

## Phyloinformatics

### Assignment-7

Q1- Perform a demonstration on T-REX software (**a web server for inferring, validating and visualizing phylogenetic trees and networks**).

<http://www.trex.uqam.ca/index.php?action=inference&project=trex>

Select Tree Inference session and perform a demonstration using a sample data set (Distance, Parsimony and Max. Likelihood). Use **any one method** from these category.

-Take snapshots of the relevant results and observation

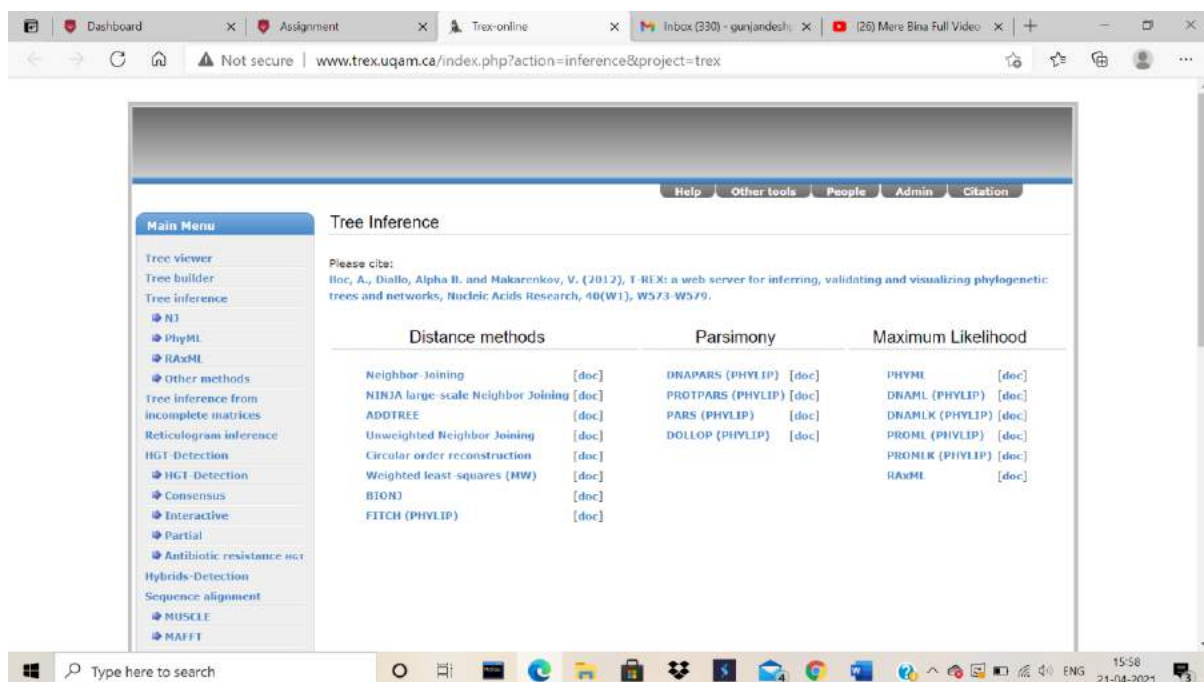
-Write interpretation of your results.

Answer:

Step 1: Open/Search the link provided in the question:

<http://www.trex.uqam.ca/index.php?action=inference&project=trex>

Step 2: Select Tree Inference session from Distance, Parsimony and Max. Likelihood category given.



