

Meeting abstract

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Fuzzy rule based unsupervised approach for gene saliency

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Clinical background

This abstract presents a novel fuzzy rule based gene ranking algorithm for extracting salient genes from a large set of microarray data which helps us to reduce computational efforts towards model building process. The proposed algorithm is an unsupervised approach and does not require any prior class information for gene ranking and microarray data has been used to form a set of robust fuzzy rule base which helps us to find salient genes based on its average relevance with already formed fuzzy rules in rule base. Fuzzy rule based ranking has been carried out to select salient genes based on their average firing strength (i.e. average true value after all the fuzzy rules applied) in order of high relevancy and only top ranked genes are utilized to classify normal and cancerous tissues for a carcinoma dataset [1]. Results validate the effectiveness of our gene ranking method as for the same no. of genes, our ranking scheme helps to improve the classifier performance by selecting better salient genes. In our case study the performance comparison for five top ranked genes is given in Table 1.

Table 1:

Ranking scheme and genes	Classifier performance	
	SVM	KNN
t-test[2] T64297, T96548, M97496, T71025 and H20709	0.8571	0.8571
Fuzzy rule based method M94132, X53416, b-actin-M, Z24727 and L08010	1.0000	1.0000

Conclusion

Results of classifiers in terms of correct rate (Table 1) show that the proposed fuzzy rule based gene ranking scheme outperforms t-test based ranking schemes.

Acknowledgements

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References

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