EVOLUTIONARY TRACE ANALYSIS OF
A ZINC METALLOENZYME – ALCOHOL DEHYDROGENASE

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2012
EVOLUTIONARY TRACE ANALYSIS OF
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SUBMITTED TO
INSTITUTE OF BIOLOGICAL SCIENCES
FACULTY OF SCIENCE
UNIVERSITY OF MALAYA

IN PARTIAL FULFILLMENT
OF THE REQUIREMENTS FOR
THE DEGREE OF MASTER OF BIOINFORMATICS
2012
ACKNOWLEDGEMENTS

Although this is a personal project paper, the success of this research has been contributed by the pool of energy and ideas from various organizations. I wish to dedicate this research especially to my parents Mr Abdul Jamil Md Ali and Madam Juriah Ismail who have been supportive in giving me the motivation and drive to complete this research.

I convey my deepest appreciation to my supervisor Dr. Saharuddin Mohamad who never gave up on me and was always there to assist me in my research. In addition to that, I personally thank all my lecturers for coaching me throughout my learning escapade in the Bionformatics and Biocomputing Division, Institute of Biological Sciences, University of Malaya.

A heartfelt thank you to the laboratory staff who have given their helping hands in this research. I convey my deepest gratitude to my course mates for their out of the world guidance and knowledge sharing sessions we had. Finally, I wish to thank everyone else including family and friends for their modest assistance.
ABSTRACT

Molecular evolution is the study of the evolutionary patterns and processes of nucleic acids and proteins to understand the phylogenetics, population genetics, biogeography, and other areas of research at the DNA, RNA and protein levels of the biological organization. Evolutionary trace method is a technique to identify evolutionary important residues and their positions in a group of protein alignment. In this study, the zinc metalloenzyme alcohol dehydrogenases (ADH) of the eukaryote Mus musculus (mouse) was used as the sequence of interest against 48 other bacteria species. BLAST was used to identify the 48 bacteria species with the closest ADH sequences to the Mus musculus ADH. Multiple sequences alignment was done in order to construct the phylogenetic tree to view the evolutionary relationship of the sequences. Partitions on the Cladogram were created to trace back to where the organisms branch off pointing to a common ancestor. Each partition was then split into smaller groups to identify similar species in the family. 29.8% of the residues in the first partition were fully conserved whilst another 47.8% of the active site residues were fully conserved.
ABSTRAK

Evolusi molekular ialah kajian corak-corak bersifat evolusi dan pemahaman proses-proses asid nukleik dan protein melalui kajian filogenetik, genetik populasi, biogeografi dan lain-lain penyelidikan di tahap DNA, RNA dan protein organisasi biologi. Kaedah jejak evolusi (Evolutionary Trace Method) ialah satu teknik mengenal pasti jejak-jejak penting bersifat evolusi dan kedudukan amino-amino asid dalam jajaran protein. Dalam kajian ini, zink enzim-metal alcohol dehydrogenase (ADH) eukariot Mus musculus (tikus) digunakan sebagai jujukan rujukan kepada 48 spesis-spesis bakteria. Program BLAST digunakan bagi mengenal pasti 48 spesis-spesis bakteria yang mempunyai jujukan-jujukan ADH terhampir dengan Mus musculus. Jujukan berbilang penjajaran (Multiple sequences alignment) dilakukan bagi membina pokok filogenetik untuk melihat hubungan evolusi antara jujukan-jujukan. Segmentasi melalui Kladogram diwujudkan bagi mengesan nenek moyang asal yang sama organisma-organisma sebelum berpecah kepada ranting. Setiap segmen dibahagikan kepada kumpulan-kumpulan yang lebih kecil bagi mengenal pasti spesis-spesis yang serupa dalam keluarga itu. 29.8% residu dalam segmen pertama adalah sepenuhnya terpelihara (fully conserved) manakala satu lagi 47.8% residu tapak aktif sepenuhnya terpelihara (fully conserved).
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Name of Degree: MASTER OF BIOINFORMATICS

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