I will be implementing a phylogenetic tree viewing program. I have been trying to get input on what Biologists who use these programs look for in deciding what type of program to use. Are there certain features that you would like to see added, what features do you currently use, are there features that are there but seem pointless to have in the program? Are there any particular things that are causing you headaches? What is clear, straightforward, and seems useful to a computer scientist might not be for a biologist, but since it is you all who are using the program, it is important to me to get your input. I have attached a questionnaire to help you with your response, but please feel free to add to it as you like. Thank you for your help and please send any responses or questions to Katie Timmerman at **timmerman.16@wright.edu**

1. What programs do you currently use and why?

2. What do you use the tree viewing program for?

3. What features below would you use?
   1. Clicking a node and getting the subtree from there
   2. Choosing 2 plus taxa and computer locates the common anscester
   3. Click a node and path from root is highlighted\
   4. Search for a taxa
   5. Hide Branches
   6. Collapse branches into a family

4. What other features would you use?

5. What types of files would like to be able to import (Newick)?

6. What kinds of files would you like to export (PDF, jpg)?

7. What kinds of options would you like for printing?

8. What are your favorite features of current programs?

9. What are the most frustrating things with current programs?

10. Do you like the idea of 3D or would you rather use a 2D item?

11. Any additional Comments: