

BT 3040: BIOINFORMATICS

Assignment 10



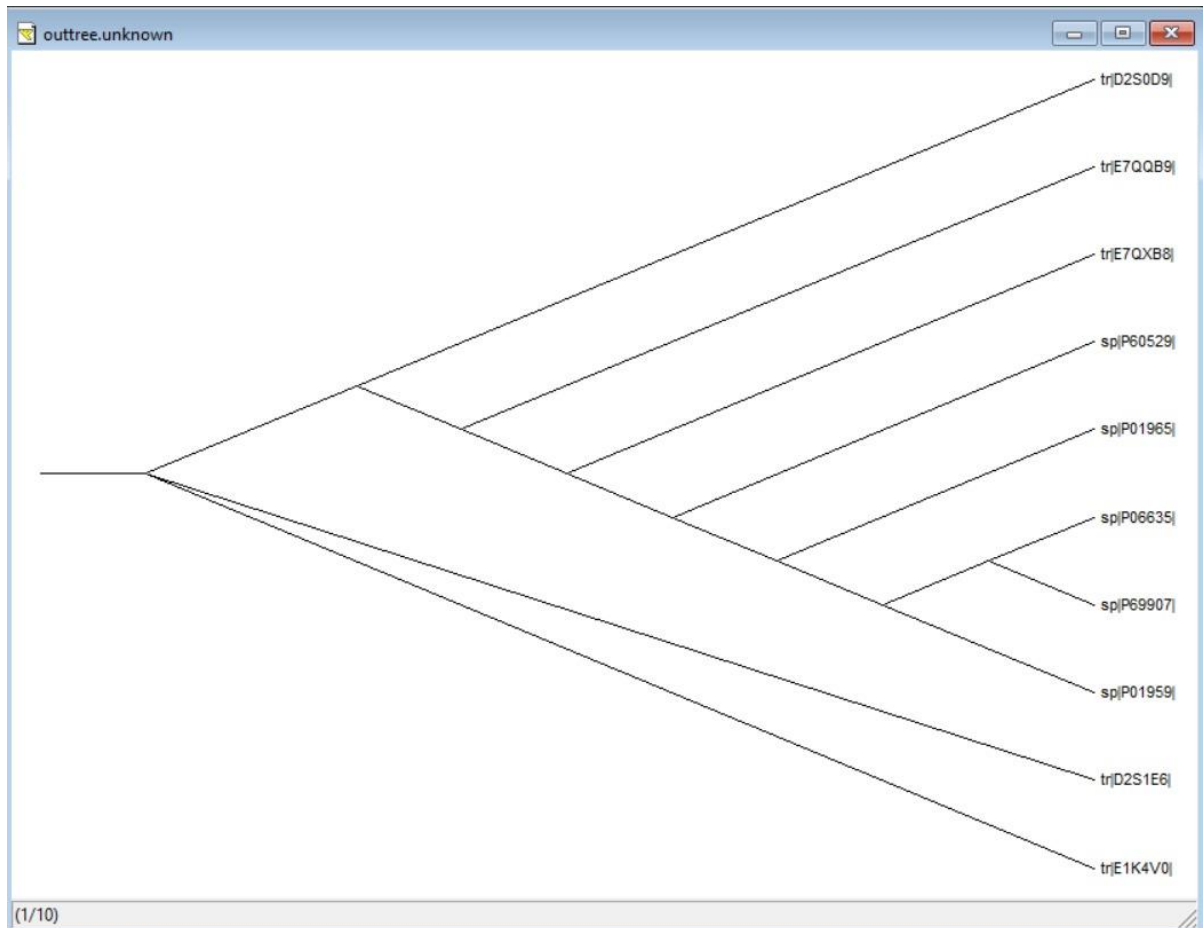
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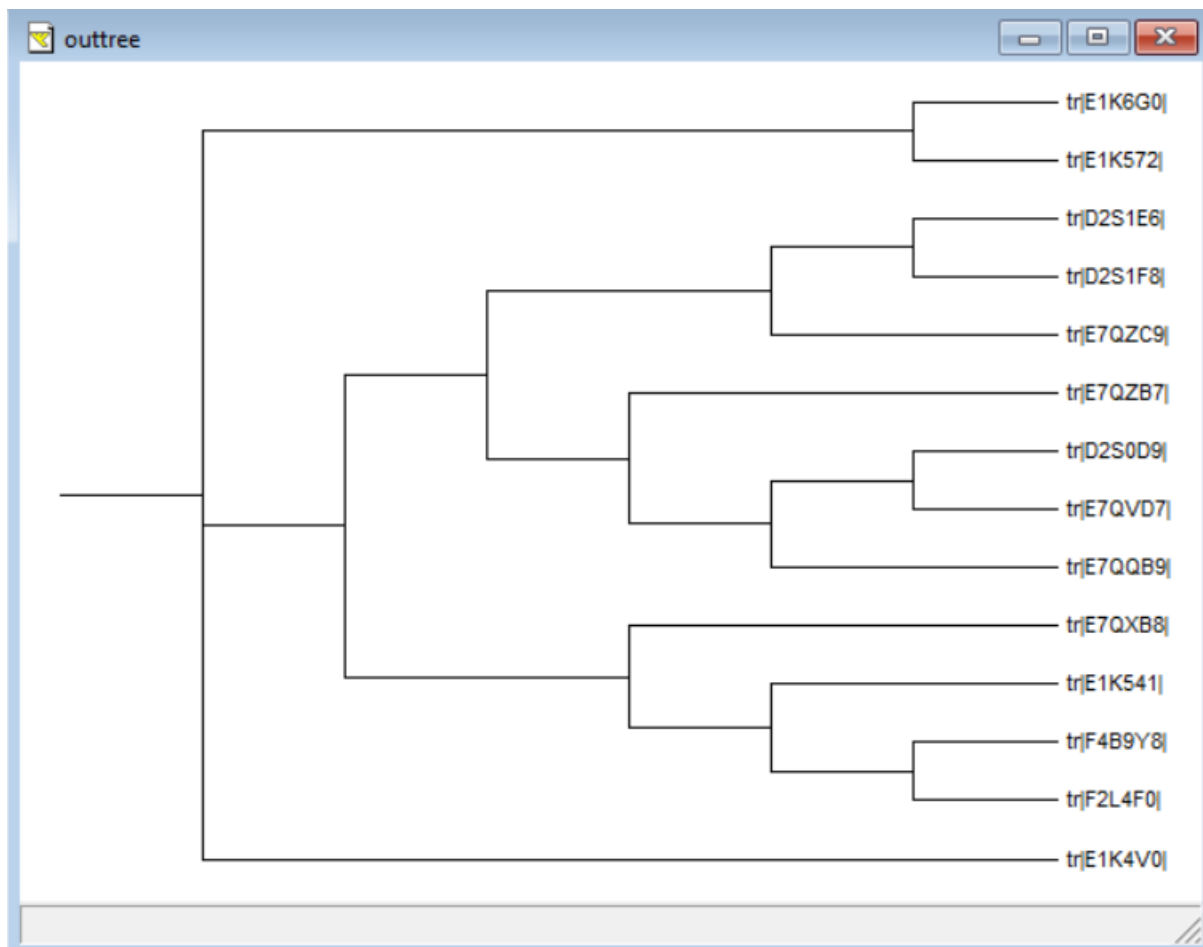
Indian Institute of Technology
Madras

