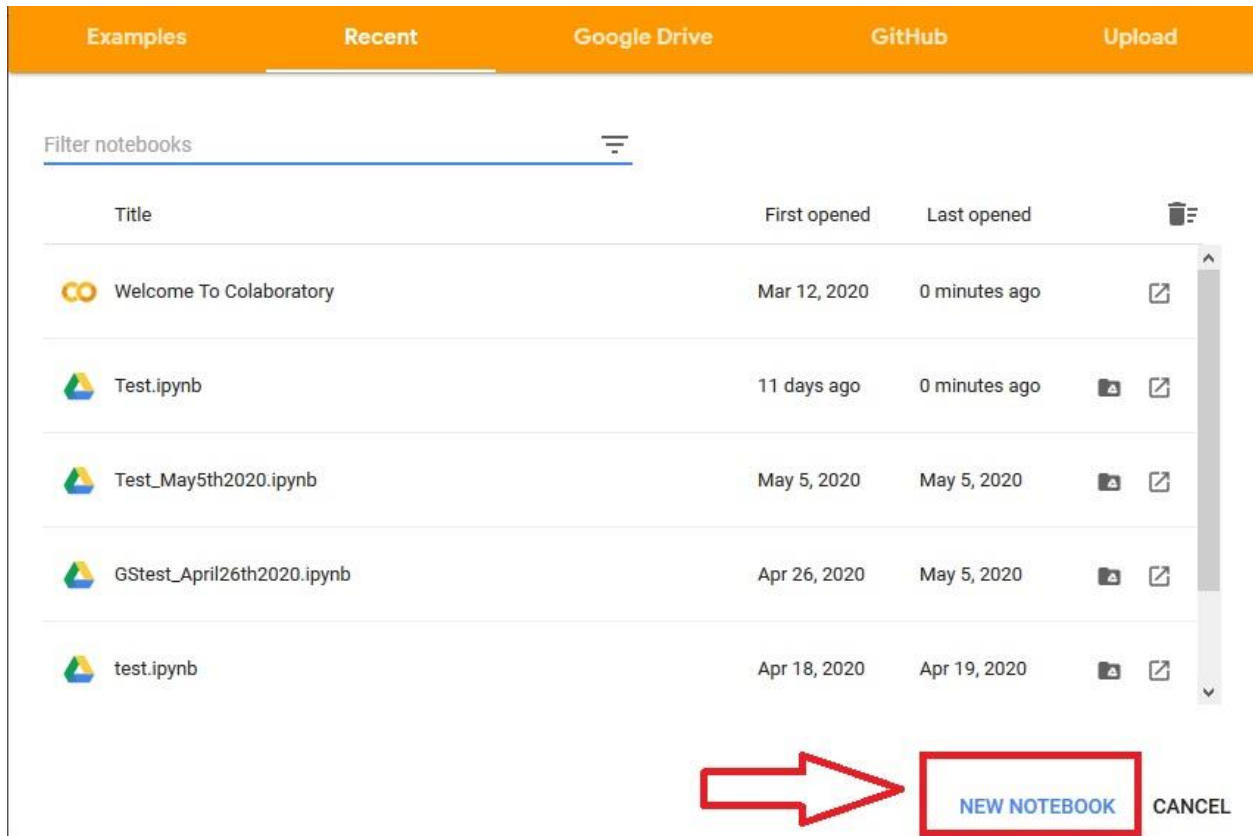
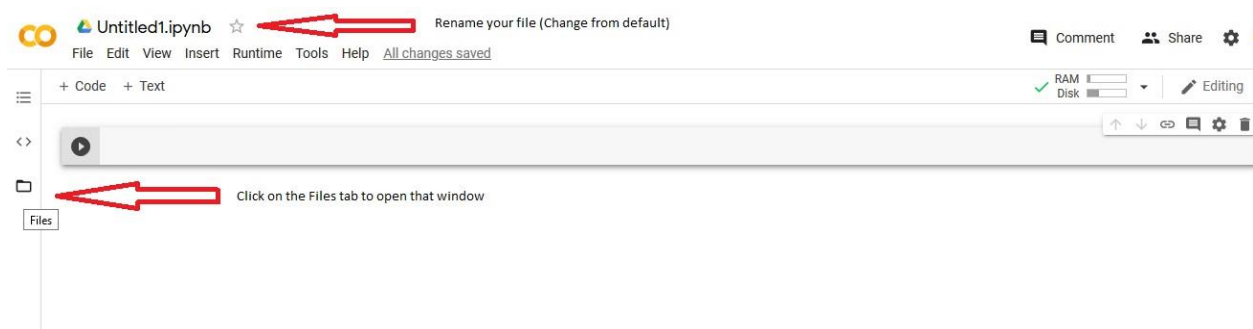


