

' Assignment-02 '

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Ans. to the question no-01

(a)

* Encoding scheme:

Each chromosomes can be represented as string of n integers, each between 1 to n , in a n -length array. In the array, the index of the array means the column and the value on string in that index represents the row.

For example, for a 4-queen problem,

row	→	2	1	4	3
column	→	1	2	3	4

1st index has value 2. This means the queen is in the 1st column at 2nd row. Similarly for others.

4			②
3			②
2	②		
1	②		

(b)

*Fitness function:

Fitness is calculated based on the number of non-attacking pairs. The maximum score for a n-queen problem is

$$\text{maxPairs} = nC_2$$

Then, we have to find the attacking pairs. There are 3 type of conflict that can happen.

1) row-conflict: The value of the array represents where in the row the queen is placed. If we found multiple queen in the same row, it means there's conflict. For every conflicting row, we take the total row-conflicting pair.

2) column-wise-conflict: By our encoding scheme there will not be any column-wise conflict.

3) Diagonal conflict: There are two diagonals. One is major and another is minor. For major diagonal, if two queens Q_1 and Q_2 share same diagonal, if,

$$Q_1[\text{column}] - Q_1[\text{row}] = |Q_2[\text{column}] - Q_2[\text{row}]|$$

for minor diagonal,

$$Q_1[\text{column}] + Q_1[\text{row}] = Q_2[\text{column}] + Q_2[\text{row}]$$

Now,

$$\text{no. of non-attacking pairs} = \left(\begin{array}{l} \text{no. of max possible} \\ \text{non-attacking pairs} \end{array} \right) - \left(\begin{array}{l} \text{No. of total} \\ \text{attacking pairs} \end{array} \right)$$

Hence, the fitness function,

$$\boxed{\text{fitness} = \text{no. of non-attacking pairs}}$$

(Ans.)

Ans. to the question no-02

(a)

* Encoding Scheme:

Each chromosomes can be represented as a string of bits in an N-length array where a bit in the array represents the group it belongs to. If the bit value is 0 it belongs to group X, and if the bit value is 1, it belongs to group Y.

0 → 'X'

1 → 'Y'

And, the index of the array represents the elements. For example, the i^{th} index represents the i^{th} element.

For example,

(b)

A fitness function:



The fitness function can be calculated by the sum of similarity scores between elements in different subset and subtracting it from the summation of the similarity scores of pairs in the same subset. So,

$$\text{Fitness} = \sum \text{similarity scores between elements in different subset} - \sum \text{similarity scores between elements in the same subset}$$

Ans. to the question no-03

(a)

A Encoding scheme:

Each chromosome can be represented as a permutation of vertex in an array where every value of the array is unique to each other, and the value represents the vertex. For example,

A	C	B	F	D
1	2	3	4	5

(b)

* Fitness function:

The fitness function can be calculated using inverse of total cost.

The total cost is calculated from the array,

$$\text{total cost} = \left(\sum_{i=1}^{N-1} \text{weight of vertex}(x_i, x_{i+1}) \right) + \left(\begin{array}{l} \text{weight of} \\ \text{vertex } 1 \\ \text{and } N. \end{array} \right)$$

here, N is the length of the array and x_i is the vertex in the i th index.

finally, fitness function,

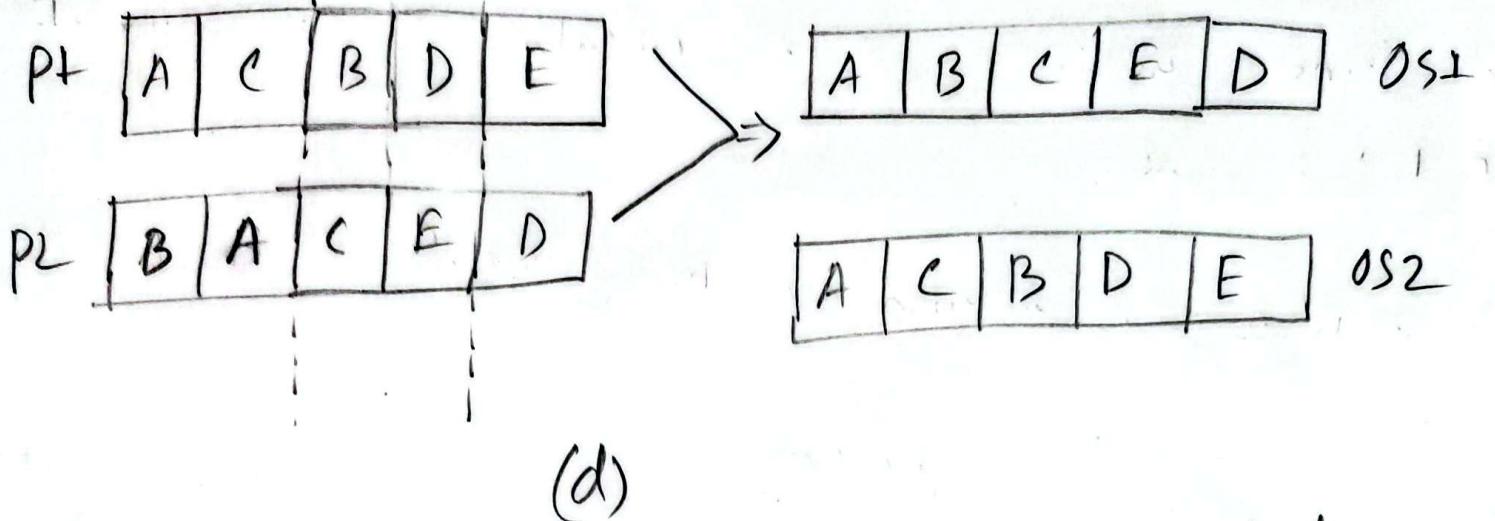
$$\text{fitness} = \frac{1}{\text{total cost}}$$

(c)

We can use 'order crossover' to perform crossover.