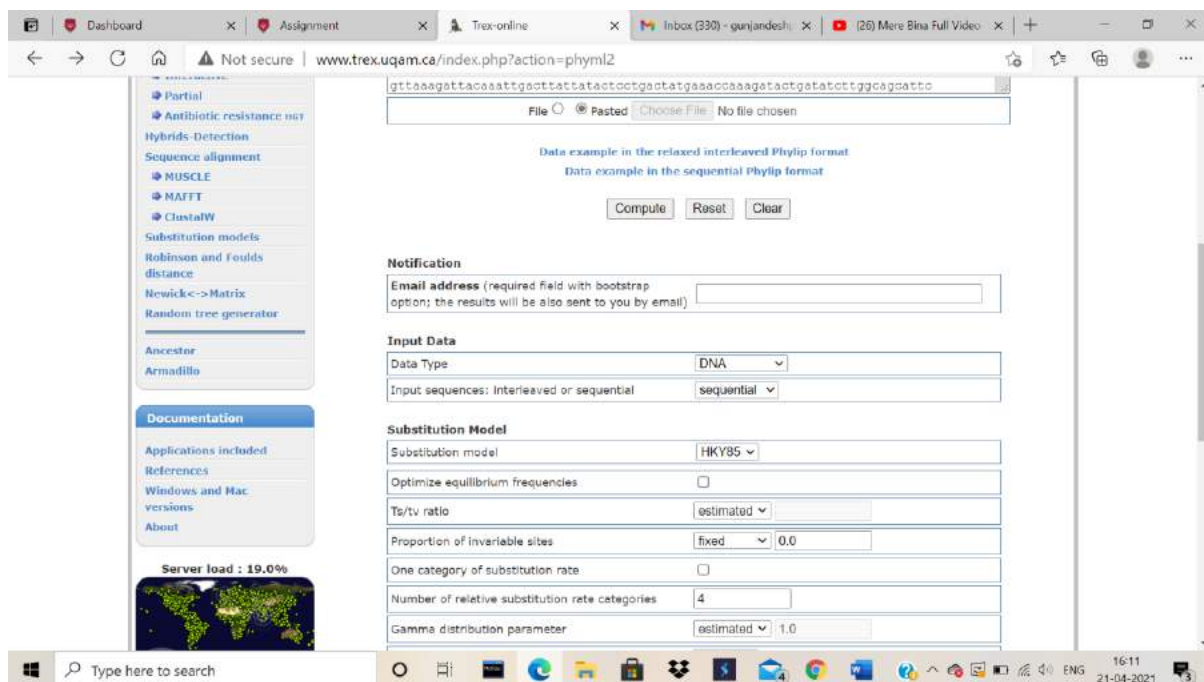
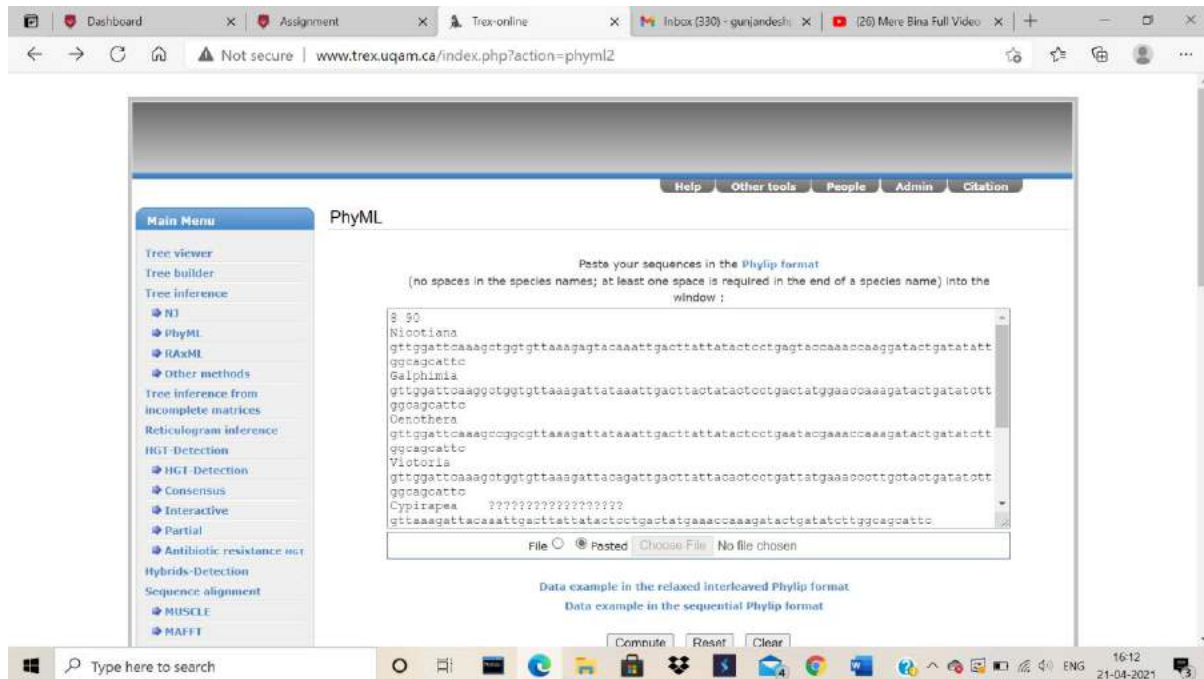
Step 3: Selected category: Maximum Likelihood

Step 4: Click on the first hit of Maximum Likelihood .i.e. PHYML.

Step 5: Select any of the two formats provided:

- Data example in the sequential Phylip format
- Data example in the relaxed interleaved Phylip format

Step 6: Selected format: Data example in the **sequential Phylip format**, paste the format in the blank box and click on compute.



Dashboard | Assignment | T-Rex-online | Inbox (330) - gunjandeshi | (26) Mere Bina Full Video

Not secure | www.trex.uqam.ca/index.php?action=phym12

'Middle' of each rate class:

**Tree Searching**

Optimize tree topology with branch lengths: ☒

Starting tree:

Starting tree file:  No file chosen

Tree topology search operations:

**Branch Support**

Non parametric bootstrap analysis: ☐ 100 replicates

Approximate likelihood ratio test:

**Citation**

"A simple, fast and accurate algorithm to estimate large phylogenies by maximum likelihood" Guindon S., Gascuel O. Systematic Biology 52(5):696-704

This site has been visited 8234 times since Friday, November 25, 2005.

Bot., A., Diallo, Alpha B. and Makarenkov, V. (2012), T-REX: a web server for inferring, validating and visualizing phylogenetic trees and networks, *Nucleic Acids Research*, 40(W1), W573-W579.

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Webmasters : Alix Boc and Alpha Bouacar Diallo

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Step 7: After computing you will find the result for PHYL:

1)Result for PHYL:

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Not secure | www.trex.uqam.ca/loadData.php?actionTrex=phymresult&id=n71t2mld8ul1ki8br1c28mio4\_21\_06\_...

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**Results for PHYL**

**Input file(s)**

[Input data](#)

