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# Reinforcement Learning Technique Based Automated Feature Analysis of Gene Expression Data

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#### Document Sections

- I. Introduction
- II. Related Works
- III. Proposed Method
- IV. Results and Discussions
- V. Conclusion

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#### Abstract:

Immunohistochemistry and reverse transcription polymerase chain reaction, it is feasible to find molecular markers that are specific to cancer; nevertheless, there are no pathognomonic molecular markers available for the vast majority of solid tumors at this time. In this paper, we develop a Reinforcement learning Technique based automated feature analysis of gene expression data. This provides support for the idea that, on average, all the validation findings and training data from each epoch were utilized. This proposed method helps to acquiring knowledge at a more leisurely pace is, in the end, what makes episodic deep RL possible as a potential choice for students to pursue. To put it another way, the slow but steady accumulation of knowledge paves the path for the rapid extension of one existing body of information. The proposed methods provide 98 percent of the accuracy result than existing ANN and DNN. The proposed framework outperformed existing methods in terms of increase accuracy rate and reduced execution time than other methods

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 **Contents**

**I. Introduction**

The majority of cancers can be classified into one of several unique subtypes depending on the kind of tissue from which they first developed. However, independent pathologists discovered only 41% agreement on the subtypes of lung adenocarcinoma [1], which illustrates that the subjective interpretation of the histology of a cancer material is prone to human mistake or prejudice [2].

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