Gene Selection for SVMs

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Abstract

The problem of classifying molecular patterns and inferring which genes are relevant in this classification will be addressed. We look at problems of predicting cancer morphologies and treatment outcomes and infer which genes are relevant in these prediction. Specifically we look at morphology data for Leukemia, Lymphoma, and Brain tumors. For treatment outcome we look at Diffuse Large B Cell Lymphoma and Medullablastomas. We state error rates for both types of problems and survival statistics for outcome prediction, all these are statistically significant. Some details will be given about the SVM classification with feature selection algorithm that was used to achieve these results.