Tree Display Survey

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Tree Display Survey, General

\bigcirc	Life Science Researcher		Bioinformatics Professional
	Geneticist		Computer Scientist / Software Developer
	Genetic Counselor		Educator
	Clinical Testing Laboratory Staff		Student
	Physician	\bigcirc	Librarian / Information Specialist
	Other Healthcare Professional		Patient / Family of Patient
	Other (please specify)		
	College or University Commercial or Industry		
2. P	ick one category that best describes your organi	ization	
	Commercial or Industry		
	Hospital / Clinical / Medical Practice		
	Non-Profit Organization		
	Government		
\bigcirc	Other (please specify)		
Mha	t is your primary reason for visiting the page tod	av2	
71110	to your primary reason for violating the page tour	шу. 	
Plea	se outline the workflow that you use with the dat	a you	are seeking today at NCBI, including other NCE
d noi	n-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

	How easy was it to use the tree display to accomplish your planned task(s)?
\bigcirc	Very easy
\bigcirc	Easy
\bigcirc	Somewhat easy
\bigcirc	Neither easy nor difficult
	Somewhat difficult
	Difficult
	Very difficult
mp	nortant, regardless of whether you used this feature today? Please check all that apply. node labels search tree
<u> </u>	filter tree (by various data attributes)
<u> </u>	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

rRNA sequences		hich of the following tree-related features that are under development would you find useful (check all t
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 28 rRNA sequences Download trees for prokaryotic 16S rRNA sequences, fungal ITS (Intergenic Transcribe Spacer) rRNA sequences, and/or fung 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	appl	y)?
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 fung 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		View kingdom-wide trees for GenBank bacterial, fungal and/or protist assemblies
pownload trees for prokaryotic 16S rRNA sequences, fungal ITS (Intergenic Transcribe Spacer) rRNA sequences, and/or fung 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		Download kingdom-wide trees for GenBank bacterial, fungal and/or protist assemblies
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		View trees for prokaryotic 16S rRNA sequences, fungal ITS (Intergenic Transcribe Spacer) rRNA sequences, and/or fungal 28S rRNA sequences
9. Would you like more information on the algorithm used to generate the tree on this page? Yes No		Download trees for prokaryotic 16S rRNA sequences, fungal ITS (Intergenic Transcribe Spacer) rRNA sequences, and/or funga 28S rRNA sequences
Yes No		Other (please specify)
Yes No		
Yes No		
Yes No	9. W	ould you like more information on the algorithm used to generate the tree on this page?
No No		
If yes, please tell us what information you would like.	\bigcirc	No .
	If yes	, please tell us what information you would like.

ree v	/iewer Survey MR-123
ee C	Display Survey, Databases (a)
	Which of the following tree-related features that are under development would you find useful (check all 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 2 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)

Tree Viewer Survey MR-123
12. Pick the scale of the dataset you typically visualize in your analyses
<u> </u>
<u> </u>
<u> </u>
>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 Viewer Survey MR-123
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)

	kely is it th	at you wo	uld recom	nmend NC	BI's Tree I	Displays t	o a friend o	or colleagi		
t at all lik	ely 1	2	3	4	5	6	7	8	Extr	emely lik
Is the	e anything	else you'd	d like to te	ell us?						

Tree Viewer Survey MR-123								
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.								