In order crossover, we choose two random point and swap their values. Then go through the array and check if there's any value that's not in the array.

For example,

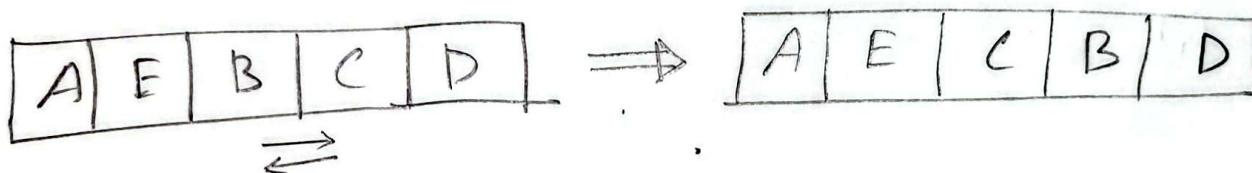


(d)

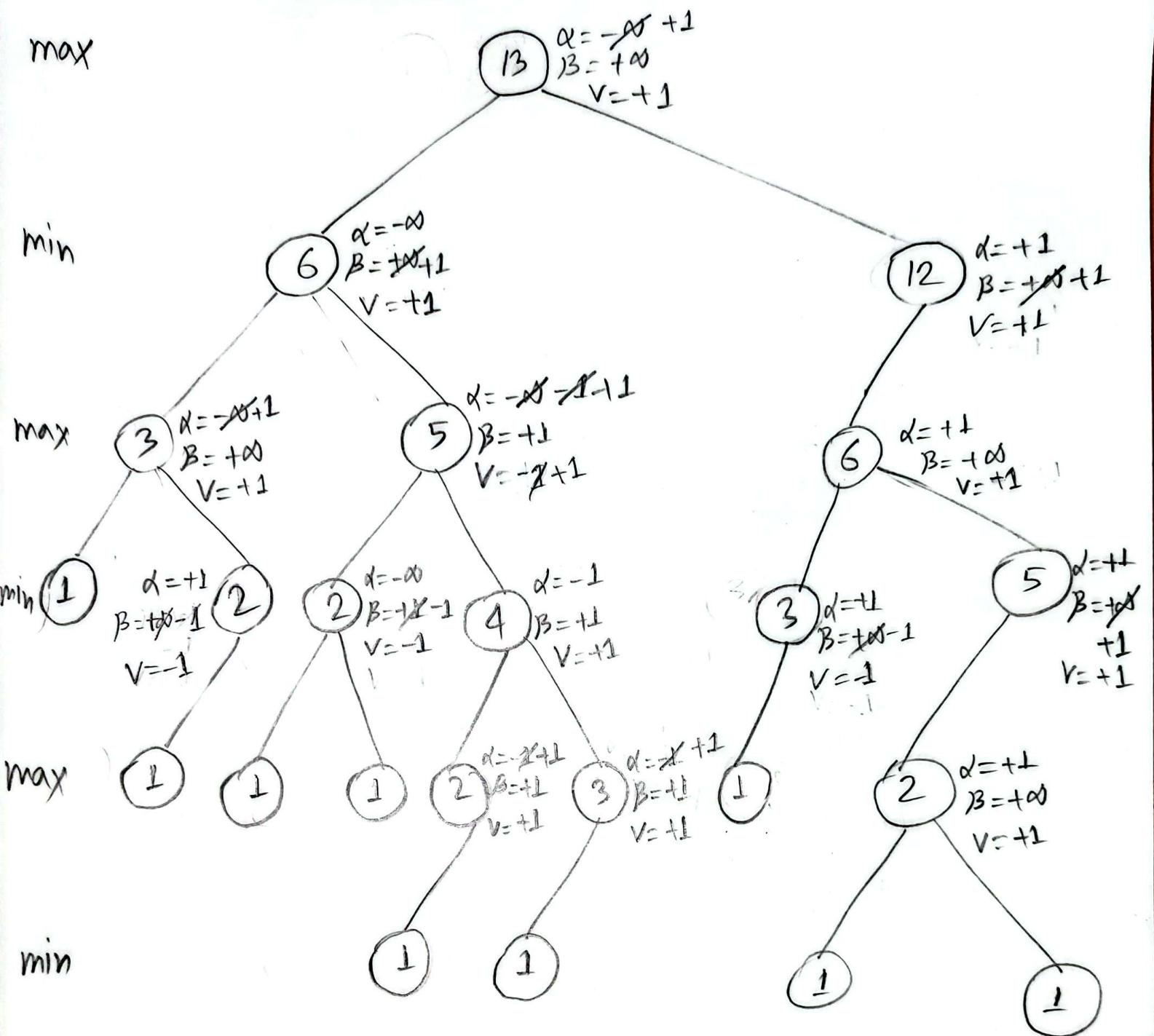
We can use 'swap mutation' to perform mutation.

In swap mutation, we choose two random points and swap their values.

For example, if we choose index 2 and 3 (0-based)



Ans. to the que. no- 04



This is the tree generated from the mini-max algorithm with alpha-beta pruning, without pruned branches. The next move should be left-child or $\lfloor N/2 \rfloor$ as it returns +1, so a win can be forced.

(Ans.)