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**CBIO – EX1  
Sequences Alignment**

1. Let two DNA squences of length and two indices . Let an arbitrary column in the alignment, there are 3 possibilities for it:
   1. of form – the column consists of two nucleotides.
   2. of form – the column consists of nucleotide in and a gap in .
   3. of form – the column consists of nucleotide in and a gap in .

Since there is at least arbitrary in an alignment and there is 3 options for each one, combinatorically there are more than possible alignments.

1. Let two DNA squences of length and are the score and trace tables as they are in the original algorithm. The entry contains the best alignment for and where .

We initialize as a matrix of zeros and override the values of the first raw and column in the following way:

We use the following recursion rule to fill the table:

Where is the score matrix of two nucleotides (and not nucleotide with gap).

The table and the final alignment are obtained the same way as in the original algorithm, starting with the entry in and traversing till .