Practical session 5

Implementing NJ

- First, we need to identify the classes (usually names).
- Second, we need to identify the relationships between classes (redundancies indicate a common root).
- Third, we need to identify the atributes (usually adjectives).
- Fourth, we need to identify actions (usually verbs).

- Prior conditions: we have created for each type of animal as many animals as the present in the zoo. For example:
- pumba = Lion(number_of_eyes, color)
- nala = Lion(number of eyes, color)
- ...
- Put each type of animal in its own list
- Put each list into a list of animals
- arnau = ZooKeeper()
- for hour in 1:24 DO:
 - for list of animals DO:
 - for animals in list DO:
 - if(animal.get_time_feeding()==hour)
 - arnau.feed(animal)

Exam

```
def estimate_emission_probabilities(PI, x):
    # Get the different states of the sequence of hidden states PI
    states_in_PI = []
    # iterate over the sequence of PI. For each state, check if it is in the list of states in PI
   # This loop is looking for the unique states in the sequence
   for i in self.PI:
        # add to the list if it is not already in the list of states
       if i not in states_in_PI:
           # add the state in the states_in_PI list
           states in PI.append(i)
   \# Get the different categories that can be found in the vector x
    categories_in_x = {}
   # Iterate over each position of x
    for i in x:
        # if the category is not in the list of categories, add it
       if i not in categories_in_x:
            # add the category to the list of categories
            categories in x .append(i)
   # a dictionary of dictionaries to store, for each state, the emission probabilities
   e = []
   # iterate over all the states of PI
    for key in states in PI:
        # create a new dictionary to store the categories of that state
       t = []
        # for each unique category
        for cat in categories_in_x:
            # initialize the counter at 0
           t[cat] = 0
        # add to the dictionary e the dictionary with the frequencies of the different categories
        e[key] = t
    # iterate over each position
    for i in range(len(x)):
        # current state at position i
        state = PI[i]
        # current category at position i
        category = x[i]
        # update the dictionary of dictionaries at state and category
        e[state][category] = e[state][category] + 1
    for state in states in PI:
       T = 0
        for cat in categories in x:
           T = T + e[state][cat]
        for cat in categories_in_x:
            e[state][cat] = int(e[state][cat]/float(T))
```

Exercise 2

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Exercise 2. (2 Pnt) Assume an exponential probability distribution with cdf = 1 - exp(-l*x). Use the inverse transform sampling technique to create a function called "sample" that takes I as parameter to generate numbers x randomly sampled from the probability distribution.

Tip: Use math.log and random.random(). Comment each line of code

def sample(l):
 u = random.random()
 # log(1-cdf) = -l*x; x = -log(1-cdf)/l
 return -math.log(1-u)/l

Exercise 2

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```
Exercise 3. (2 Pnt) Fix (five errors) and comment the code. WHAT IS THE PURPOSE OF
THIS CODE? '''
def prob_x_and_pi(prior_prob, transition_prob, emission_prob, x, pi):
    # Initialize the probability with the prior at state in position i-1
    p = prior prob[pi[0]] # prior of the hidden state
    # counter to store the state of previous position.
    si = pi[0]
    for ii in range(len(pi)):
        p = p*emission prob[pi[ii]][x[ii]]*transition prob[si][pi[ii]] # move from
state <u>si to pi and emission from state pii and x</u>
        si = pi[ii]
    return p # return p
```

Exercise 4 (2 Pnt)

Reconstruct phylogenetic tree from the following distance matrix using UPGMA approach:

```
      OTUS
      A
      B
      (CD)
      E
      F

      A
      0
      6
      29
      24
      30

      B
      6
      0
      31
      26
      28

      (CD)
      29
      31
      0
      32
      15

      E
      24
      26
      32
      0
      30

      F
      30
      28
      15
      30
      0
```

What would be the topology of this tree? (Parentheses indicate the order of grouping):

a) ((EAB(CDF)); b) ((EA(B))(CD)F); c) (((AB)(CD)F)E); d) (E(AB))((CD)F)If in the previous exercise dF(CD) - d(CD)=9, what is the distance of the both taxons C and D to their most recent common ancestor?

