Comparison of Ataxia Telangiectasia Mutated's Nucleotide Sequence in Different Model Organisms

Reviewed by Mudith Ekanayake

You have given a nice and long introduction for the project which I found interesting. I have some comments for the materials and methods section. You have done a good job in this section. It is better if you can cite the appropriate papers for the tools you have used. For example, paper for MAFFT is Katoh *et al*., 2002 (Katoh, et al. "MAFFT: a Novel Method for Rapid Multiple Sequence Alignment Based on Fast Fourier Transform." *OUP Academic*, Oxford University Press, 15 July 2002, academic.oup.com/nar/article/30/14/3059/2904316). You can find these from the tutorials or by just searching in the web.

In addition to the steps you have carried out in the project, you can perform model selection using tools such as ProtTest, JmodelTest or SMS. Furthermore if you want to improve your alignments by removing poorly aligned regions you can trim your alignments by carrying out GBlocks or TrimAl. These are just additional steps for generating better output results.

In the results section I think you have showed the same tree twice with and without bootstrap support. The tree with bootstrap support will be enough for this section and you can include all the other trees as supplementary materials. When visualizing it is better to use visualizations from the visualization tool you use. In this section you can include the AIC/BIC scores as well. You can find them in the bottom of the RAxML-NG log file. You have nicely concluded it by addressing your question of interest. In conclusion, I found this paper well formatted and well explained. Good luck with the project and the final presentations.