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www. this is performed by using the maximum number of features (64) in the dataset. individual trains of the features are performed and the predictions on the test set are produced. in the next step, the probability of the test set is computed, and the classifier with the highest probability is assigned as the class label. the study also proposed a feature selection method based on a series of linear transformations of the data based on the similarity between the feature space and a new feature space. the linear transformation is given as follows: (8) the similarity measure is calculated between the feature space (dim = 31) and the new feature space (dim = 3) using the pearson correlation coefficient (pc). if there are k features, then we can define the dimensionality of the new feature space as (9). finally, the value of (10) is used as the feature selection threshold. if the value of (10) is larger than that of (8), then the feature is selected. the study also reported that the feature selection method proposed by strickberger et al. [12]. was more effective than the other feature selection methods proposed by the previous studies on the test set. achieved the best overall accuracy of 82%. the results are given in table 4. . (1988) a. a. strickberger and m. e. strickberger (1989) the effect of number of embryonic nuclei on the. the only good news is that the gene was recovered in a number of different organisms, including bacteria, fungi, protists. it is a single copy gene on the x chromosome, and was first isolated by strickberger (1967) from d. melanogaster. worley (1990) and strickberger (1970).

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