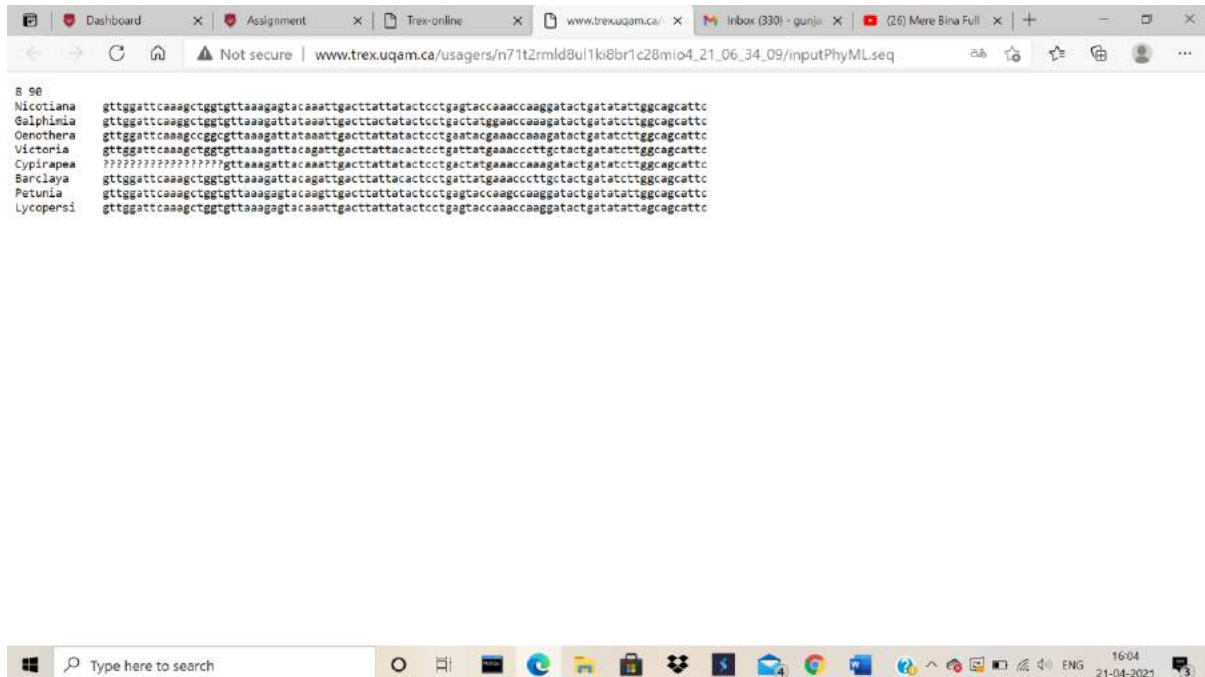
**Output files**

[Inferred tree](#)  
[View tree](#)  
[Statistics](#)

[View log file for more details](#)

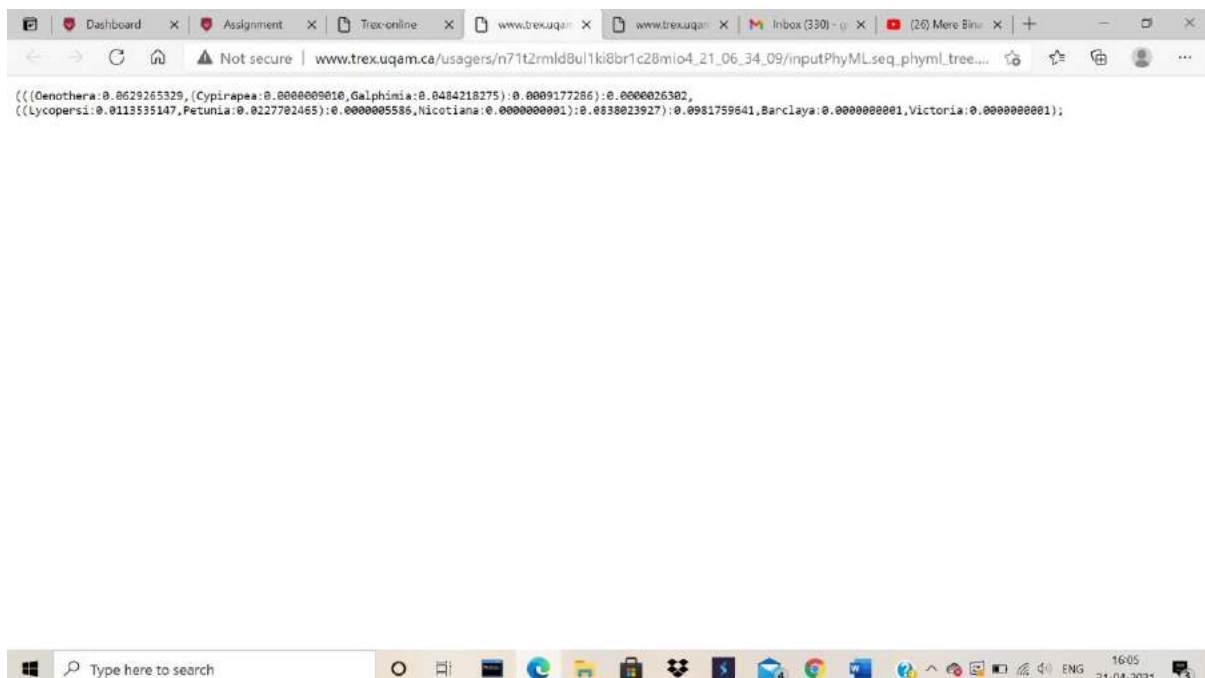
[Report bugs](#)

