

**DESIGN AND ANALYSIS OF CONSTRUCTION AND
RECOMBINATION MODULE USING IDURY-WATERMAN
ALGORITHM FOR FRAGMENT ASSEMBLY APPLICATION**

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UNIVERSITI TEKNOLOGI MARA



HAFIFI BIN MOHD RAFI

FACULTY OF ELECTRICAL ENGINEERING

UNIVERSITI TEKNOLOGI MARA (UiTM)

SHAH ALAM

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Hafifi Bin Mohd Rafi
(2008562065)

ABSTRACT

There is several algorithms use in sequencing of DNA fragment. This paper presents a study on design and analysis of construction and recombination module using Idury-Waterman algorithm and fragment assembly application using Verilog. This algorithm will be implemented on the Xilinx ISE 12.4 software to model the sequence and optimize the last sequence of DNA. The DNA sequences will be overlapped in every fragment. Combination of Eulerian path and de Bruijn graph concept will guide the overlaps process between the DNA sequences. Step by step on how the fragment move and overlap to each other. The result of the proposed algorithm, verifies the validity of proposed algorithm.

TABLE OF CONTENTS

CHAPTER	LIST OF TITLE	PAGE
	TITLE	i
	DECLARATION	iii
	ACKNOWLEDGEMENT	iv
	ABSTRACT	v
	LIST OF FIGURE	vi
	LIST OF TABLE	xi
	LIST OF ABBREVIATION	xii
1	INTRODUCTION	1
	1.1 Introduction	1
	1.1.1 Shotgun Sequencing Fragment Assembly	3
	1.2 Objectives of Project	4
	1.3 The DNA Fragment Assembly Problem	4
	1.4 Scope Of Project	5
	1.5 Significant of Project	5

CHAPTER 1

INTRODUCTION

1.1 INTRODUCTION

Since the advent of rapid DNA sequencing methods in 1976 [1], scientist has had the problem to inferring DNA sequences from sequenced fragment. Shotgun sequencing is a well-established biological and computational method used in practice. Many conventional algorithms for shotgun sequencing are based on the notion of pair wise fragment overlap. While shotgun sequencing infers a DNA sequence given the sequences overlapping fragments, a recent and complementary method, called sequencing by hybridization (SBH) [2], infers a DNA sequence given the set of oligomers that represents all sub words of some fixed length, k . The study of DNA sequence, can analysis of construct and recombination module using Idury-Waterman algorithm for fragment assembly application.

Idury-Waterman algorithms are a fairly new, non-analytical optimization technique that can give solutions to hard optimization problems that traditional techniques fail to solve. It is based on a simulated evolution, where processes such as crossover, mutation and survival of the fittest help to “evolve” good solutions to a given problem. In this study, it shows how Idury-Waterman algorithms [2] can be used to optimize DNA sequence. As an important aspect of bioinformatics, the main problem of Genome Sequencing is DNA Fragment Assembly. The capability of algorithm in assembly affects the quality and efficiency of sequencing directly.