THESIS NAME

A Thesis

Presented in Partial Fulfillment of the Requirements for the Degree of Master of Science in the Graduate School of Nile University

By

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 $\mathrm{June},\,2020$

Nile University

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Abstract

Abstract goes here ...

To my beloved family

ACKNOWLEDGMENTS

ACKNOWLEDGMENTS goes here \dots

Contents

		Page
Abs	tract	. iv
Ded	ication	. v
Ack	nowledgments	. vi
List	of Tables	. ix
List	of Figures	. X
Cha	pters:	
1.	Introduction	. 1
	1.1 Motivation	
	1.3 Thesis Outline and Summary of Contributions	
2.	Literature Survey	. 3
	2.1 Introduction 2.2 Section 1 2.2.1 Sub-Section 1	. 3
3.	Methodology	. 5
4.	Results and Discussions	. 6
	4.1 Section	
5.	Conclusions and Future work	. 7
	5.1 Conclusion	
6.	Proof of equation	. 8

7.	Appendi	x B Tit	le		 	 	 	 	 	•	 			 9
Bibli	ography			• • •	 	 	 	 	 		 	 		 10

List of Tables

Tab	ble			Pa	ge
4.1	Table one caption	 	 		6

List of Figures

Figu	ıre													Pa	ge
1.1	Chapter 1 figure 1 caption	 	 				•		 •				 •		1

LIST OF ABBREVIATIONS

Symbol	Definition
cDBG	Combact de bruign graph
DAG	Directed asyclic graph
GTF	Gene transfer format

Introduction

1.1 Motivation

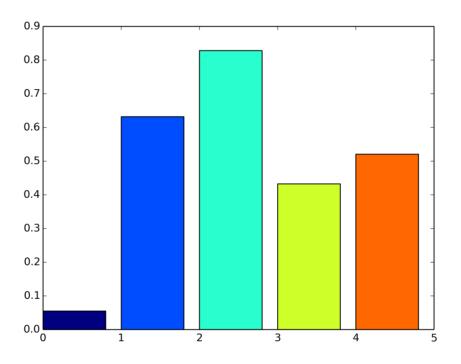


Figure 1.1: Chapter 1 figure 1 caption

1.2 Problem Statement

Lorem Ipsum is simply dummy text of the printing and typesetting industry. Lorem Ipsum has been the industry's standard dummy text ever since the 1500s, when an unknown printer took a galley of type and scrambled it to make a type specimen book. It has survived not only five centuries, but also the leap into electronic typesetting, remaining essentially unchanged. It was popularised in the 1960s with the release of Letraset sheets containing Lorem Ipsum passages, and more recently with desktop publishing software like Aldus PageMaker including versions of Lorem Ipsum.

1.3 Thesis Outline and Summary of Contributions

Literature Survey

2.1 Introduction

Lorem Ipsum is simply dummy text of the printing and typesetting industry. Lorem Ipsum has been the industry's standard dummy text ever since the 1500s, when an unknown printer took a galley of type and scrambled it to make a type specimen book. It has survived not only five centuries, but also the leap into electronic typesetting, remaining essentially unchanged. It was popularised in the 1960s with the release of Letraset sheets containing Lorem Ipsum passages, and more recently with desktop publishing software like Aldus PageMaker including versions of Lorem Ipsum. [?].

Protein alignment is commonly used for studying distantly related species as proteins are well-conserved over long evolutionary periods. A good example is the rapidly evolved species like bacteria so that it will fit for homologs detection due to the consistency of amino acids discarding the effect of DNA synonymous mutations [?]. On the other hand, nucleotides alignment is better to use in studying the same or closely related species for overcoming the effect of the mutation on amino acids, like frame-shifting, insertion-deletion pairs, and replacement events, which may lead to proteins change. Furthermore, it is possible to infer nucleotides sequences that follow a specific convergence distribution [?], also studying the non-coding sequences and measuring the evolutionary distance cannot be done using proteins.

2.2 Section 1

Local and global alignments are the two primary methods that all alignment tools were built on top of them in order to control the alignment completeness. In the local alignment, we align two sequences that may be similar or divergent to find the highest similar local sub-sequence matches; this is applicable even when dealing with large sequences. Whereas the global sequence alignment is very much appropriate when aligning closely-related sequences with the same or nearly equal lengths as the sequence-alignment is performed from the sequence start position then extends until finding the maximum match. Two primary strategies for sequence-alignment were developed, pairwise strategy of sequence alignment (PSA), and the multiple sequence alignment (MSA). PSA aligns 2 sequences in every single process, while multiple sequences can be aligned using MSA. MSA outperformed PSA when it came to aligning multiple sequences of families for providing insightful information from the biology perspective. Also, MSA is mandatory in comparative studies to identify and quantify conserved regions in whole sequence family as well as for the estimation of evolutionary distance between sequences and profiling the ancestral sequences [?].

2.2.1 Sub-Section 1

Lorem Ipsum is simply dummy text of the printing and typesetting industry. Lorem Ipsum has been the industry's standard dummy text ever since the 1500s, when an unknown printer took a galley of type and scrambled it to make a type specimen book. It has survived not only five centuries, but also the leap into electronic typesetting, remaining essentially unchanged. It was popularised in the 1960s with the release of Letraset sheets containing Lorem Ipsum passages, and more recently with desktop publishing software like Aldus PageMaker including versions of Lorem Ipsum.

2.2.1.1 Sub-Sub-Section 1

Methodology

Results and Discussions

4.1 Section

4.1.1 Subsection

4.1.1.1 Sub Sub section

Col 1	Col 2	Col 3
1	2	3
1	1	2

Table 4.1: Table one caption

Conclusions and Future work

5.1 Conclusion

Lorem Ipsum is simply dummy text of the printing and typesetting industry. Lorem Ipsum has been the industry's standard dummy text ever since the 1500s, when an unknown printer took a galley of type and scrambled it to make a type specimen book. It has survived not only five centuries, but also the leap into electronic typesetting, remaining essentially unchanged. It was popularised in the 1960s with the release of Letraset sheets containing Lorem Ipsum passages, and more recently with desktop publishing software like Aldus PageMaker including versions of Lorem Ipsum.

5.2 Future directions

Proof of equation

Appendix A goes here...

Appendix B Title

Bibliography