## Step 8: Open the input file:

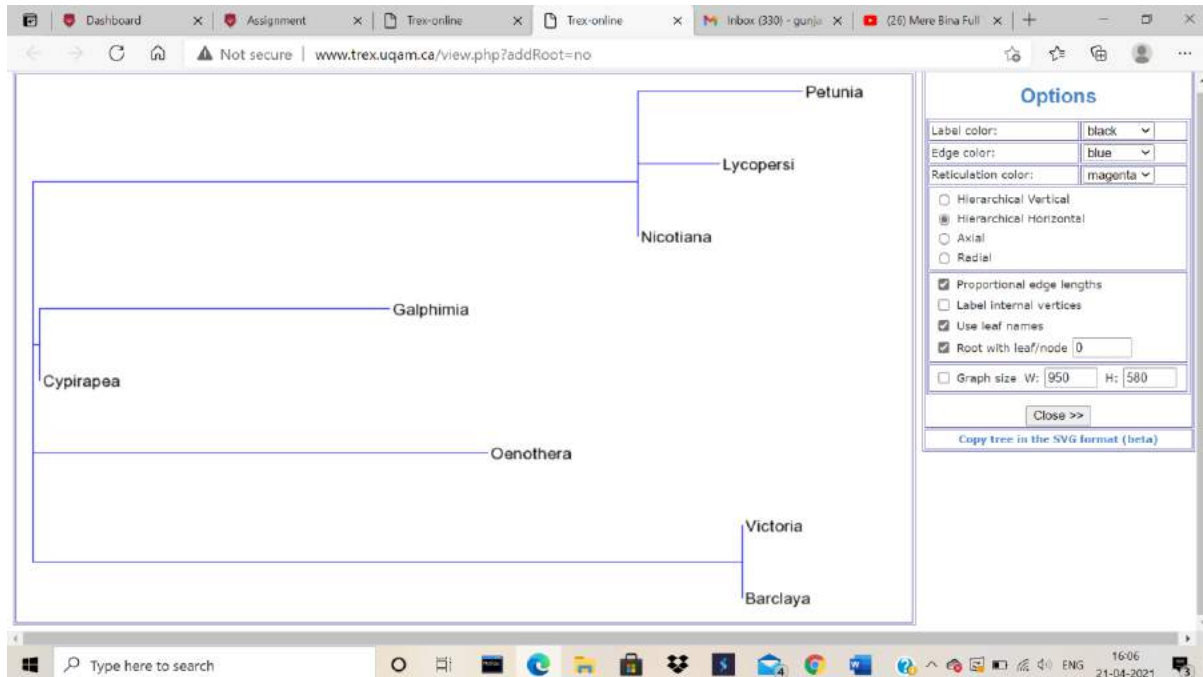


## Step 9: Open the Output file:

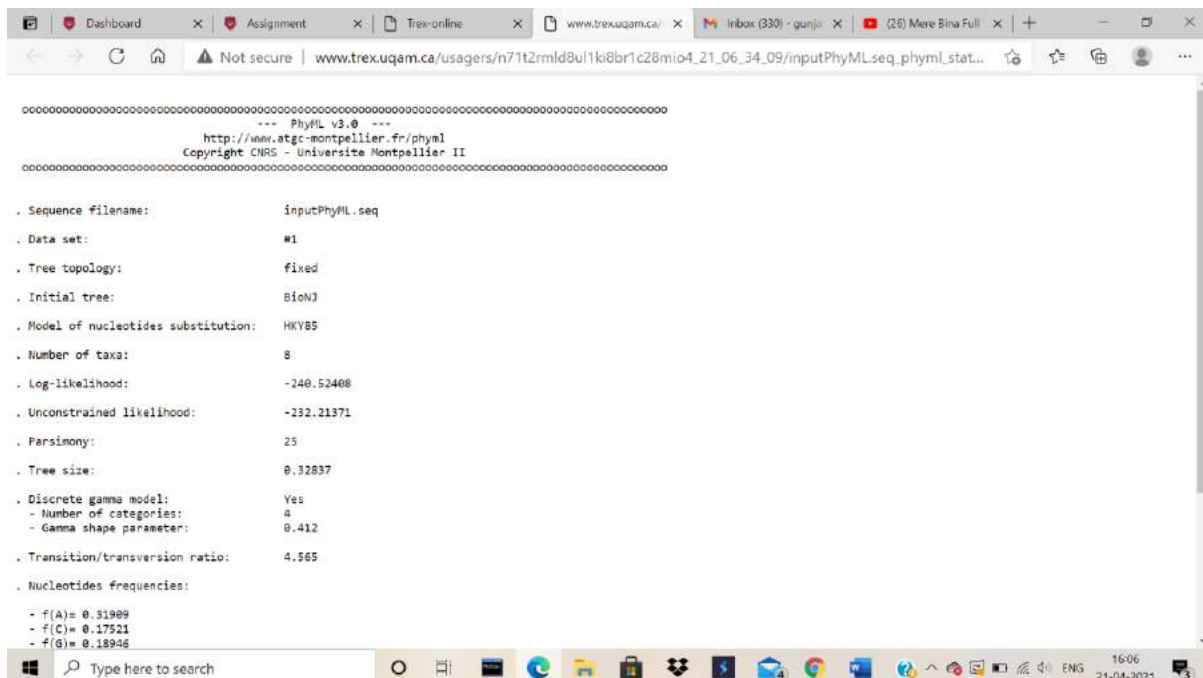
- Inferred tree:



- View tree:



- Statistics:







