Shahizan 2020

#Gene\_selection #cancer\_microarray\_data #cuckoo\_search #evolutionary\_operators #Machine\_learning

# Gene Selection Using Hybrid Multi-Objective Cuckoo Search Algorithm With Evolutionary Operators for Cancer Microarray Data

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Summary

The paper’s innovative approach to gene selection from cancer microarray data using a hybrid multi-objective cuckoo search algorithm is quite intriguing. The use of bio-inspired algorithms in solving complex problems, such as selecting relevant genes from high-dimensional and noisy data sets, showcases the potential of computational intelligence in advancing healthcare. The successful application of this algorithm, as demonstrated by the improved results in the study, could pave the way for more efficient and accurate diagnostic tools in the future.



Quotable

The hybrid multi-objective cuckoo search algorithm presented in this paper demonstrates the potential of computational intelligence in advancing healthcare, offering an innovative approach to gene selection from cancer microarray data. By addressing the challenge of selecting relevant genes from high-dimensional and noisy data sets, it paves the way for more efficient and accurate diagnostic tools in the future.

### Aim of Paper

The aim of this paper is to present a novel gene selection algorithm for cancer microarray data using a hybrid multi-objective cuckoo search with evolutionary operators. The paper describes the motivation, methodology, and results of the proposed algorithm, and compares its performance with other existing methods. The paper also discusses the implications and limitations of the algorithm, and suggests directions for future research.

### Key insights

* The web page is a research paper on **gene selection using hybrid multi-objective cuckoo search algorithm with evolutionary operators for cancer microarray data**.
* The paper proposes and develops a **hybrid algorithm** that combines **cuckoo search**, **multi-objective optimization**, and **evolutionary operators** to select the most relevant and informative genes from high-dimensional cancer microarray data sets.
* The paper evaluates the performance of the hybrid algorithm on **seven publicly available cancer microarray data sets** and compares it with **cuckoo search** and **multi-objective cuckoo search** algorithms.
* The paper reports that the hybrid algorithm **outperforms** the other two algorithms in terms of **accuracy**, **F-measure**, and **number of selected genes**. The paper also shows that the hybrid algorithm can **adapt** to different data sets and **avoid** local optima and parameter tuning issues.

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