```
a) 3,0; b) 1,5; c) 1,0; d) 2,0
''' ((A:3.0,B:3.0):1.5,E:1.5):14.75,
((CD):7.5,F:7.5):14.75)
```

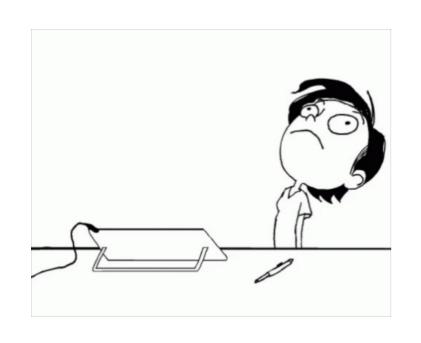
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Exercise 5 (2 Pnt).

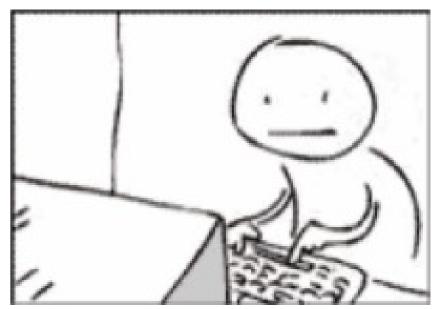
Write in <u>pseudocode</u> (NO NEED TO BE PYTHON FRIENDLY) an algorithm for <u>evolving in forward a sequence</u> of n nucleotides for x generations given a transition matrix M between nucleotides.

1.1.1

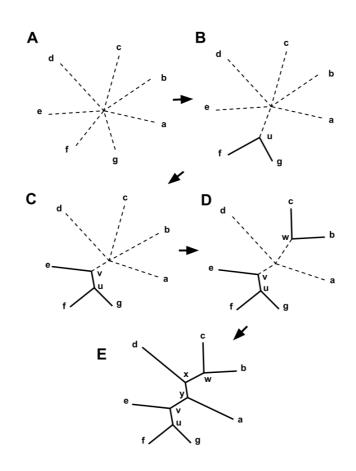
Stuff going on during the exam...







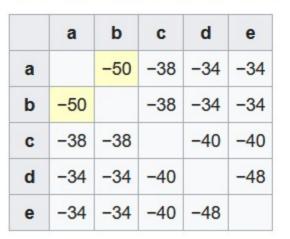
Implement the NJ algorithm



Implement the NJ algorithm

$$Q(i,j) = (n-2)d(i,j) - \sum_{k=1}^n d(i,k) - \sum_{k=1}^n d(j,k)$$

	a	b	С	d	е
а	0	5	9	9	8
b	5	0	10	10	9
С	9	10	0	8	7
d	9	10	8	0	3
е	8	9	7	3	0



Implement the NJ algorithm

$$\delta(a,u) = rac{1}{2}d(a,b) + rac{1}{2(5-2)}\left[\sum_{k=1}^5 d(a,k) - \sum_{k=1}^5 d(b,k)
ight] = rac{5}{2} + rac{31-34}{6} = 2 \ \delta(b,u) = d(a,b) - \delta(a,u) = 5-2 = 3$$

$$\delta(f,u)=rac{1}{2}d(f,g)+rac{1}{2(n-2)}\left[\sum_{k=1}^nd(f,k)-\sum_{k=1}^nd(g,k)
ight] \ \delta(g,u)=d(f,g)-\delta(f,u)$$

$$d(u,k)=\frac{1}{2}[d(f,k)+d(g,k)-d(f,g)]$$

$$d(u,c) = \frac{1}{2}[d(a,c) + d(b,c) - d(a,b)] = \frac{9+10-5}{2} = 7$$

$$d(u,d) = \frac{1}{2}[d(a,d) + d(b,d) - d(a,b)] = \frac{9+10-5}{2} = 7$$

$$d(u,e) = \frac{1}{2}[d(a,e) + d(b,e) - d(a,b)] = \frac{8+9-5}{2} = 6$$

	u	C	d	е
u	0	7	7	6
С	7	0	8	7
d	7	8	0	3
е	6	7	3	0