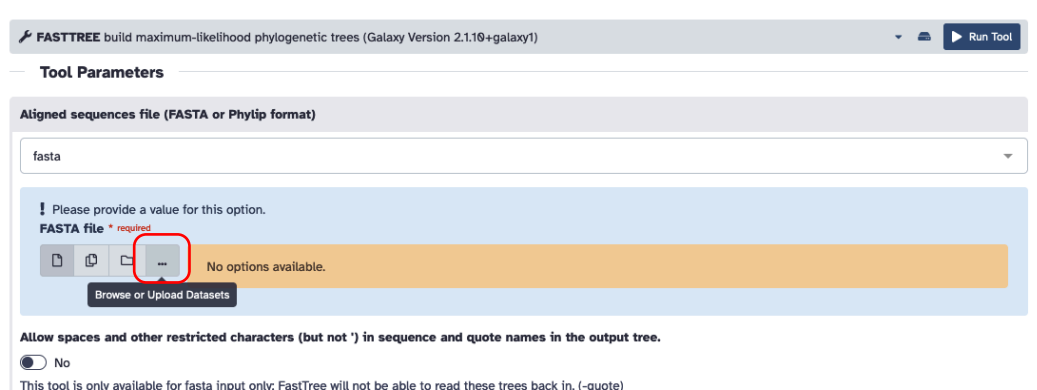
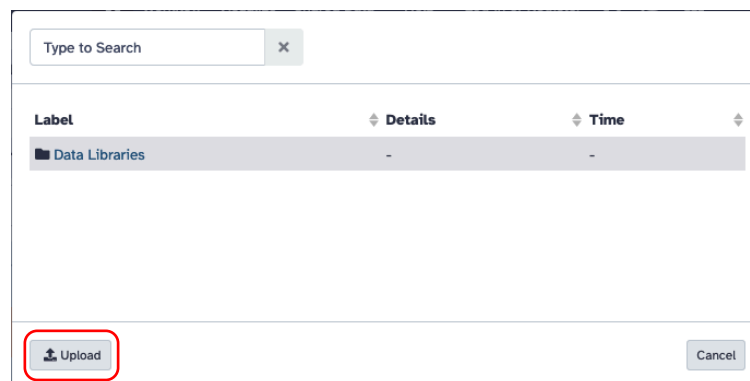


Build a Phylogeny with FastTree @

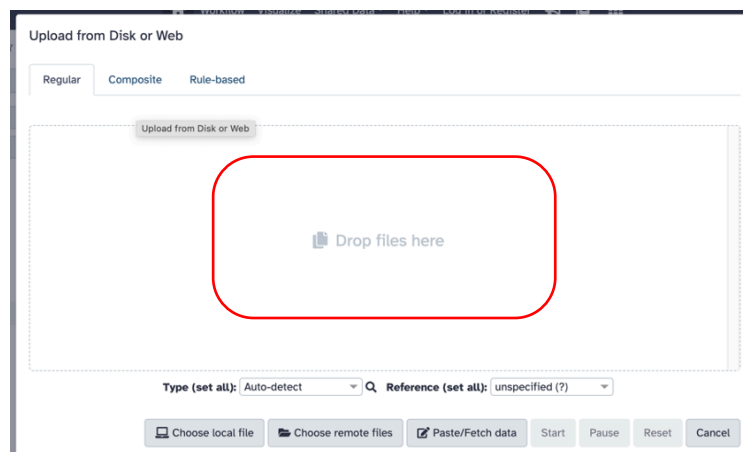
1. Go to FastTree page on Galaxy: https://usegalaxy.org/root?tool_id=fasttree
2. Upload the alignment file (.aln)
 - i. Click on “...” under **FASTA file** in the **Aligned sequences file** section

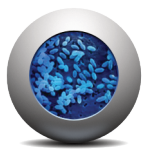


- ii. Click on “**Upload**” in the pop-up window



- iii. Drag and drop the alignment file into the “**Drop files here**”





- iv. Click “**Start**” to start the upload process

Upload from Disk or Web

Regular Composite Rule-based

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.

	argentina_snp.aln	61.2 MB	Auto-detect		unspecified (?)		0%	
--	-------------------	---------	-------------	--	-----------------	--	----	--

Type (set all): Auto-detect Reference (set all): unspecified (?)

Start

- iv. Wait for the upload process to finish

Regular Composite Rule-based

	argentina_snp.aln	61.2 MB	Auto-detect		unspecified (?)		100%	
--	-------------------	---------	-------------	--	-----------------	--	------	--

- 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.

FASTREE build maximum-likelihood phylogenetic trees (Galaxy Version 2.1.10+galaxy1) Run Tool

Tool Parameters

Aligned sequences file (FASTA or Phylip format)

fasta

FASTA file *

... t: argentina_snp.aln

History

search datasets

Unnamed history

64.1 MB

t: argentina_snp.aln

3. Select “**Nucleotide**” in the **Protein or nucleotide alignment** section. “**GTR+CAT**” will be automatically selected as the **Nucleotide evolution model**

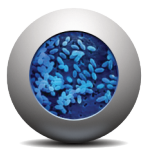
Protein or nucleotide alignment


Select Value

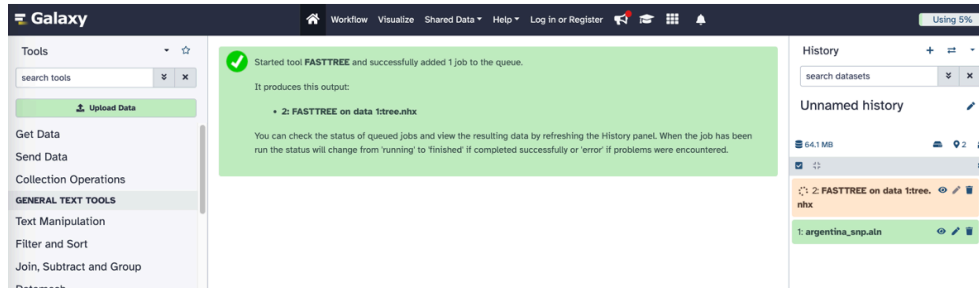
Nucleotide

Protein

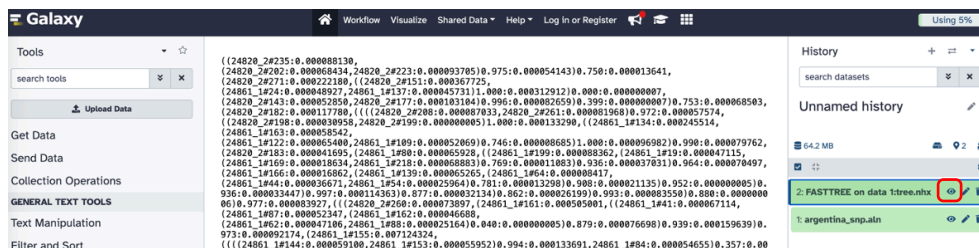
GTR+CAT



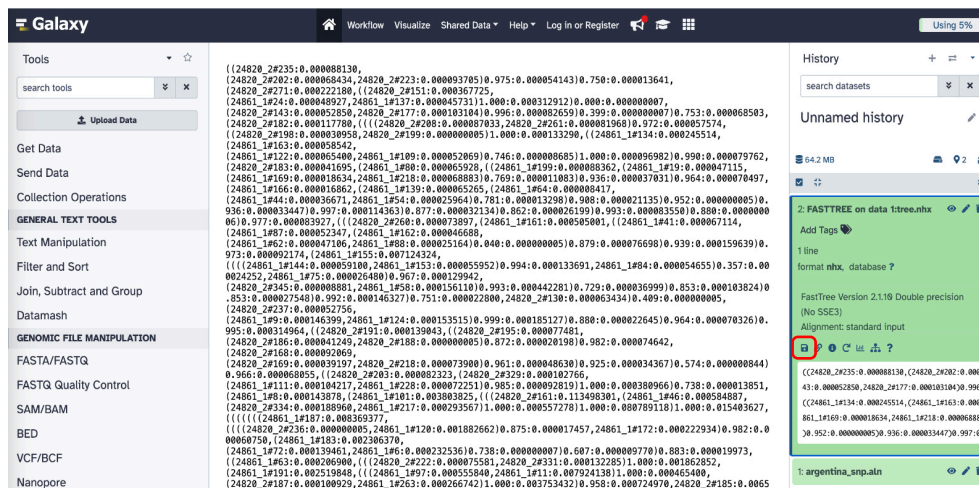
- Click on  to start running FastTree
- Wait for all items in the **History** sidebar turn green. (grey means the job is pending; orange means the job is running, green means the job is completed.)



- Once the FastTree job is completed, you can view the output by clicking on  of the job



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



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

