

Building Phylogenetic Trees

What is a phylogenetic Tree?

- How the observed differences between sequences are developed through evolution.
- The distance between sequences.

Steps of Building Phylogenetic Trees

1. Collect sequences in one FASTA format file.
2. Perform multiple sequence alignment (global).
3. Draw phylogenetic trees (different approaches).
4. Bootstrapping the phylogenetic tree
5. View and edit the tree for presentation.

Building Phylogenetic Trees

Observe:

Extracting sequence, alignment, and tree building with Jalview.

<https://www.jalview.org/>

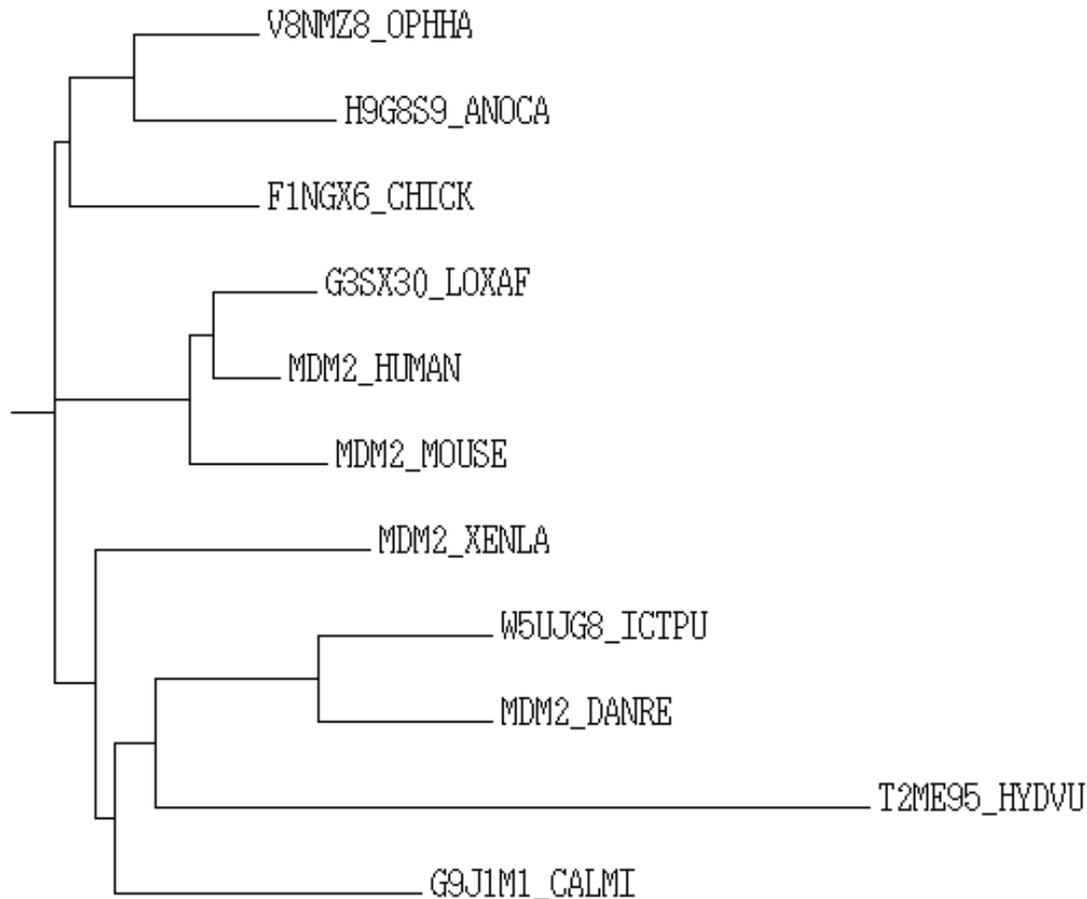
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Practice:

1. Load sequence in FASTA format to Clustal Omega to perform alignment.
2. Download the tree file save in your GMS6014/XXX folder.
3. View the tree with the Phylodendron tree printer.

