

Universiti Teknologi MARA

**Comparative Revision of Artificial Intelligent
Methods for Discovering Gene Expression**

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DECLARATION

I certify that this thesis and the system to which it refers, are the product of my own individual work, and that any ideas from the work of other people, published or otherwise, are fully acknowledged in accordance with the standard referencing practices of the discipline. I also acknowledge the helpful guidance and support of my supervisor, Pn.Shuzlina bt. Abd Rahman.

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ABSTRACT

Gene expression analysis is one of the studies in bioinformatics. There are many methods and approaches use in gene expression analysis. Some methods that are currently being used, such as fuzzy ART, neural network, and Bayesian method were used in gene expression analysis. The problem that occurred in supervised learning is that the output and error rates that been provided were momentous. The reason in conducting this research is to determine the best methods, between two approaches for gene expression analysis. For this research, the approach used is supervised learning and the methods that were used are multi layer feedforward and k-Nearest Neighbour. The methodology that will be use for this research are knowledge acquisition, implementation that consists of three phase; experiment, result and analysis, experiments and observation, and evaluation and findings. After a series of experiments, the multi layer feedforward is the better method in determining gene expression especially protein genes rather than k-Nearest Neighbour. It is because the accuracy of the output is more precise and can be used for further analysis. The presentation of multilayer feedforward is clear and well-defined. The accuracy of the results is important for usage of others. This research can be a good reference for the advancement and development of gene expression analysis.

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