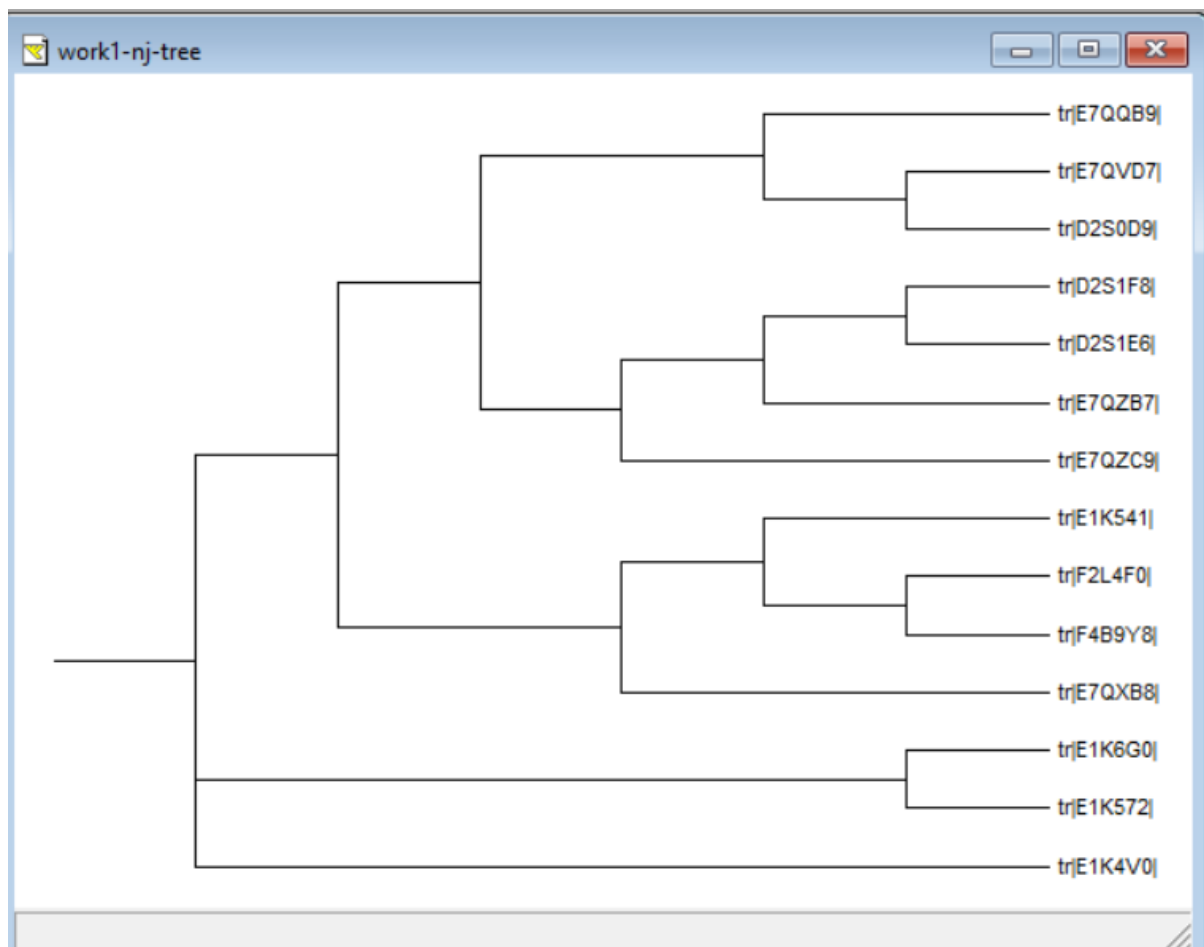
Q1) Obtain the consensus phylogenetic tree for the following two sets of sequences:

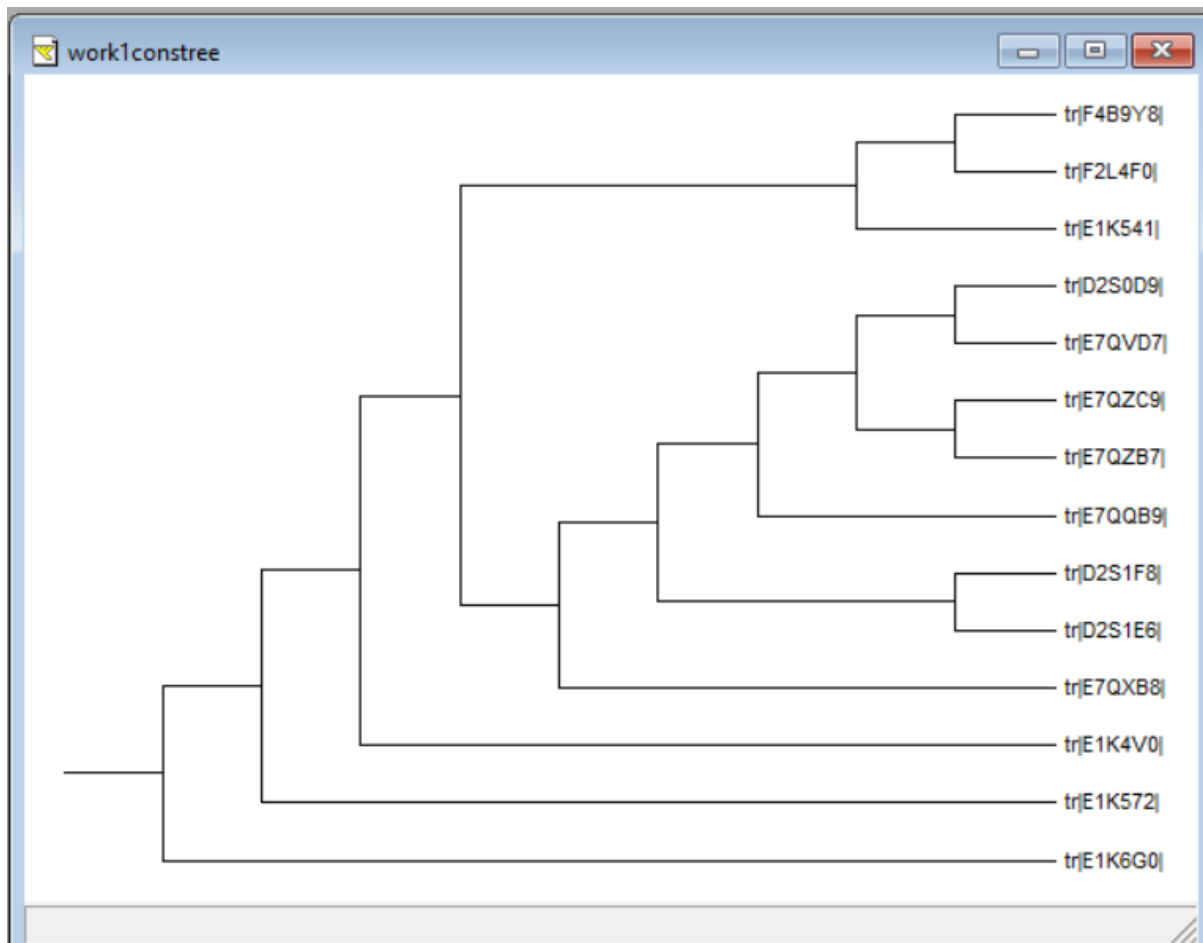
Set 1: tim.dat

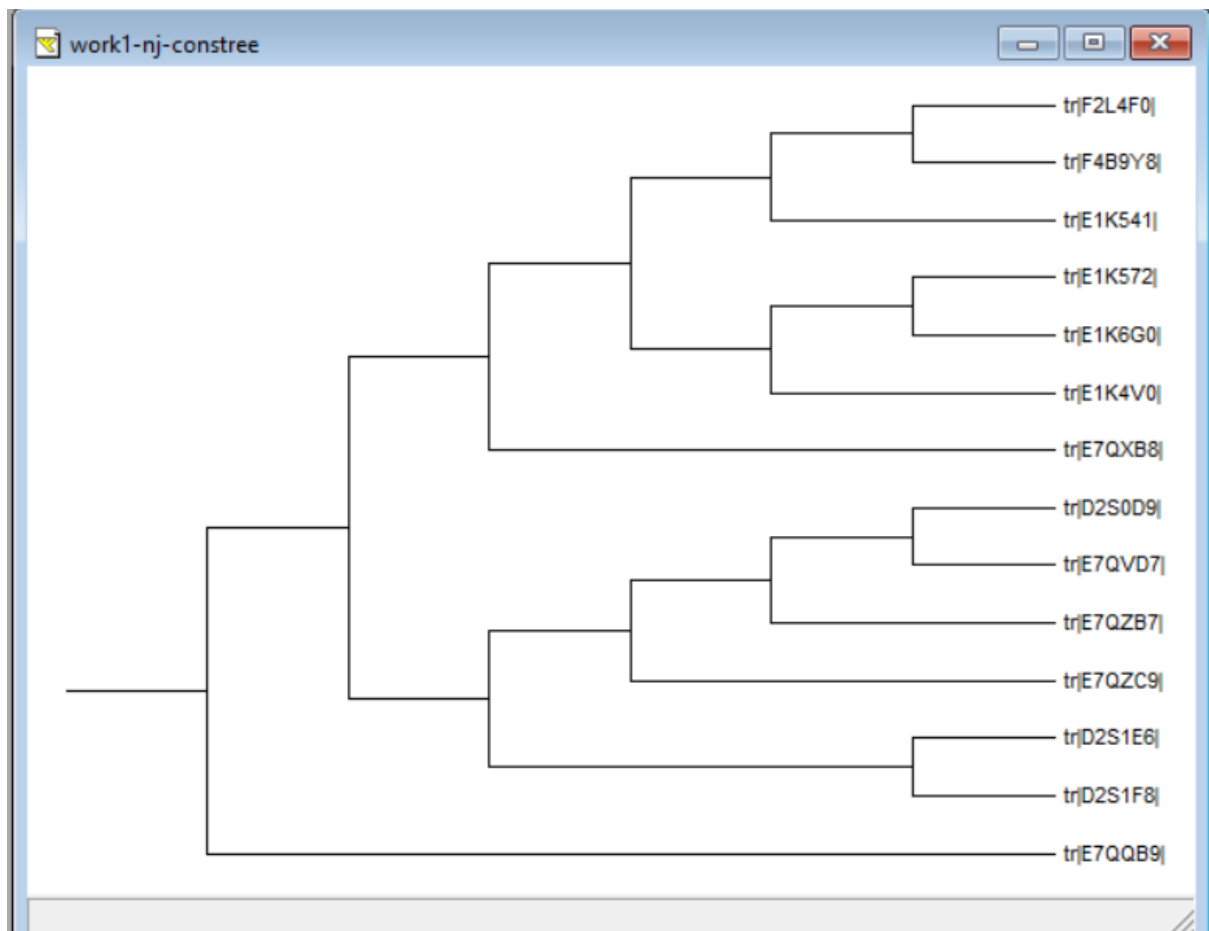
All the files in 'tim_dat' folder





