

Bioinformatics Bonus Assignment

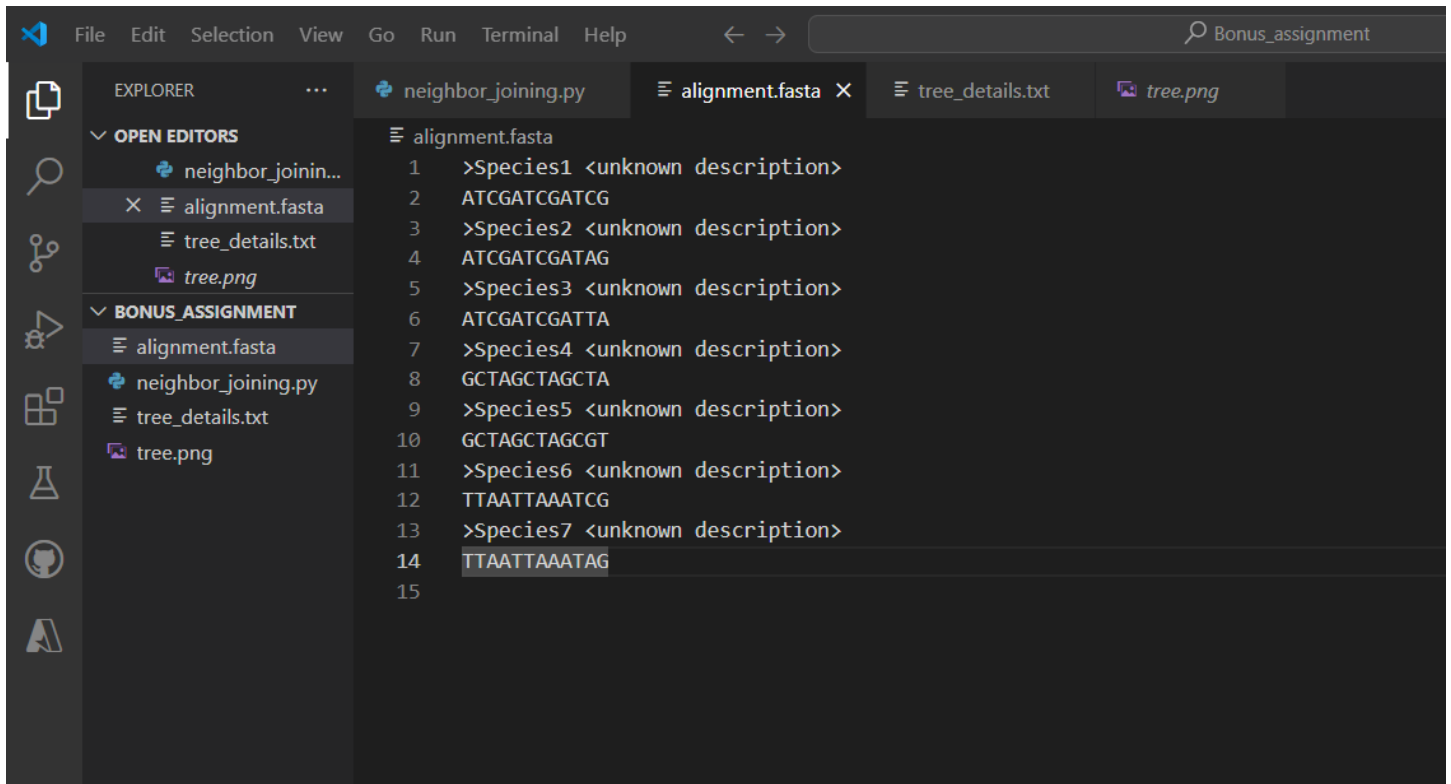
Results Explained

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1. Input:

