

1. a.)  $\{ \langle n \rangle \# \langle p \rangle \# \langle q \rangle : n = p \times q \}$ , where  $\langle n \rangle$  is product of two prime numbers and  $\#$  is the delimiter.

b.)  $\{ \langle n \rangle : n = p \times q \text{ for some primes } q \text{ and } p \}$  where  $\langle n \rangle$  is the product of two prime numbers.

c.)  $\{ \langle A \rangle \# w : A \text{ accept } w \}$ , where  $\langle A \rangle$  is the string encoding of NFA  $A$  and  $\#$  is the delimiter.

d.)  $\{ \langle A \rangle : A \text{ accepts } w \text{ for some } w \}$ , where  $\langle A \rangle$  is the string encoding of NFA  $A$



2.

$$2.) \quad a.) \quad F(n) = 2n^2 - 18n$$

Proof:

for  $O(n)^3$ :

let  $C = 3$ .

$$\lim_{n \rightarrow \infty} \frac{2n^3 - 18n}{3n^3}$$

$$\Rightarrow \lim_{n \rightarrow \infty} \frac{2}{3} = \lim_{n \rightarrow \infty} \frac{2}{3} - \lim_{n \rightarrow \infty} \frac{6}{3n^2} = \frac{2}{3}$$

for  $O(n^4)$

let  $C = 1$

$$\lim_{n \rightarrow \infty} \frac{2n^3 - 18n}{1n^4} = 0 < 1$$

for  $O(n^2 \log n)$

A  $C > 0$  cannot be found since all 'n' goes

to  $\infty$ ,  $\lim_{n \rightarrow \infty} \frac{2n^3 - 18n}{(n^2 \log n)}$  will also go to  $\infty$ .

b.) for  $3n^2 2^{2n}$  is  $2^{o(n)}$

let  $c = 3$ .

$$\lim_{n \rightarrow \infty} \frac{3n^2 2^{2n}}{2^{3n}}$$

$$\Rightarrow \lim_{n \rightarrow \infty} \frac{3n^2}{2^n} = 0 < 1$$

3.

- A. An algorithm that compass protein structures using shape analysis and 3D coordinates of atoms in the protein to find differences in protein structures that are infected or find early stages of a disease to treat it beforehand. Comparing protein structures is crucial for in silico functional analysis of unknown proteins. It is also used to comprehend the evolutionary connections between proteins.
- B. Text string is not the best option for input the data of the protein structures since the whole algorithm is based on comparisons, the best input would be graphs or jpeg. But in these both options I would choose graphs since they would have the best outcomes for the comparison of the protein structures and analysis of proteins.
- C. Make two protein structures with one that has 100% accuracy and other one with 60-70% comparison, once the whole algorithm is done you will have a result of how much percentage of the protein are completely damaged and how much of it is getting infected and how much percentage of them are not infected at all, this information can be used to understand the situation and better treat the disease