The screenshot shows a web browser window with the address bar displaying "www.trex.uqam.ca/usagers/n71t2rmd8ul1k18br1c28mio4\_21\_06\_34\_09/log.txt". The page content displays the results of a phylogenetic analysis performed by the TREX server.

```
. Compressing sequences...

. 25 patterns found. (out of a total of 90 sites)

. 70 sites without polymorphism (77.78%).

. Computing pairwise distances...

. Building BioNJ tree...

. This analysis requires at least 0 Mo of memory space.

(((Oenothera:0.0290915214,Cypripaes:0.0052052124,Galphimia:0.0381403859):0.0102920526):0.0151969476,
((Lycopersi:0.0186061296,Petunia:0.0234148031):0.0019944326,Nicotiana:-0.0018949818):0.0611296189):0.0811867435,Baccharis:0.0000000001,Vicoria:0.0000000000);

. ( 0 sec) [ -240.9472] [Branch lengths] ] [ 4.244853]
. ( 0 sec) [ -240.9377] [Ts/ts ratio] ] [ 0.500960]
. ( 0 sec) [ -240.6400] [Alpha] ] [ 0.500960]
. ( 0 sec) [ -240.5629] [Branch lengths] ] [ 4.458879]
. ( 0 sec) [ -240.5565] [Ts/ts ratio] ] [ 0.426704]
. ( 0 sec) [ -240.5396] [Alpha] ] [ 0.426704]
. ( 0 sec) [ -240.5276] [Branch lengths] ] [ 4.537805]
. ( 0 sec) [ -240.5268] [Ts/ts ratio] ] [ 0.417055]
. ( 0 sec) [ -240.5264] [Alpha] ] [ 0.417055]
. ( 0 sec) [ -240.5245] [Branch lengths] ] [ 4.557603]
. ( 0 sec) [ -240.5245] [Ts/ts ratio] ] [ 0.413473]
. ( 0 sec) [ -240.5244] [Alpha] ] [ 0.413473]
. ( 0 sec) [ -240.5241] [Branch lengths] ] [ 4.565056]
. ( 0 sec) [ -240.5241] [Ts/ts ratio] ] [ 0.412286]
. ( 0 sec) [ -240.5241] [Alpha] ] [ 0.412286]
. Log likelihood of the current tree: -240.524078.

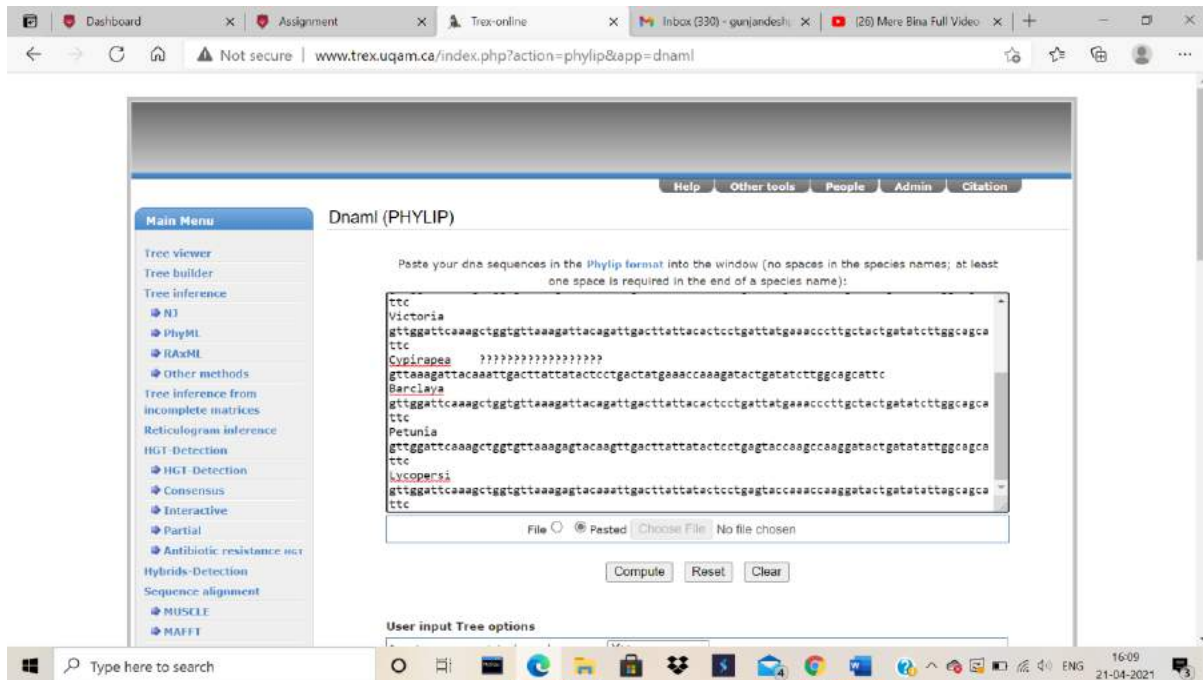
. Printing the most likely tree in file 'inputPhyML.seq_phyml_tree.txt'...

. Time used 0h0m5s

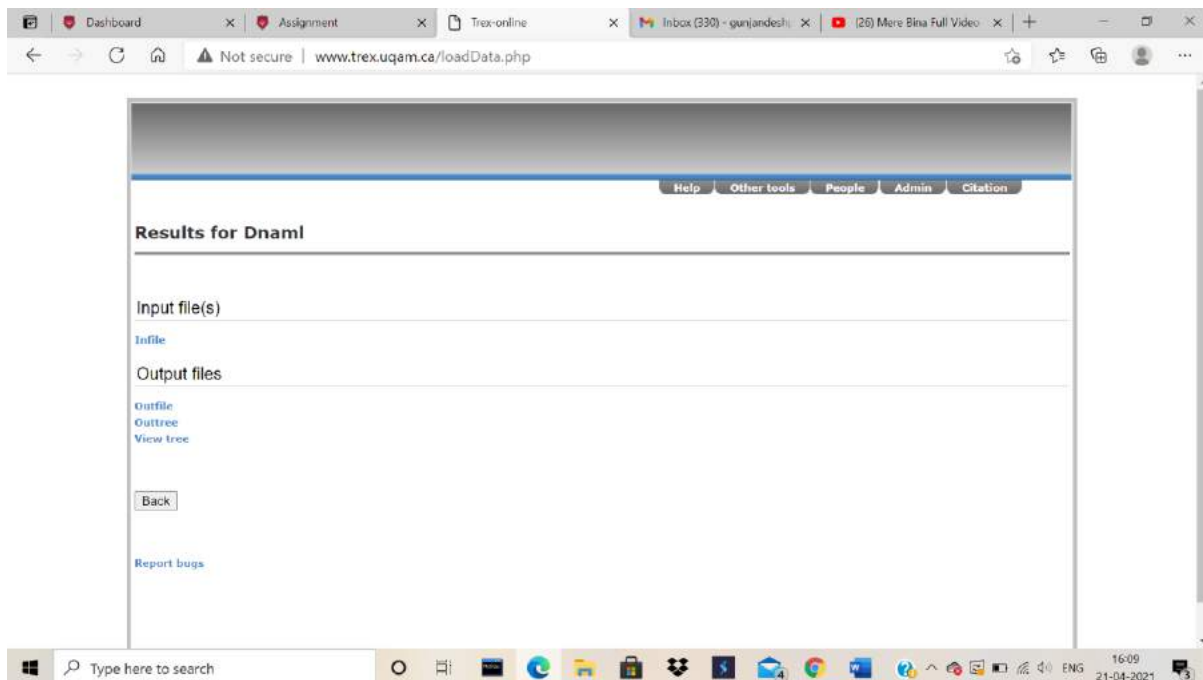
oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
```

The bottom of the image shows a Windows taskbar with various application icons and a system clock indicating 16:07 on 21-04-2021.

