

# About.txt

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*           Summer Training 2014
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* Project: Implementation of Bioinformatics Algorithms
*           to Compare DNA Sequences in Java
*           (Using Dynamic Programming)
*
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*           Project Description
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The Project is a compilation of three DNA comparison techniques:

## 1) Longest Common Subsequence --

This comparison technique is based on finding out the longest set of characters occuring in order (not necessarily adjacent) in both the input strings.

Example:

ATCTGAT and TGCATA

The longest possible subsequence is TCTA.

```
A T - C - T G A T
- T G C A T - A -
```

## 2) Global Sequence Alignment --

This comparison technique is based on finding the overall best alignment of the input strings based on the common characters (in order).

Example:

ACGC and GACTAC

The best global alignment is along characters ACGC.

```
-ACG-C   -AC-GC
GACTAC   GACTAC
```

## 3) Local Sequence Alignment --

This technique has the most practical application as many researches require the comparison of parts of DNA sequences to find common traits. In

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this the best and the longest local alignment of characters in the strings is sought.

Example:

CGTGAATTCAT and GACTTAC

Alignment:

GAATTCA GAATT-C  
GACTT-A GACTTAC

```
/******  
* NOTE: The '-' symbol in the above string resembles *  
* 'character insertion' while that in the lower *  
* string resembles 'character deletion' *  
*****/
```