Bioinformatics II: Alignment Dynamic Programming

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Before we start, lets remember!

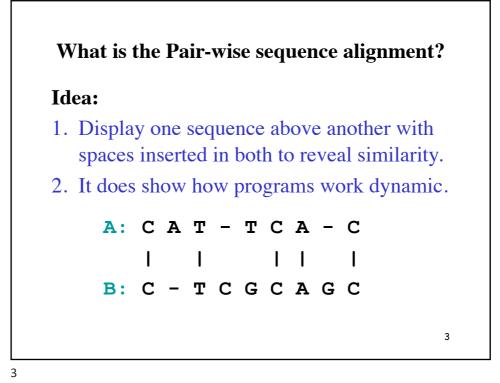
• How many types of changes which can present between two sequence alignment?

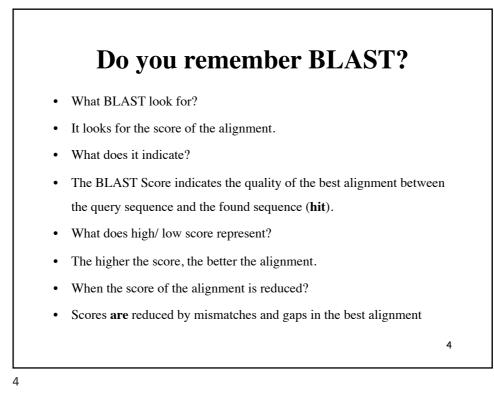
- 1. A mutation that replace one character with other.
- 2. An insertion that adds one or more positions.
- 3. A deletion that deletes one or more positions.

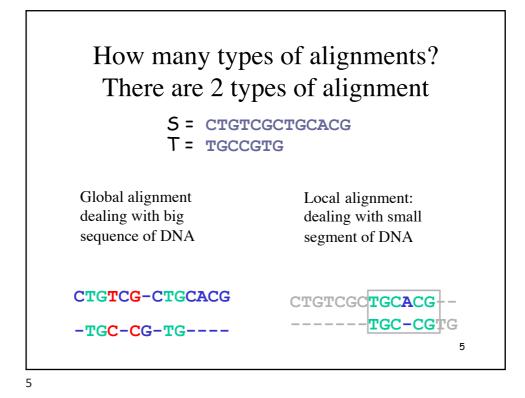
2

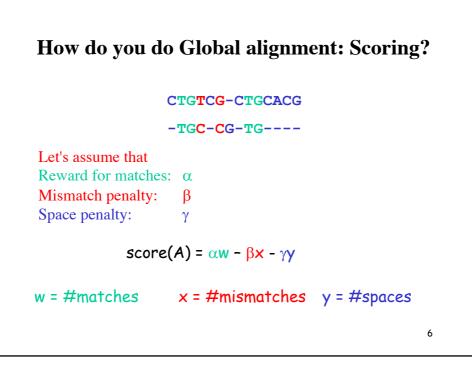
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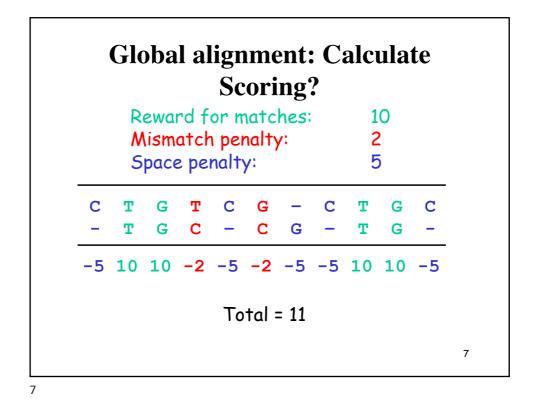
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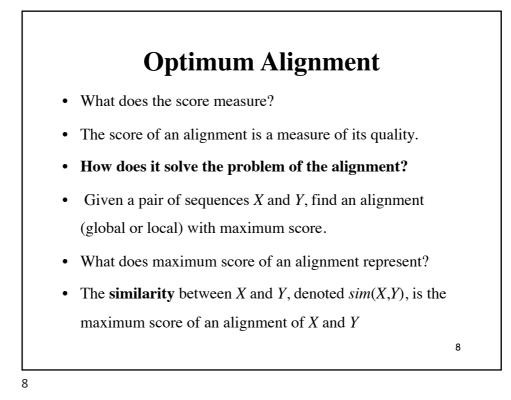


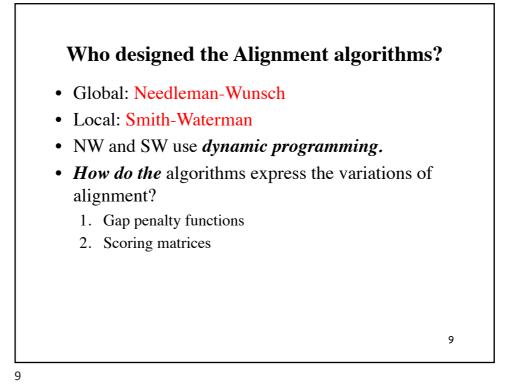










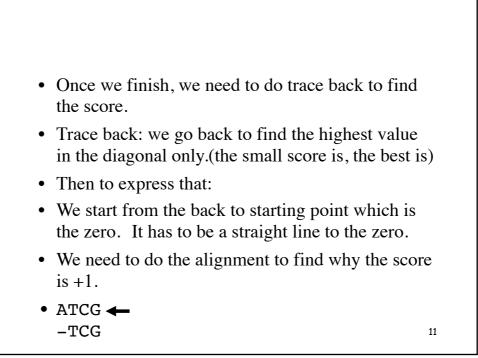


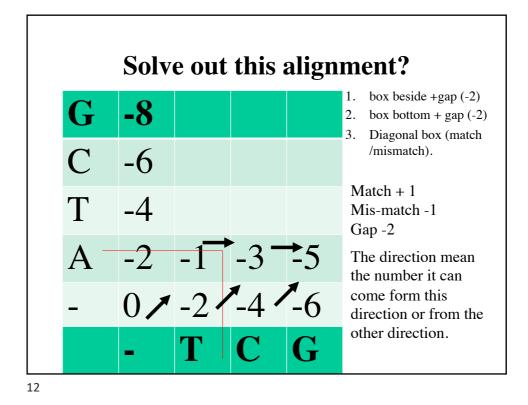
Follow the role to find the Global alignment in two sequencing?

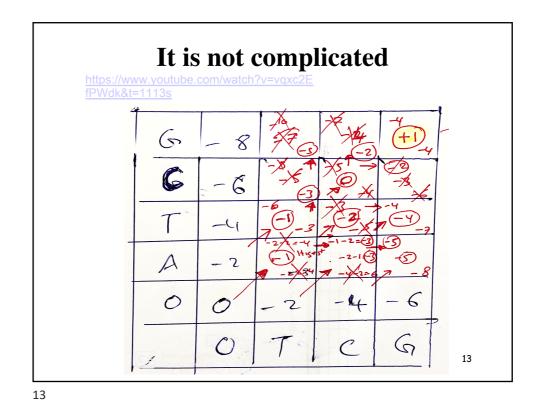
Two seq. ATCG and TCG? Scoring ?

- Match 2
- Mis-match -2
- Gap -2

- Rules:
- 1. Put the gap in the first.
- 2. The higher is score the best because it shows the maximum alignment.
- 3. The first box always zero.
- 4. Add the initial column and row by adding gap value -2.
- 5. To calculate the score, it will be the highest value in the diagonal.







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