













## CONCLUSION

In this paper, various algorithms are used to find the cancer affected genes in the sample dataset. That are K-Means, Kernel based fuzzy clustering, fuzzy c-means and modified fuzzy c-means. The sample dataset which is used for this research work are DLBCL, MLL, SRBTCM, and EWS. The specified algorithms are not well functioned, in a cancer genes. So, the modified fuzzy c-means algorithm is proposed to grasp the cancer genes.

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