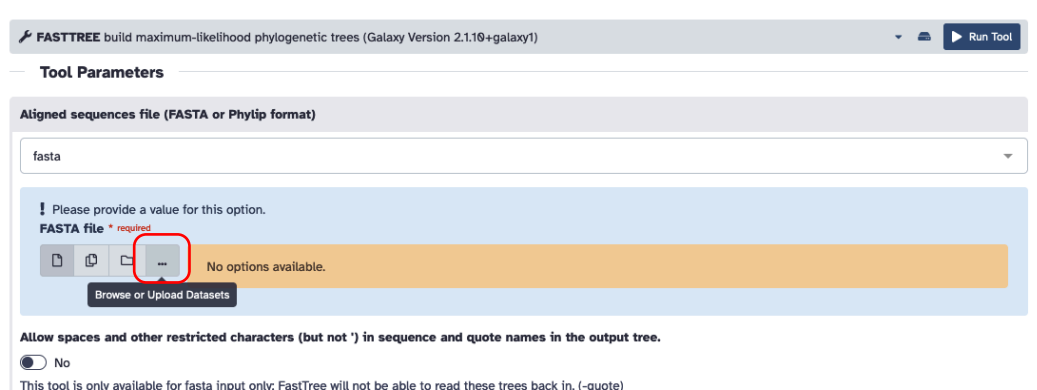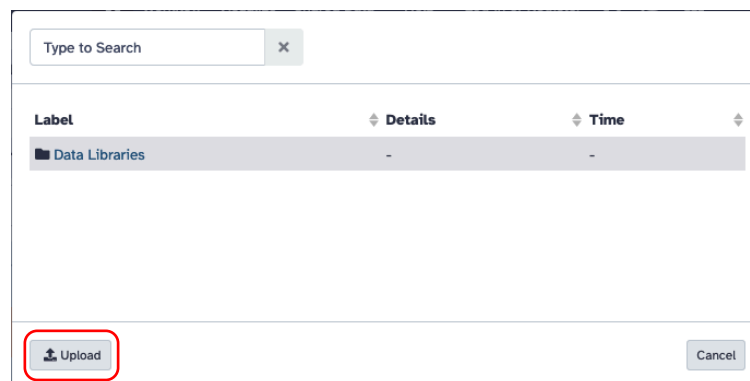**G**lobal
Pneumococcal
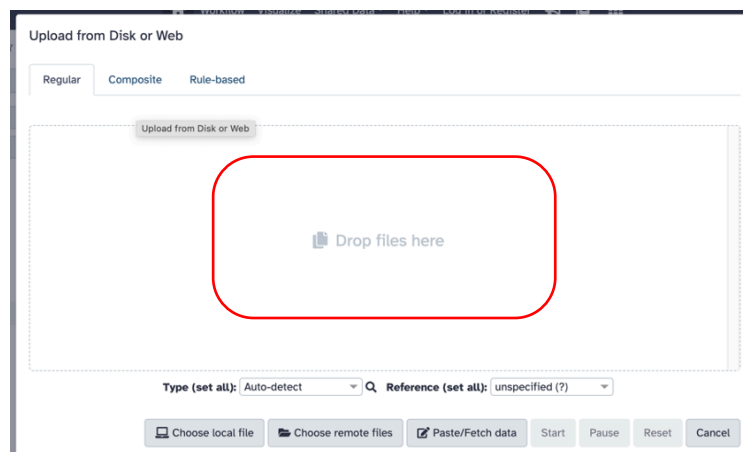**S**equencing
Project

Build a Phylogeny with FastTree @ Galaxy

1. Go to FastTree page on Galaxy: https://usegalaxy.org/root?tool_id=fasttree

2. Upload the alignment file (.aln)

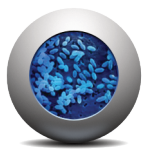   i. Click on "**…**" under **FASTA file** in the **Aligned sequences file** section

    ii. Click on "**Upload**" in the pop-up window

    iii. Drag and drop the alignment file into the "**Drop files here**"

iv. Click "**Start**" to start the upload process

iv. Wait for the upload process to finish

iv. Once the upload process is finished, you can close the pop-up window. The uploaded alignment should be ready to use once it is highlighted in green in the **History** sidebar. The alignment file will also be automatically selected if it is the only file uploaded.

