**Project Report**

**on**

**Implementation of Waterman Algorithm In Python**

Department of Computer Science and Engineering

(2013-15)



Submitted To: Submitted By:

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***DECLARATION***

We hereby declare that this mini project titled **IMPLEMENTATION OF WATERMAN ALGORITHM IN PYTHON** submitted for the partial fulfilment of the requirement for the award of degree in **Master OF TECHNOLOGY IN COMPUTER SCIENCE & ENGINEERING** at GALGOTIAS COLLEGE OF ENGINEERING & TECHNOLOGY GR. NOIDA is an authentic record of our work carried out under the guidance of Mr. Manish Kumar Singh.

Signature:

Name :

Roll No. :

Date :

This is to certify that the above statement made by the candidate is correct to the best of my knowledge.

**Signature of Supervisor**

**(Mr. Manish Kumar Singh)**

**(Assistant Professor)**

**Date:**

III

***CERTIFICATE***

This to certify that this report titled **“IMPLEMENTATION OF WATERMAN ALGORITHM in Python”** embodies the original and has not been submitted for the award of any other degree, work done by ANIL KUMAR GUPTA for partial fulfilment of the requirement for the award of degree in **MASTER OF TECHNOLOGY IN** **COMPUTER SCIENCE & ENGINEERING** at GALGOTIAS COLLEGE OF ENGINEERING & TECHNOLOGY GR. NOIDA.

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**IV**

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***ABSTRACT***

**IMPLEMENTATION OF WATERMAN ALGORITHM IN PYTHON** is a local [sequence alignment](http://en.wikipedia.org/wiki/Sequence_alignment); that is, for determining similar regions between two strings or [nucleotide](http://en.wikipedia.org/wiki/Nucleotide_sequences) or [protein sequences](http://en.wikipedia.org/wiki/Protein_sequence). Instead of looking at the [total sequence](http://en.wikipedia.org/w/index.php?title=Global_sequence_alignment&action=edit&redlink=1), the Smith–Waterman algorithm compares segments of all possible lengths and [optimizes](http://en.wikipedia.org/wiki/Mathematical_optimization) the similarity measure.

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***TECHNOLOGY USED***

***OPERATING SYSTEM -*** WINDOW-7

***TOOL***- PYTHON 3.3

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