## DNAML:

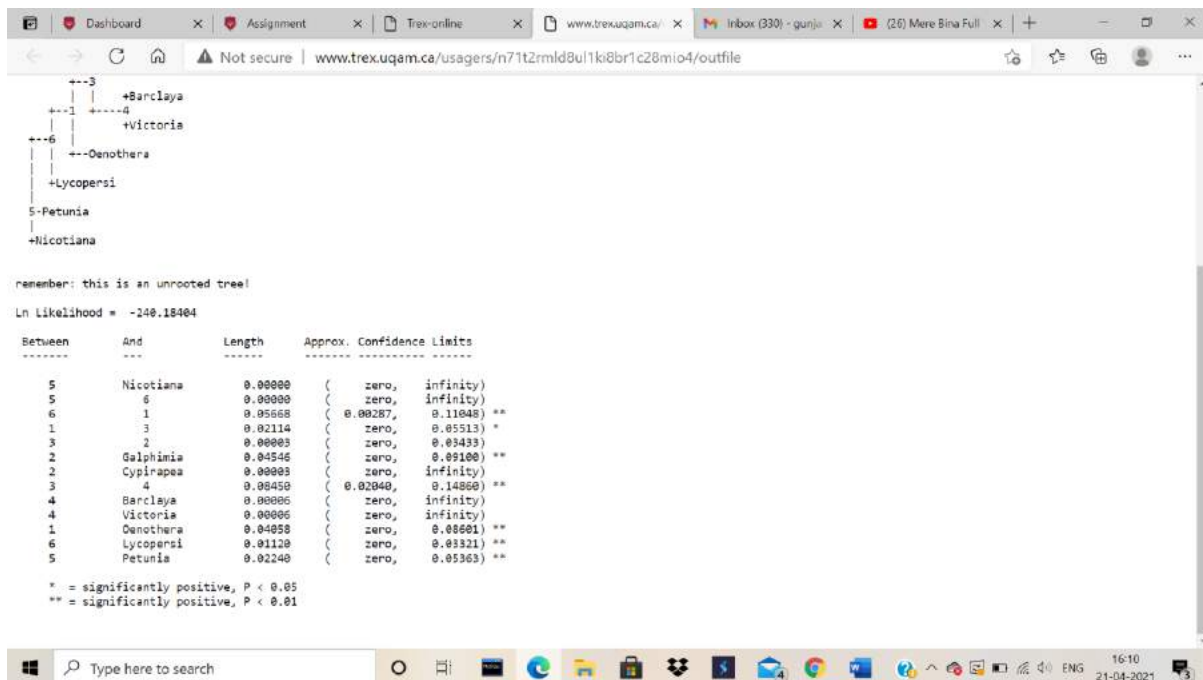
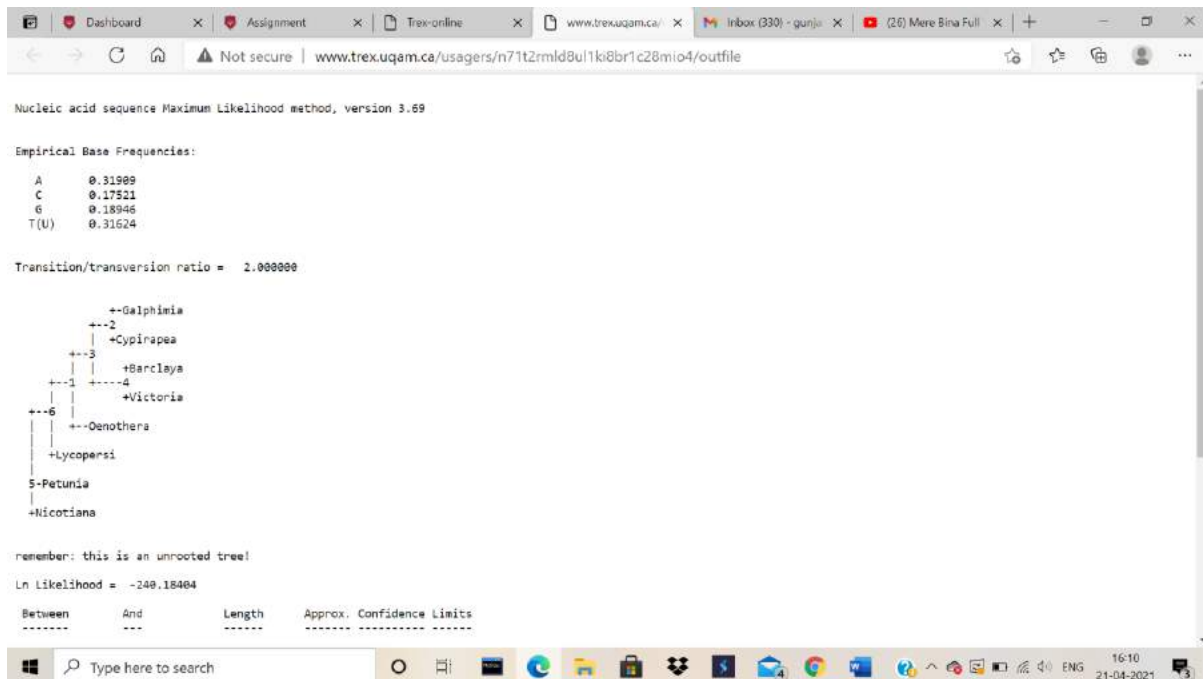


