Algorithms for Bioinformatics

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What is the role of algorithms in Biology/Bioinformatics? Procedure that solves a problem

1. solve pratical problems.
2. model a phenomenom + simulation.
3. consider the biological system a computational device.

Types of problem we will work on

1. strings: sequences on alphabet
2. alignment

1 Turing Machines

simple explanation of turing machines
`turing.org.uk/book/update/tmjavar.html`

2 Problems

2.1 Alignment

DNA: AGTC

1. Compare sequences for different *organism*.
2. Align them with a **query**, to find the active regions (or active parts) relevant for this sequence. (example: **BLAST**)
3. Global alignment (pairwise alignment): include the sequences completely.
4. Local alignment (pairwise alignment): include the sequence partially.

1st: `ACGTCCCATG`
2nd: `TCGCCCTG`
$global \rightarrow 0CG1CCC2TG$ 0==mismatch 1==insertion 2==deletion
$local \rightarrow CGCCCTG$ i'm happy with this and i dont care about what is not aligned.
The algorithm used maximize a **score**.

How to define the score?

1. insertion
2. deletion
3. mismatch
4. match

with this we already moved to the **model a phenomenom** part. The actual number differ wrt the phenomenom and wrt the time it happens (the first insertion is different than the second). This issue of define the score lead us to the definition of **score Matrices**