Tutorial 9, Step by Step

1. Create Cipres user account. (http://www.phylo.org/sub_sections/portal/)
2. Create a folder for the project - provide a descriptive name.
3. In the folder your just created open the data subfolder and upload the file (Haemophilus_influenzae_16S.fasta)
4. Go to the tasks subfolder and create a new task. (We need to align our sequences before we construct our tree)
5. Choose the 'MAFFT' alignment tool. Click on the task subfolder and run the task we just created. Click the view status button. You can then click the refresh button to see when the task is complete. The task should take a few minutes to run.
6. Once the task is complete, click on the View link. Inspect the output.MAFFT file by View, then click 'Save to current folder'.
7. We will be using the RAxML maximum likelihood method. This algorithm requires the input to be in Phylip format. We can convert the fasta alignment to the Phylip format using the Readseq tool. Create a new task using the Readseq tool. Be sure to select your parameters so that the input format is fasta and the output is Phylip. Save the outfile.phy file to your data folder.
8. Create a new task using the RAxML-HPC Blackbox maximum likelihood algorithm. Change the sequence parameter from nucleotide to protein. Use the Phylip file as your input file. When the task is complete download the output file marked RAxML_bestTree.result to your desktop.
9. Use the iTOL web interface. Open your web browser and go to the iTOL website http://itol.embl.de/. Go to the Data Upload tab and then upload your tree. Give the tree a name.Then you will have your tree displayed. Change the display from circular mode to normal mode. Export the tree and show your work to TA. Also, answer this question: From your analysis which coronavirus is most closely related to human SARS?