Instructions to run the Pipeline:

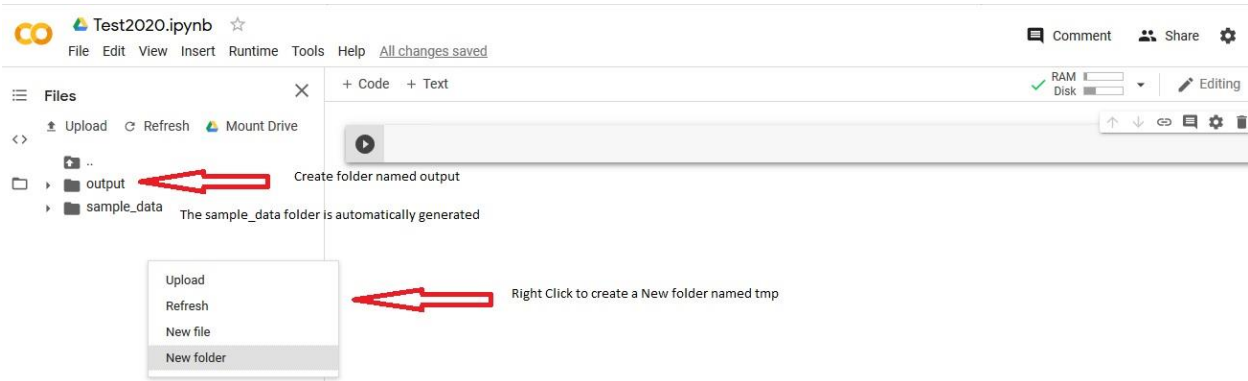
1. Open Google Collab: <https://colab.research.google.com/notebooks/welcome.ipynb> and Click on New Notebook. Sign into your google account. The output from the python script will be stored in your google drive.



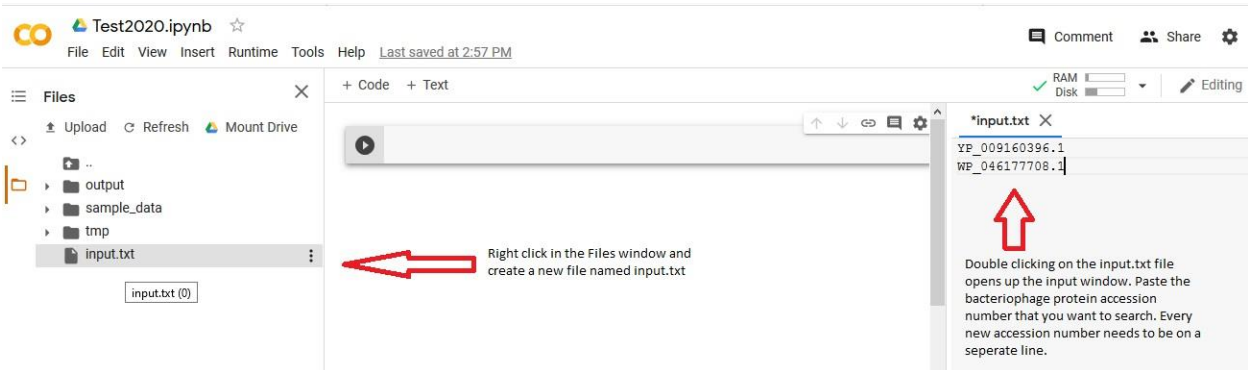
2. Rename your notebook. Then click on the File tab to open it.