3. Select "**Nucleotide**" in the **Protein or nucleotide alignment** section. "**GTR+CAT**" will be automatically selected as the **Nucleotide evolution model**
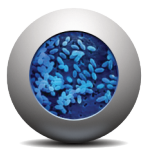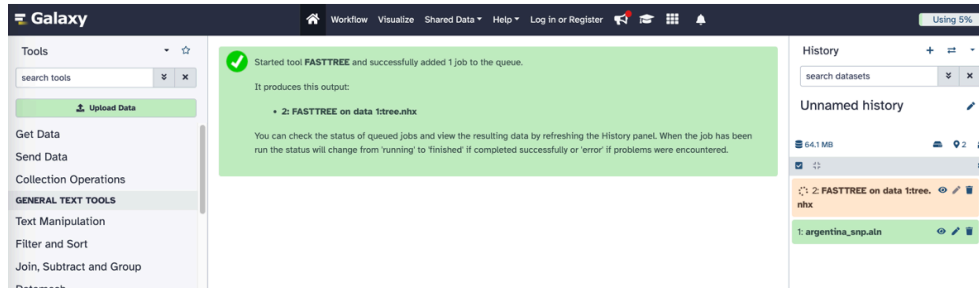
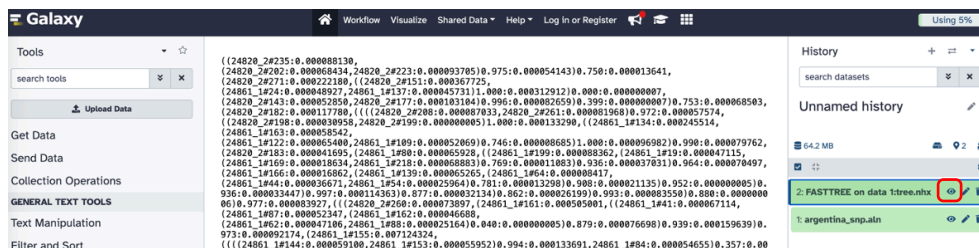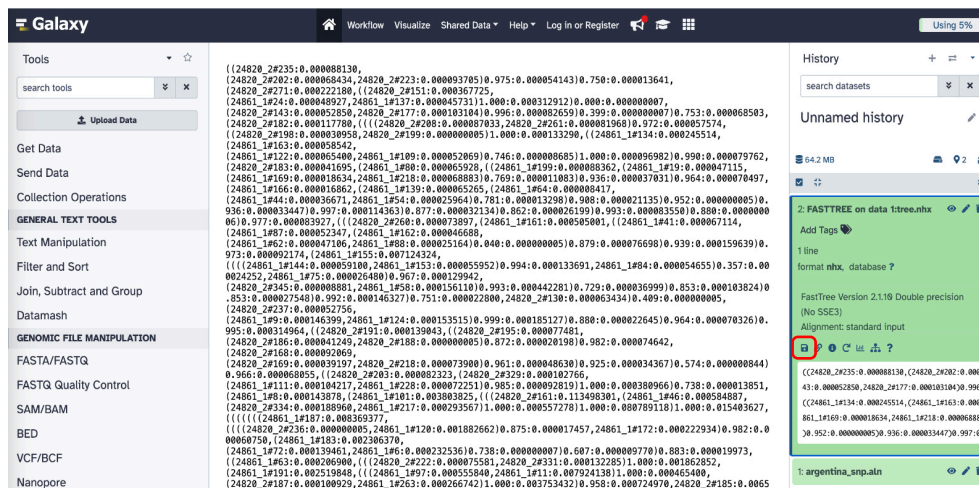4. Click on **▶ Run Tool** to start running FastTree

5. Wait for all items in the **History** sidebar turn green. (grey means the job is pending; orange means the job is running, green means the job is completed.)

6. Once the FastTree job is completed, you can view the output by clicking on 👁 of the job

7. Download the tree file (.nhx) by clicking on the job and then clicking on 💾

8. The downloaded tree file (.nhx) can be used to generate a [Microreact](#) visualisation