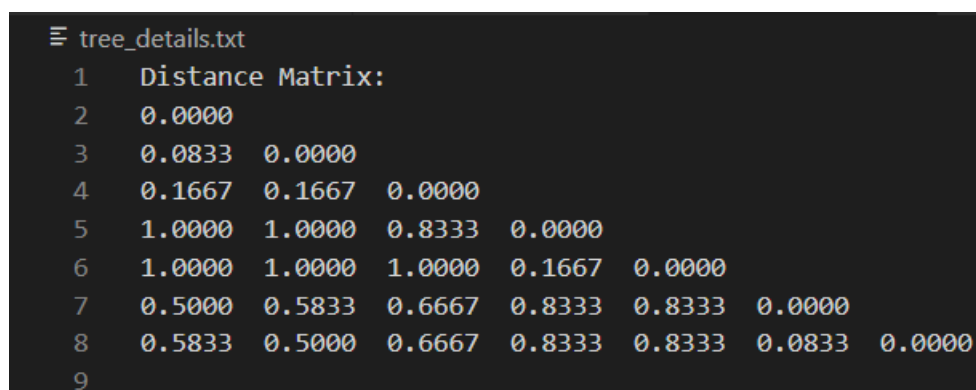
Read FASTA file then do multiple sequence alignment and get the distance Matrix to use it as my input.

FASTA file used:



```
alignment.fasta
1  >Species1 <unknown description>
2  ATCGATCGATCG
3  >Species2 <unknown description>
4  ATCGATCGATAG
5  >Species3 <unknown description>
6  ATCGATCGATTA
7  >Species4 <unknown description>
8  GCTAGCTAGCTA
9  >Species5 <unknown description>
10 GCTAGCTAGCGT
11 >Species6 <unknown description>
12 TTAATTAAATCG
13 >Species7 <unknown description>
14 TTAATTAAATAG
15
```

My Distance Matrix used as input:

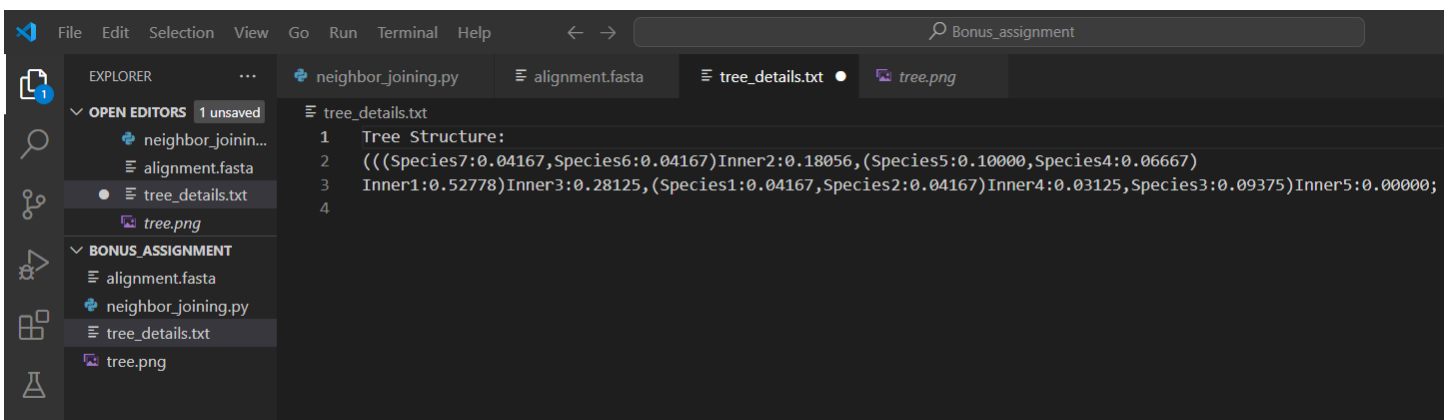


```
tree_details.txt
1  Distance Matrix:
2  0.0000
3  0.0833  0.0000
4  0.1667  0.1667  0.0000
5  1.0000  1.0000  0.8333  0.0000
6  1.0000  1.0000  1.0000  0.1667  0.0000
7  0.5000  0.5833  0.6667  0.8333  0.8333  0.0000
8  0.5833  0.5000  0.6667  0.8333  0.8333  0.0833  0.0000
9
```

2. OUTPUT:

Text file

Detailing the tree distances between the sequences and which nodes are grouped together to which parents.



