

For the 3 fitness functions shown in the slides, the first one is the most common one to implement. It calculates the summation of all differences between the target DNA and the competing DNA and use that value as a base for the fitness consideration. In this case, if the competing DNA has more different genes when compared to the target DNA, the fitness score will be lower, because the final fitness score is $1/\text{total fitness value}$.

The second one will most likely show the difference between the target DNA and the competing DNA more obviously. Since the difference between the target DNA character and the competing DNA character could be minute, this fitness function enlarges the difference by squaring the differences. In that case, even if the competing DNA has only one gene different from the target DNA, it will be readily visible.

The third fitness function is likely a different version of the first fitness function. In the first fitness function, the immediate differences between the target DNA and the competing DNA are used as calculation base, which means the result varies. The differences between characters from the 2 DNAs won't be the same, the final fitness score will change from time to time. In the third function however, the numerical differences between the DNA characters are not considered, but rather the "existence of difference". If 2 characters are different, a value of 1 is added, no matter what the difference between them is. In this case, the final fitness score will stay more consistent even when the differences are large.

Program result:

When using the first fitness function, penalty ranges about 200 – 350

When using the second fitness function, penalty ranges from 8000-14000

When using the third fitness function, penalty ranges from 8 – 150

All fitness functions were experimented with more than 10 runs.

In that case, the third fitness function would be the best to implement.

It shows fairly obvious changes and the values won't go as crazy as the second one.