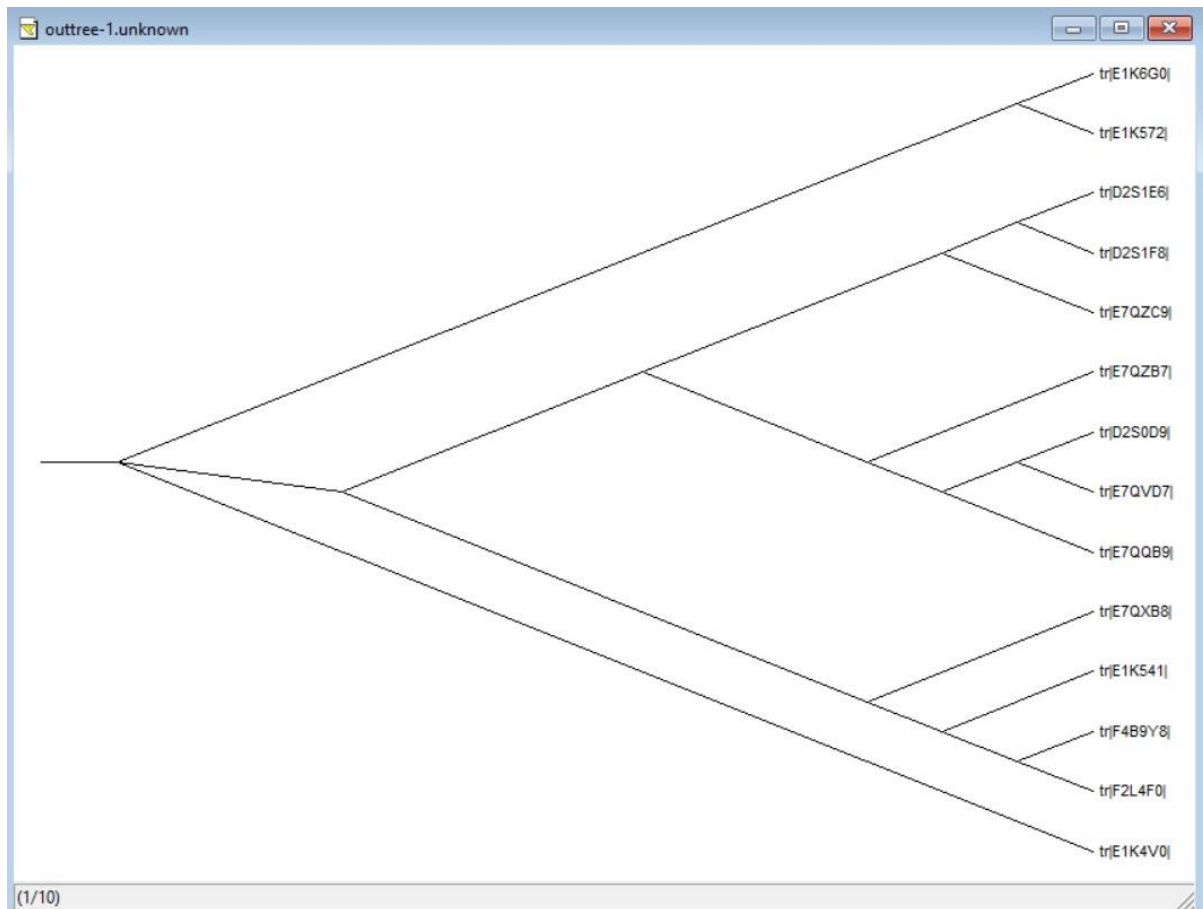


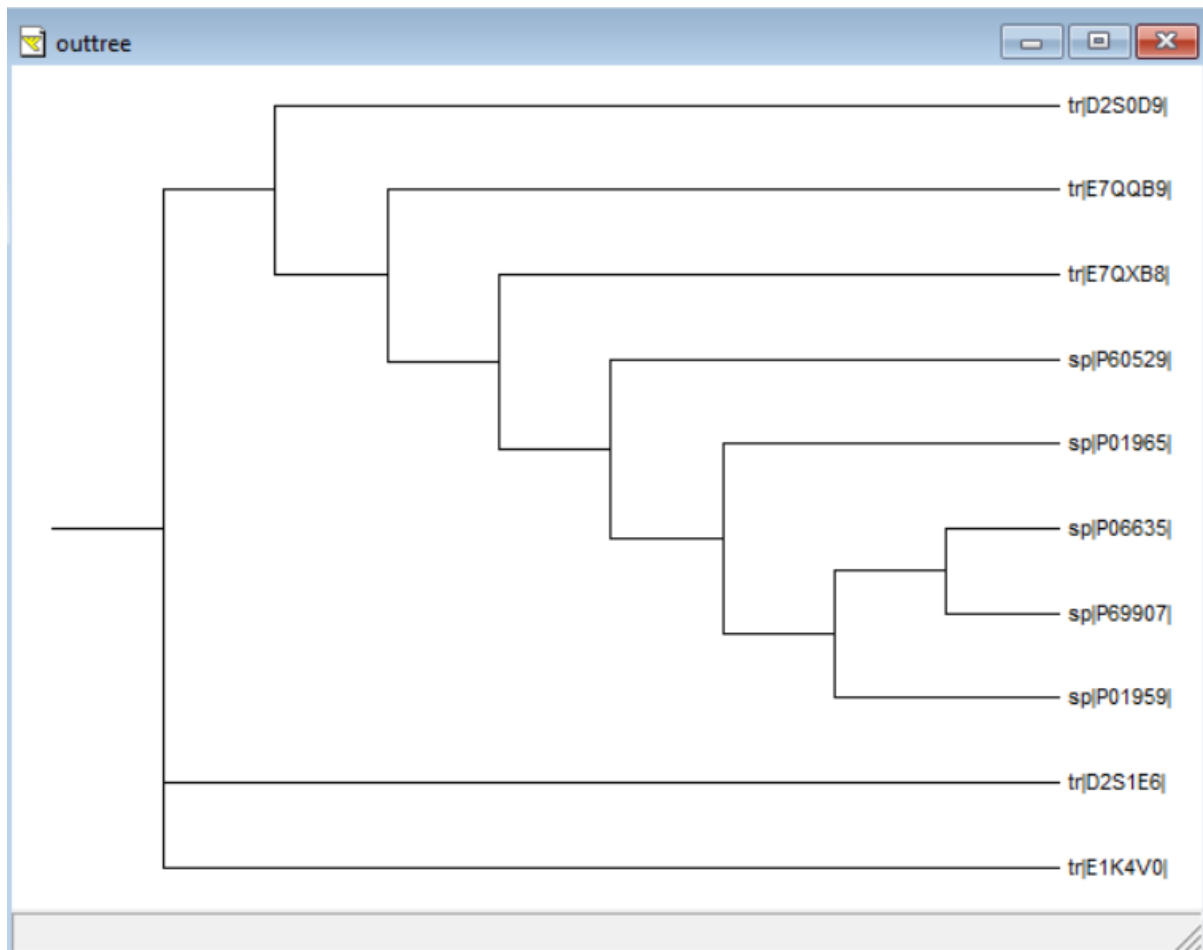


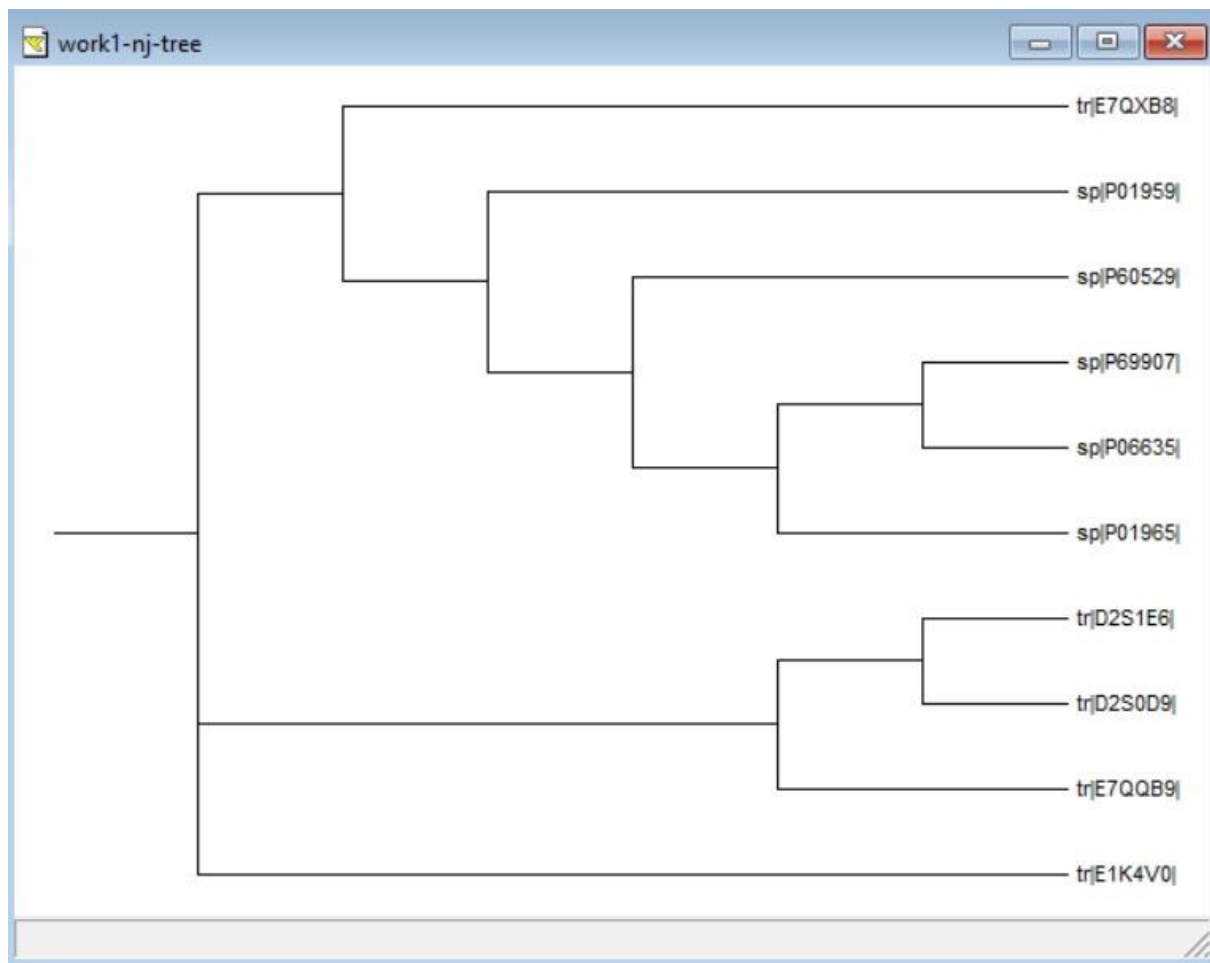


