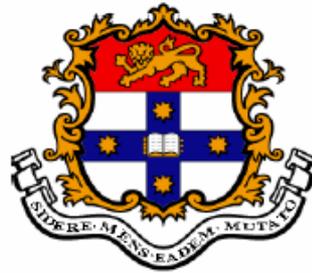


A Novel Quartet-Based Method for Inferring Evolutionary Trees from Molecular Data



A thesis submitted in fulfilment of the requirements for the
degree of Doctor of Philosophy

School of Information Technology
Faculty of Engineering and Information Technology

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Science is nothing but perception
Plato (Ancient Greek
Philosopher
428-348 BC)

To my mother

To my father

أهداء الى امي وابي

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Finally, I would like to thanks my parent for their ever lasting support of my work and study.

Declaration

I, Monther Tarawneh, do hereby declare that this submission is my own work and that, to the best of my knowledge and belief, it contains no material previously published or written by another person, nor material which to a substantial extent has been excepted for the award of any degree or diploma of a university or other institute of higher learning, except where due acknowledgments were made in the text.

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Monther A Tarawneh

Abstract

Molecular Evolution is the key to explain the divergence of species and the origin of life on earth. The main task in the study of molecular evolution is the reconstruction of evolutionary trees from sequences data of the current species.

This thesis introduces a novel algorithm for inferring evolutionary trees from genetic data using quartet-based approach. The new method recursively merges sub-trees based on a global statistical provided by the global quartet weight matrix. The quartet weights can be computed using several methods. Since the quartet weights computation is the most expensive procedure in this approach, the new method enables the parallel inference of large evolutionary trees.

Several techniques developed to deal with quartets inaccuracies. In addition, the new method we developed is flexible in such a way that can combine morphological and molecular phylogenetic analyses to yield more accurate trees. Also, we introduce the concept of critical point where more than one possible merges are possible for the same sub-tree. The critical point concept can provide information about the relationships between species in more details and show how close they are. This enables us to detect other reasonable trees.

We evaluated the algorithm on both synthetic and real data sets. Experimental results showed that the new method achieved significantly better accuracy in comparison with existing methods.

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