other Healthcare Professional
- Other (please specify)
- Bioinformatics Professional
- Computer Scientist / Software Developer
- Educator
- Student
- Librarian / Information Specialist
- Patient / Family of Patient

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)

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)

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)

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

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)

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?

**Please write to us at [suggest@ncbi.nlm.nih.gov](mailto:suggest@ncbi.nlm.nih.gov) if you would like to provide additional feedback on NCBI's tree displays.**