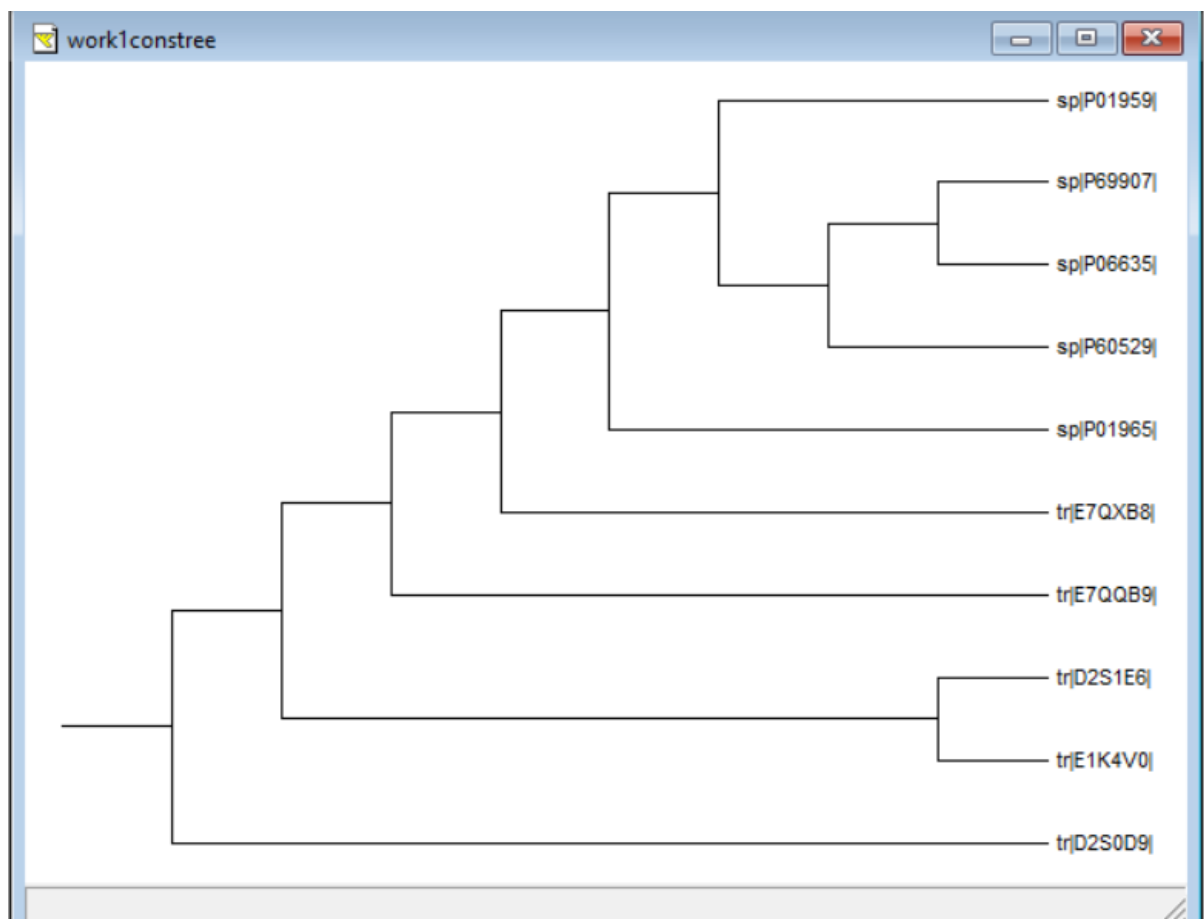
Set 2: tim-hemo.dat

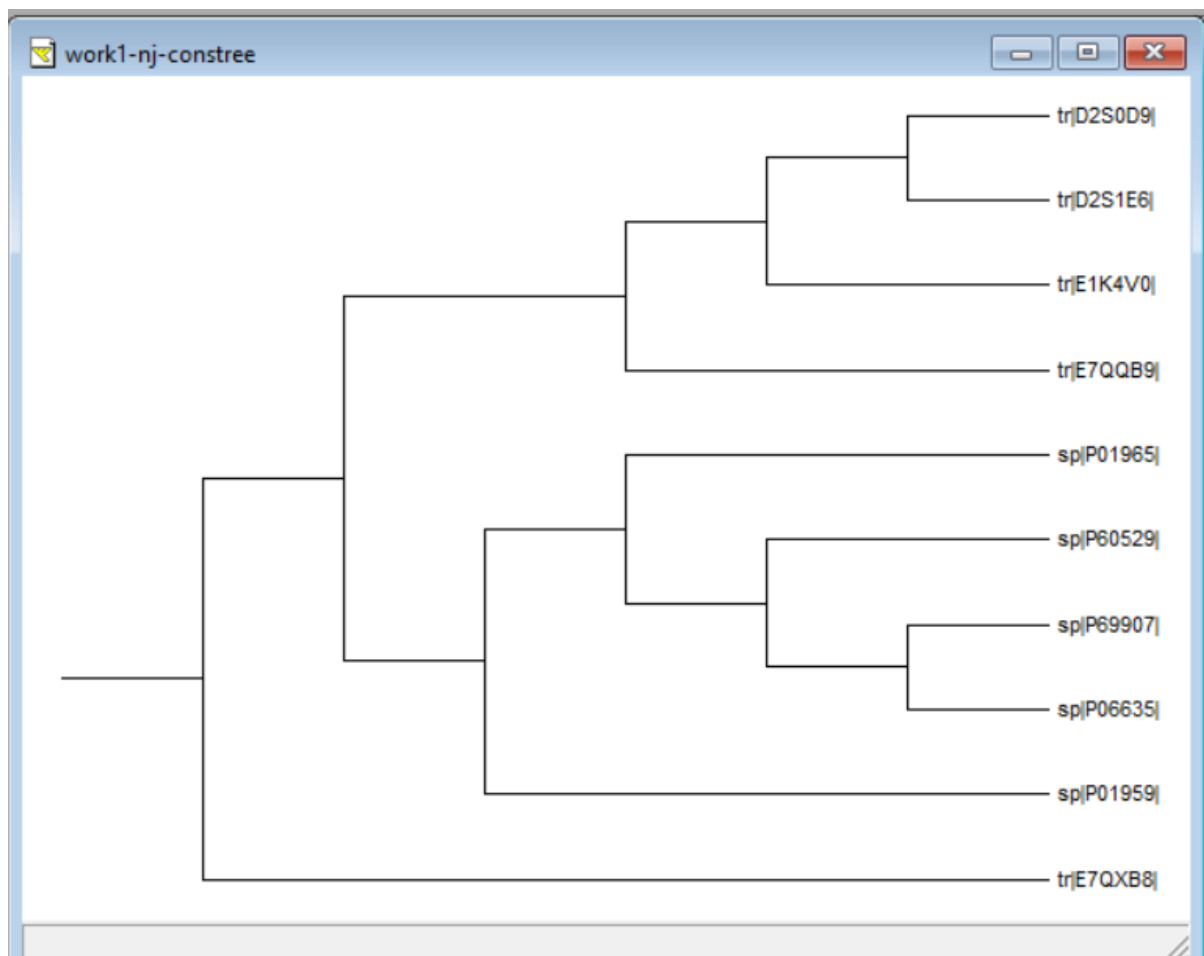
All the files in 'tim_dat_hemo' folder











Q2) Obtain the weight matrix for the following sequences

MVLSPADKTNVKGKVGAGHAGEYGAAAW
MKRLPADPPCVKGKVKAKAGDYGATTW
MALSAADKTNVKS KVGGHAGEYGAATS
MVLSAADKTNVKS KAGGNAGEWWAAAW
MVLSAADKTNVKS KVLNAGEFGAAAW
ALLPIRTTYHKKCASGHIPEEKDLNNV
DEASSLKGHHIKKLEADALLIPLSASS