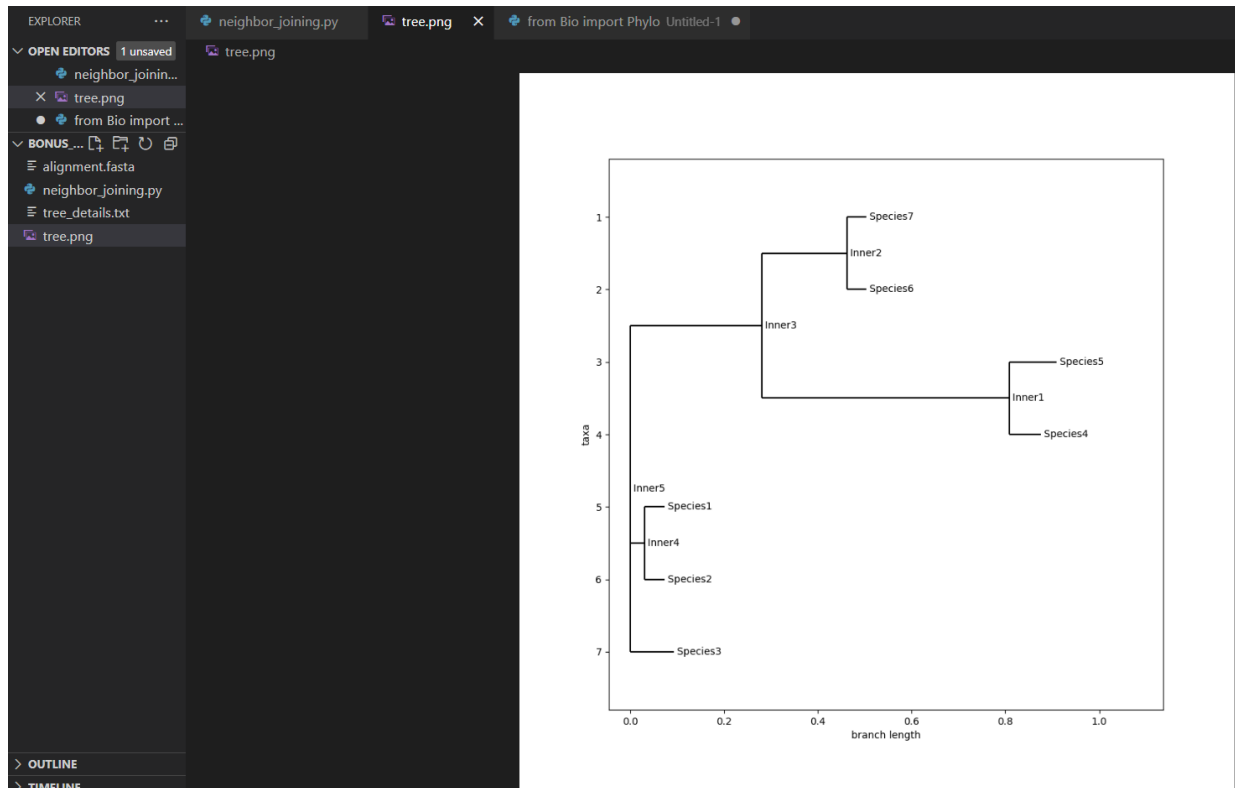
The screenshot shows a code editor with a dark theme. The Explorer panel on the left shows a project named 'Bonus_assignment' with files 'alignment.fasta', 'neighbor_joining.py', 'tree_details.txt', and 'tree.png'. The 'tree_details.txt' file is open in the editor, showing the following content:

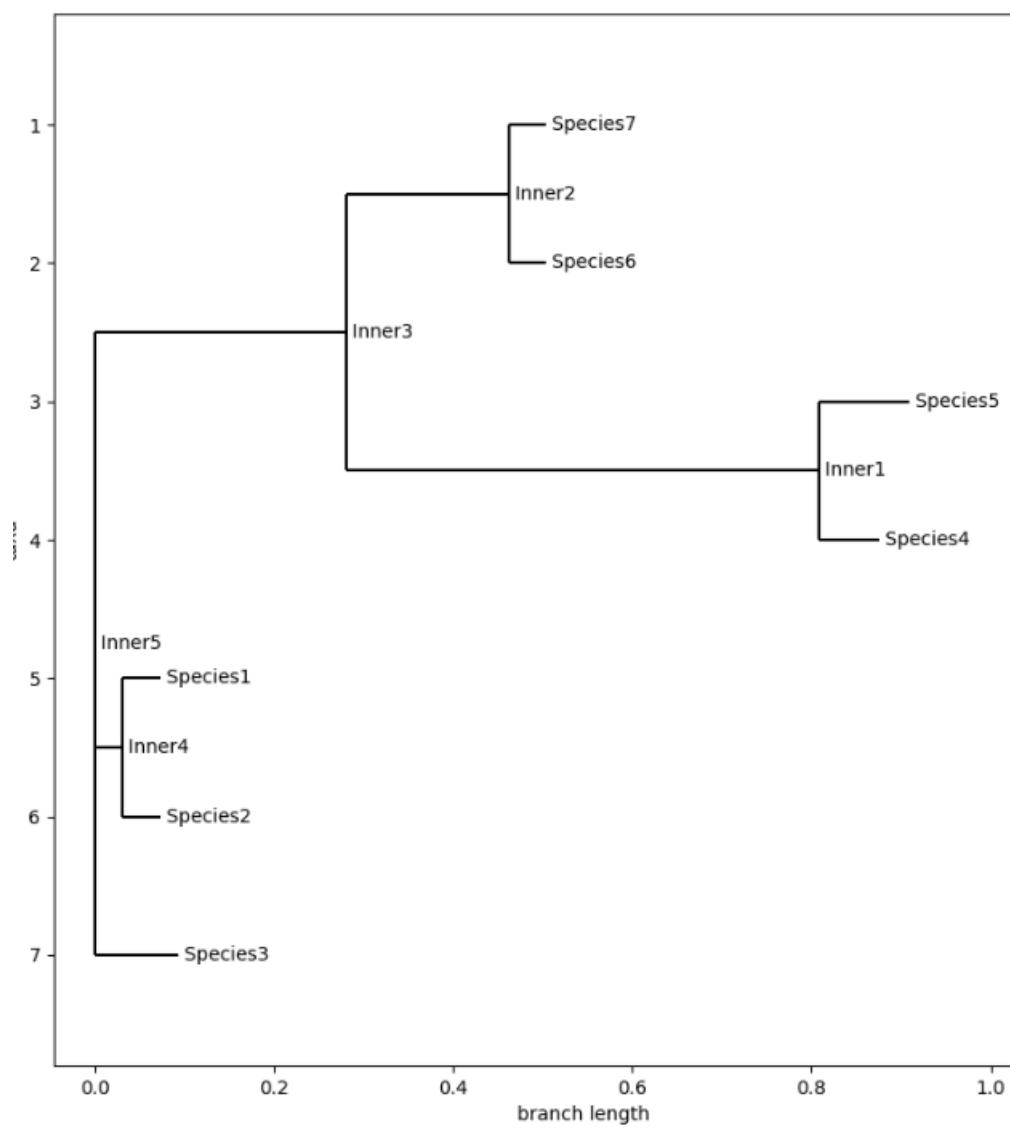
```
1 Tree Structure:
2 (((Species7:0.04167,Species6:0.04167)Inner2:0.18056,(Species5:0.10000,Species4:0.06667)
3 Inner1:0.52778)Inner3:0.28125,(Species1:0.04167,Species2:0.04167)Inner4:0.03125,Species3:0.09375)Inner5:0.00000;
4
```

A text file is made called “`tree_details.txt`” stores the distances between the species and the nodes [for this example have 5 nodes] which are called inner1, inner2, ..., inner5.

Tree figure

Using the **Phylo** library I reconstruct and save an image of the tree calling it “tree.png”





With distances print on the tree figure