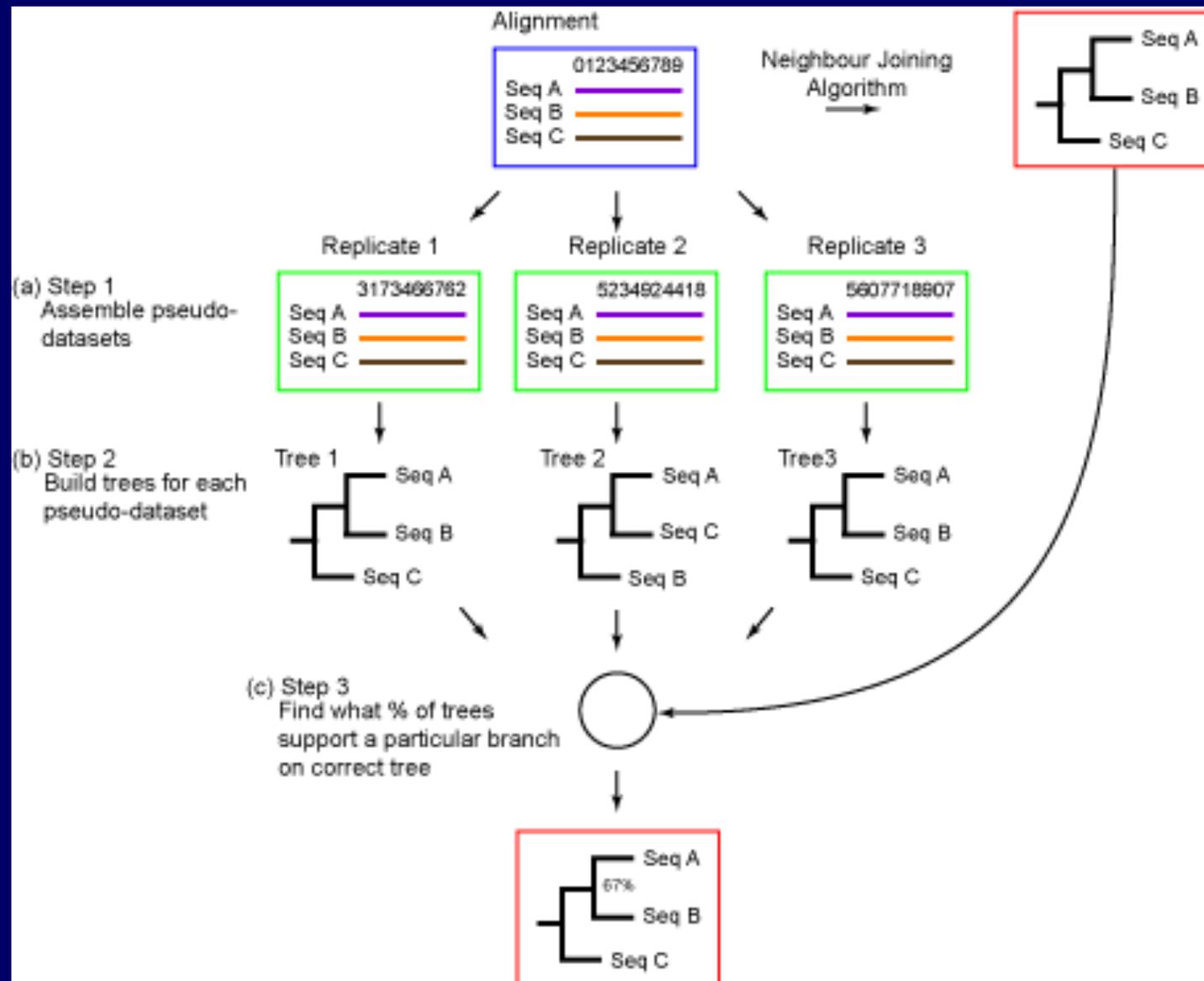
Phylogenetic Trees

Phylogenetic tree



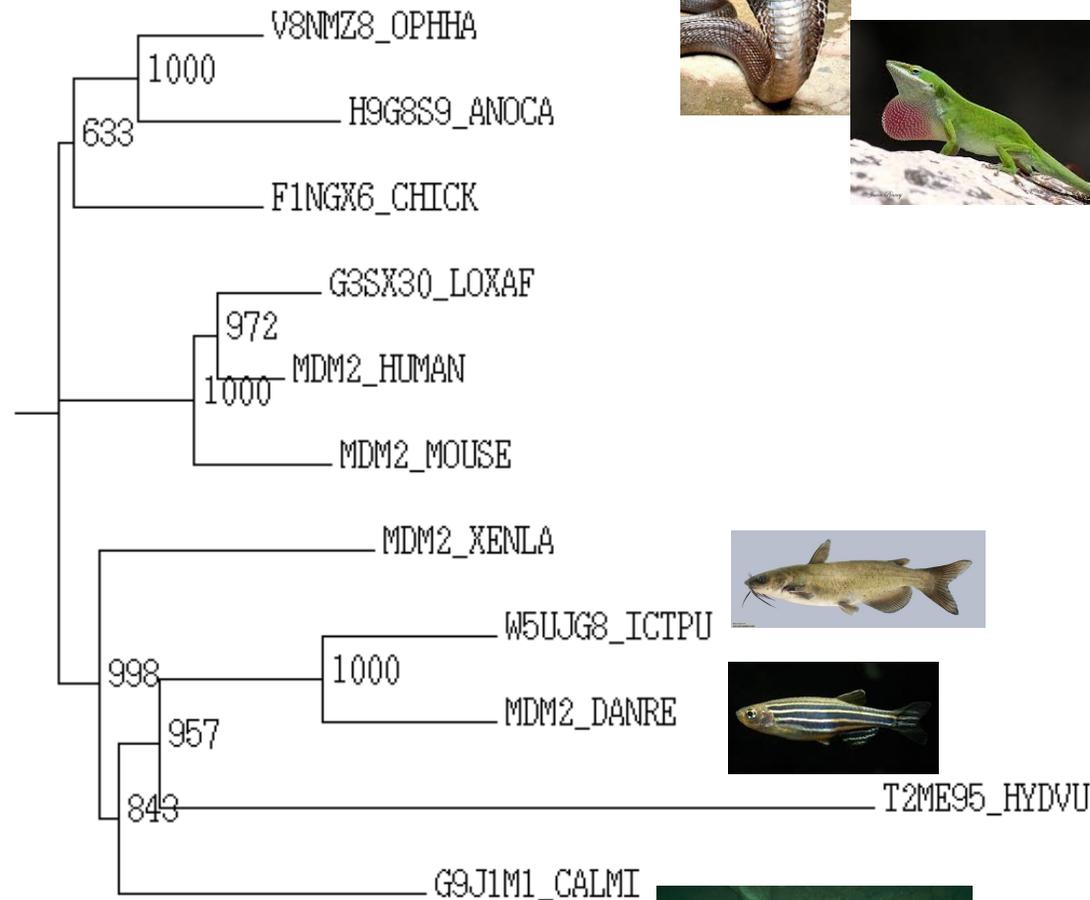
LOXAF: African Elephant

Bootstrapping

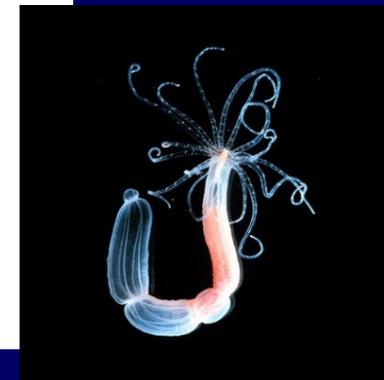


Phylogenetic Trees – boot strap

Phylogenetic tree



LOXAF: African Elephant



Practice –Download GEO dataset with job file

Retrieval of information.

- Using web interface.
- Using FTP client

- Using command line tools.
 - Generic Linux file transfer tools - always available in Linux/MacOs.
 - Specialized tool – fastq-dump
 - Let the script do the job – when you need large amount of files or large file that will take hours to download.

RNA-Seq – Download dataset

- Command line (with a few samples):
 - `$ module load sra`
 - `$ fastq-dump --gzip SRRxxxx SRRyyyy`
- With the .sbatch job file (for large data set)
 - `$sbatch myjob.sbatch`
 - Use “`$ squeue -u <yourUserName>`” to monitor progress.
 - Use “`$ls -l`” to make sure files size are correct.

RNA-Seq – Download dataset

```
#!/bin/sh
#SBATCH --job-name=GetSRA
#SBATCH --mail-type=ALL
#SBATCH --mail-user=xxxxx@ufl.edu
#SBATCH --output=GetSRA_%j.log
#SBATCH -t 12:00:00
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=3gb

pwd; date

module load sra/2.10.3

fastq-dump --gzip SRR1618640 SRR1618641 SRR1618642 SRR1618643
```

Transfer the file to your folder in HiPerGator and submit the job (\$sbatch *filename*)