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## Hamming in Scala

Readme (readme)

Test Suite (../hamming)

## Hamming

Write a program that can calculate the Hamming difference between two DNA strands.

A mutation is simply a mistake that occurs during the creation or copying of a nucleic acid, in particular DNA. Because nucleic acids are vital to cellular functions, mutations tend to cause a ripple effect throughout the cell. Although mutations are technically mistakes, a very rare mutation may equip the cell with a beneficial attribute. In fact, the macro effects of evolution are attributable by the accumulated result of beneficial microscopic mutations over many generations.

The simplest and most common type of nucleic acid mutation is a point mutation, which replaces one base with another at a single nucleotide.

By counting the number of differences between two homologous DNA strands taken from different genomes with a common ancestor, we get a measure of the minimum number of point mutations that could have occurred on the evolutionary path between the two strands.

This is called the 'Hamming distance'.

It is found by comparing two DNA strands and counting how many of the nucleotides are different from their equivalent in the other string.

- 1 GAGCCTACTAACGGGAT
- 2 CATCGTAATGACGGCCT
- 3 ^ ^ ^ ^ ^ ^ ^ ^

The Hamming distance between these two DNA strands is 7.

## Implementation notes

The Hamming distance is only defined for sequences of equal length. This means that based on the definition, each language could deal with getting sequences of equal length differently.

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The Scala exercises assume an SBT project scheme. The exercise solution source should be placed within the exercise directory/src/main/scala. The exercise unit tests can be found within the exercise directory/src/test/scala.

To run the tests simply run the command sbt test in the exercise directory.

For more detailed info about the Scala track see the help page (http://help.exercism.io/getting-started-with-scala.html).

## Source

The Calculating Point Mutations problem at Rosalind view source (http://rosalind.info/problems/hamm/)



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