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| **Agenda**  Date: 04/8/22 | | |
|  | Item |  |
| 1. | What I’ve done since last meeting.   * Raxml finished the tree of 500 members, have named them and stuff. It looks like what we would expect but Rh proteins are really far away from the rest. * Used deep tmhmm to predict the topologies of 500 sequences, tried on all 60,000 in big file but running it took up all the storage on my computer so I had to abort **[1]** * Redid 7 member tree properly to include using model-ng to work out the evolutionary model for each helix. |  |
| 2. | Questions, issues.   * Realised my 500 member tree doesn’t have the most reproducible method for creating it so might have to do it again, probably with the deep tmhmm method. * Can’t seem to add anything to my github repository from the command line so would be good to chat about that. **[2]** * Can’t work out how to parse the file generated from running deep tmhmm, but haven’t looked into it much **[3]** * I need to work out how to use the remote server you set up for me last week **[4]** |  |
| 3. | Feedback.  [1] How far did it get? If it’s storage (as opposed to RAM) which is the problem then running it on a machine with sufficient storage would avoid the problem, and knowing how much it used per sequence would let us calculate the requirement.  [2] Are you getting an error message, unable to authenticate, or unfamiliar with the CLI syntax? How we approach this depends on which problem it is.  [3] The program gives you GFF3 output, which is a standard in bioinformatics, and there are options, including <https://biopython.org/wiki/GFF_Parsing> and <https://pypi.org/project/gff3/> - if you need something custom we can manage that.  [4] It works just like running your Mac at the command-line (it’s essentially the same operating system… not exactly the same, but the essentials are very similar) |  |
| 4. | What I plan to do before next meeting. |  |
| 5. | The Next Thing. |  |
| 6. | The next meeting. |  |