3. In the File window that opens up – Right click (PC users) or CTRL + Click (Mac users) to create two new folders names – “output” and “tmp”

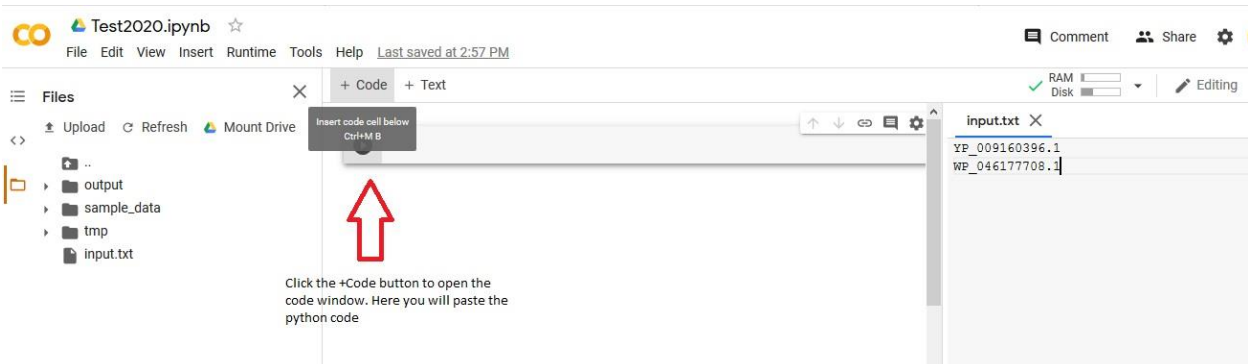


4. Right click and create a file named “input.txt”. Clicking on the file will open it up in the main window – Paste your phage protein accession numbers in the file on separate lines. Sample accession numbers can be found here: <https://github.com/genomesolver/CSPpipeline/blob/master/input.txt>

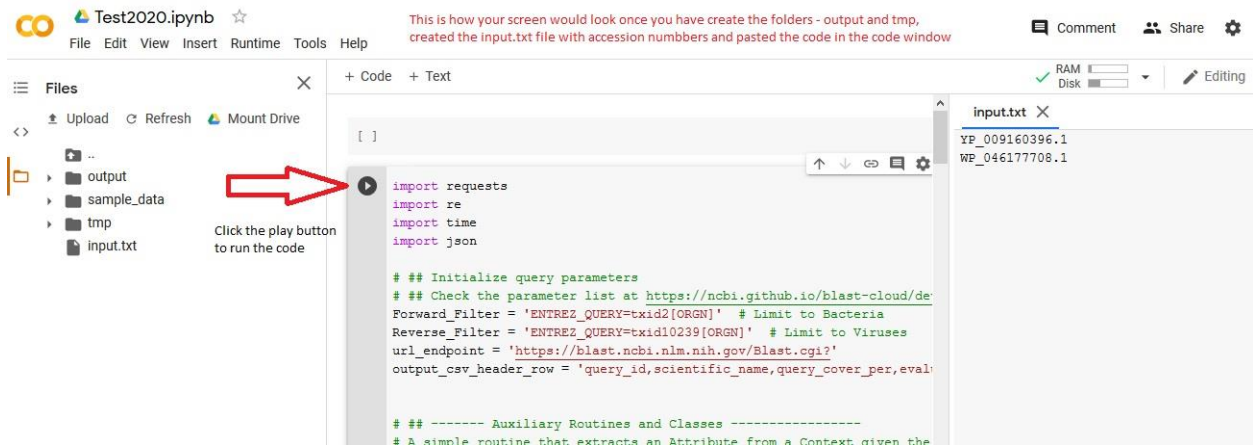


5. Click the +Code button in the central panel to open the code window. Here you will paste the python code. Code can be copied from here:

<https://raw.githubusercontent.com/genomesolver/CSPpipeline/master/blast.py>



6. Based on the instructions above, your collaborate window will look like the screenshot below. The final step is click on the play button to run the code



7. The output folder will contain the results of the “Forward” and “Reverse” Blast. You can download the output data in the .csv format and upload your results to the Community Science Pipeline database:

https://docs.google.com/forms/d/e/1FAIpQLSe8SmjjAdZrAKWBWlxcpmICIQTV_FC1cgKWgUL_OqWdyRkCgg/viewform

