Abstract

Classification of DNA repair genes into ageing and non-ageing is a vital process to identify faulty genes. Classifying genes into ageing and non-ageing human genome ranges over ten thousand. The ratio of ageing genes in the human genome is very less. There is a need for classifying ageing genes accurately in order to understand the complex processes occurring in living organisms. Data mining approach is routinely applied to classify DNA repair genes using various characteristics and feature. This paper proposes to build classification models that allow us to discriminate between ageing-related and non-ageing related DNA repair genes, in order to enhance value their different properties of genes classification performance should be evaluated by applying different kinds of classification algorithms like pruning, multiperceptron and Logistics. It will helpful for biomedical researchers, gene analyzer, patients and different kinds of end user.

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Index Terms

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