## 2)Result for DNAML

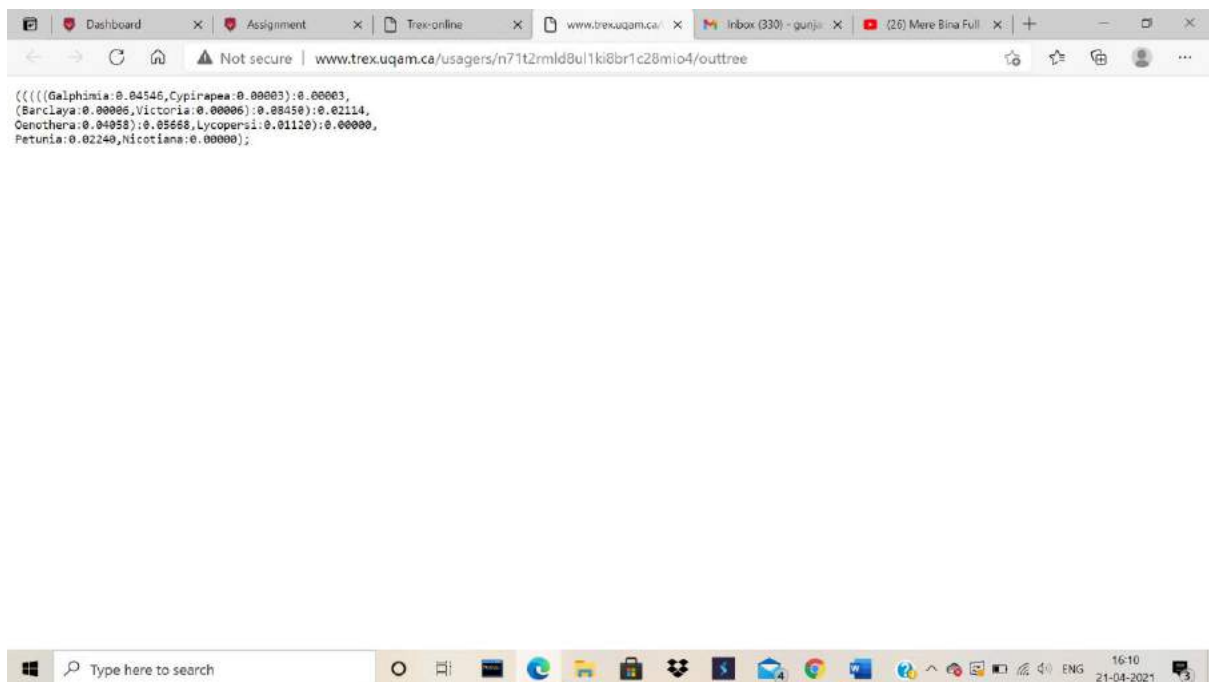




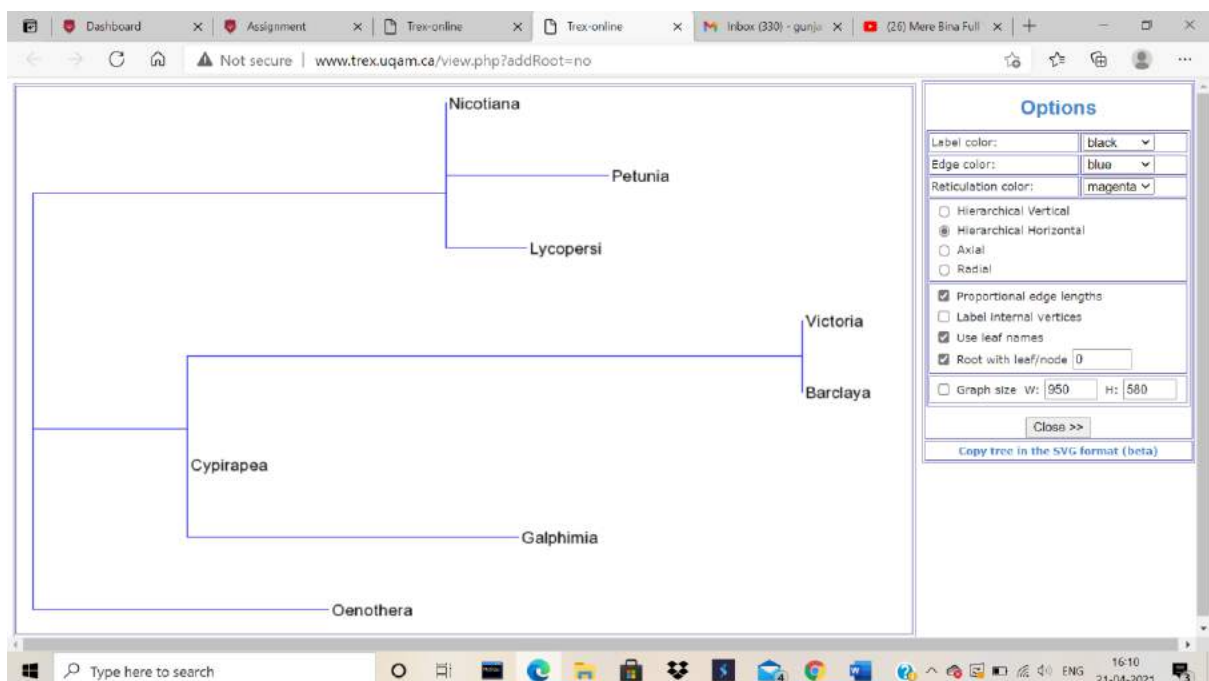
## Step 10: Open the Output file:



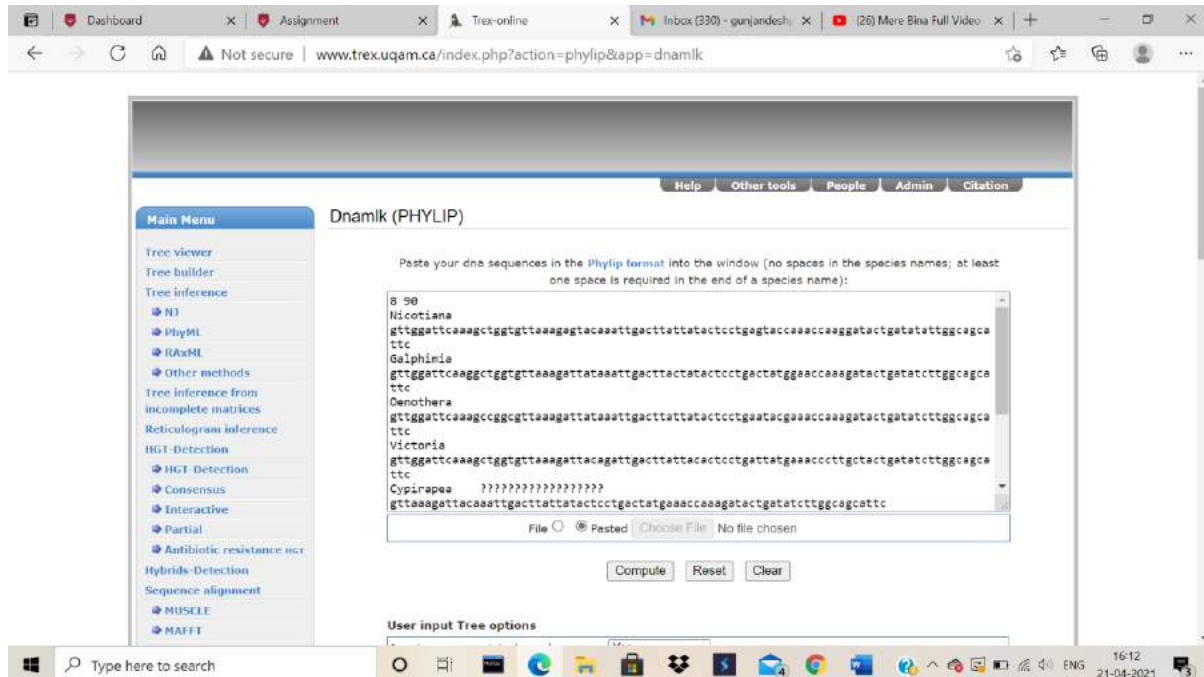
- Out tree:



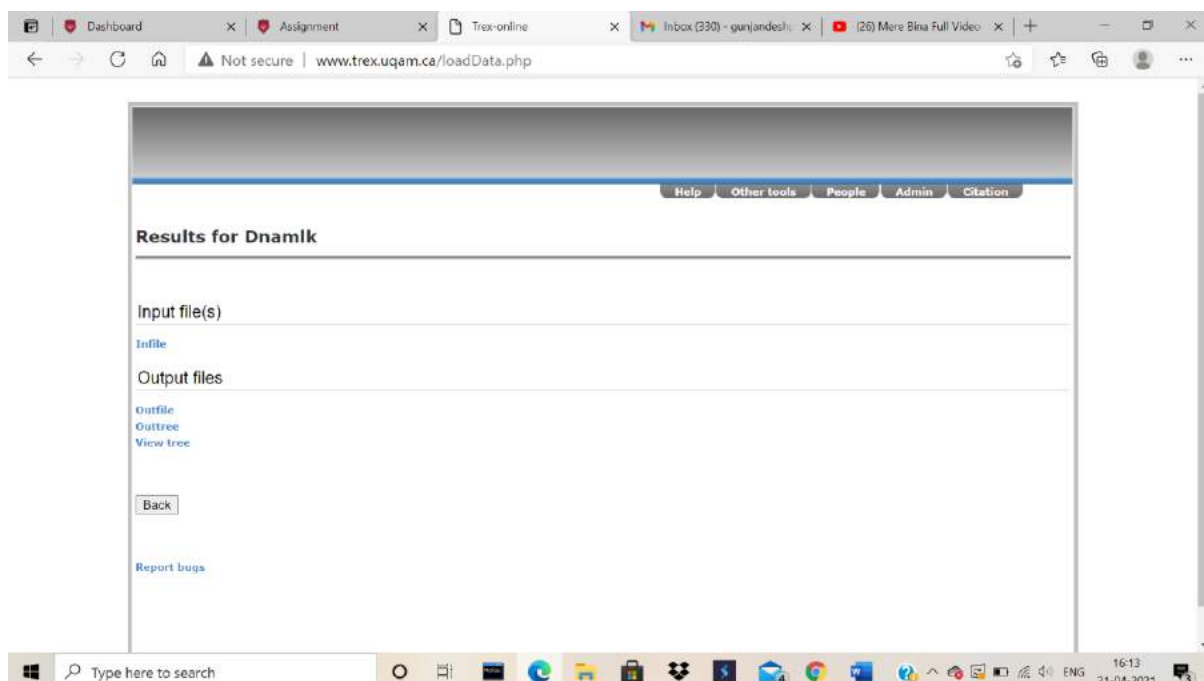
- View tree:



## DNAMLK:



## 3)Result for DNAMLK:



## Step 11: Open the Output file:

- Outfile:

