

Objectives

- Demonstrate how to construct and visualise a phylogenetic tree
- Steps:
 - 1. Align sequences using MAFFT Server
 - 2. Create an ML phylogeny using IQTREE Server
 - 3. Visualise using Nextstrain

MAFFT Server:

https://mafft.cbrc.jp/alignment/server/index.html IQTREE Server: http://iqtree.cibiv.univie.ac.at

Warning – Web servers

Data is sent to the Osaka University (Japan) who operate the MAFFT server.

Data is sent to the Wien University (Germany) who operate the IQTREE server.

Alternatives if working with sensitive data:

- Use a local program like UGENE/MEGA, tutorial linked on course website.
- Install and run through command line (not covered).

Step 1: Align you sequences using MAFFT

Open the MAFFT server in your browser: https://mafft.cbrc.jp/alignment/server/index.html

Demonstration on using MAFFT Server

Input:					
Paste protein or DNA sequences in fasta format. Example					
or upload a plain text file: Choose file No file chosen					
Use <u>DASH</u> to add homologous structures (protein only)					
Ouput original plus DASH sequences Output original sequences only					
Give structural alignment(s) externally prepared					
Allow unusual symbols (Selenocysteine "U", Inosine "i", non-alphabetical characters, etc.) Help					

Step2: Align you sequences using IQTREE

Open the server in your browser:

https://www.hiv.lanl.gov/content/sequence/IQTREE/iqt ree.html

Demonstration on using IQTREE Server

Paste your alignment here [Sample Input] or upload your alignment file Include HIV-1/SIVcpz subtype reference sequences

Step3: Visualise Tree in Auspice

Open the webapp in your browser: https://auspice.us/

Demonstration on using Auspice

Note: Auspice does NOT transmit data to any server. All computation after the website loads happens in your browser!

Questions? + Resources

- IQTree webserver tutorial:
 - 1. https://www.iqtree.org/doc/Web-Server-Tutorial
 - 2.http://www.iqtree.org/doc/Web-Server-Tutorial
- IQTree webserver paper:
 - 1. https://academic.oup.com/bib/article/20/4/1160/4 106928
- Advanced in depth CLI Tutorial:
 - 1. https://github.com/mmatschiner/tutorials/blob/ma ster/multiple_sequence_alignment/README.md
 - 2.https://github.com/mmatschiner/tutorials/tree/master/ml_phylogeny_inference