Code:

```
#BT3040 | Assignemnt 10 | Q2 | Atharva Mandar Phatak | BE21B009 |

import math

def sequence_to_matrix(input_sequence, sequence_length):
    amino_acids = ['A', 'C', 'D', 'E', 'F', 'G', 'H', 'I', 'K', 'L', 'M', 'N',
                    'P', 'Q', 'R', 'S', 'T', 'V', 'W', 'Y']
    matrix = []

    for i in range(0, len(input_sequence), sequence_length):
        subsequence = input_sequence[i:i+sequence_length]
        row = [0] * len(subsequence)
        for j, aa in enumerate(subsequence):
            row[j] = aa
        matrix.append(row)

    return matrix

input_sequence =
'MVLSPADKTNVKGKVGAGHAGEYGAAAWMKRLPADPPCVKGKVKAKAGDYGATTWMALSAADKTNVKS KVGGHAGEYG
AATSMVLSAADKTNVKS KAGGNAGEWWAAAWMVLSAADKTNVKS KVLNAGEFGAAAWALLPIRTTYHKKCASGHIPE
EKDLNNVDEASSLKGHHIKKLEADALLIPLSASS'
sequence_length = 27
amino_acid_matrix = sequence_to_matrix(input_sequence, sequence_length)

def count_amino_acids(matrix):
    amino_acids = ['A', 'C', 'D', 'E', 'F', 'G', 'H', 'I', 'K', 'L', 'M', 'N',
                    'P', 'Q', 'R', 'S', 'T', 'V', 'W', 'Y']
    amino_acid_counts = [[0] * len(matrix[0]) for _ in
                           range(len(amino_acids))]
```

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    for row in matrix:
        for i, amino_acid in enumerate(row):
            amino_acid_counts[amino_acids.index(amino_acid)][i] += 1

    return amino_acid_counts

def calculate_weight_matrix(amino_acid_counts):
    num_rows = len(amino_acid_counts)
    num_cols = len(amino_acid_counts[0])

    weight_matrix = [[0] * num_cols for _ in range(num_rows)]

    for i in range(num_rows):
        for j in range(num_cols):
            n = amino_acid_counts[i][j]
            weight_matrix[i][j] = round(math.log((n + 1/20) / (8/20)), 2)

    return weight_matrix

# Count amino acids
amino_acid_counts = count_amino_acids(amino_acid_matrix)

# Calculate weight matrix
weight_matrix = calculate_weight_matrix(amino_acid_counts)

from tabulate import tabulate
print("Alignment Matrix")
print(tabulate(amino_acid_counts, headers=["{}".format(i+1) for i in
range(len(amino_acid_matrix[0]))], tablefmt="grid", numalign="centre"))
print("")
print("")
print("Weight Matrix")
print(tabulate(weight_matrix, headers=["{}".format(i+1) for i in
range(len(weight_matrix[0]))], tablefmt="grid", numalign="centre"))

```

Output:

a) Alignment Matrix

Alignment Matrix																									
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	1	1	1	0	3	5	0	0	0	0	0	0	1	1	1	3	1	5	0	0	0	0	5	5	3
0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	5	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	4	2	0	0	5	0	0	4	0	0
0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0
0	1	0	0	0	0	1	4	0	0	1	7	1	5	0	1	0	1	0	0	0	1	0	0	0	0
0	1	5	1	0	1	0	0	0	0	0	0	0	1	0	1	0	0	1	1	0	0	1	1	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	2	0	0	0	0	0	0	1	1
0	0	0	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	5	1	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	1	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2

b) Weight Matrix

Weight Matrix																					
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	
0.97	0.97	0.97	-2.08	2.03	2.54	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	0.97	0.97	2.03	0.97	2.54	-2.08	-2.08	
-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	0.97	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	
0.97	-2.08	-2.08	-2.08	-2.08	-2.08	2.54	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	-2.08	0.97	
-2.08	0.97	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	-2.08	-2.08	0.97	2.54	
-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	
-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	-2.08	1.63	-2.08	-2.08	2.32	1.63	-2.08	-2.08	2.54	-2.08	
-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	1.63	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	1.63	-2.08	-2.08	-2.08	
-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	-2.08	0.97	
-2.08	0.97	-2.08	-2.08	-2.08	-2.08	0.97	2.32	-2.08	-2.08	0.97	2.87	0.97	2.54	-2.08	0.97	-2.08	0.97	-2.08	-2.08	-2.08	
-2.08	0.97	2.54	0.97	-2.08	0.97	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	0.97	-2.08	-2.08	0.97	0.97	-2.08	
2.54	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	
-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	2.32	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	1.63	-2.08	-2.08	-2.08	
-2.08	-2.08	-2.08	0.97	1.63	-2.08	-2.08	0.97	0.97	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	0.97	-2.08	-2.08	
-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	-2.08	

Complete output in 'Q2_Output.txt'