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In [1]: import numpy as np
import sys
from tqdm import trange

file = open('dna.txt','r')
s = file.readline()
s = s[:-1]
t = file.readline()
file.close()

sys.setrecursionlimit(1000)
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In [2]: def cost(s,t):
    F = np.zeros((len(s)+1,len(t)+1))
    for i in range(1,len(s)+1):
        F[i,0] = F[i-1,0] + 2

    for j in range(1,len(t)+1):
        F[0,j] = F[0,j-1] + 2

    for i in trange(1,len(s)+1):
        for j in range(1,len(t)+1):
            F[i,j] = min(F[i-1,j]+2,F[i,j-1]+2,F[i-1,j-1]+(1-int(s[i-1]==t[j-1])))
    return F[-1,-1]
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In [3]: c_s_t = cost(s,t)
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In [4]: c_s_t/len(s)
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Out[4]: 0.0223
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These two sequences are serving the same function