A Comparison of Validation Methods for Learning Vector Quantization and for Support Vector Machines on Two Biomedical Data Sets

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Abstract. We compare two comprehensive classification algorithms, support vector machine (SVM) and learning vector quantization (LVQ), with respect to different validation methods. The generalization ability (test set error rate) is estimated by "multiple hold out" and "leave one out" cross validation method. The $\xi\alpha$-method, a further estimation method, which is only applicable for SVM and is computationally more efficient, is also used. Calculations on two different biomedical data sets, generated from experimental data measured in our laboratory, are presented. The first data set contains 748 feature vectors with relatively low number of components. Features are extracted from center-of-pressure (COP) signals of posturographic investigations of 48 young adults. Two different classes are labeled as "with" and "without" alcoholic impairment. This classification task aims the detection of small unknown changes in a relative complex signal with high interindividual variability. The second data set contains 6432 feature vectors with relatively high dimensionality (207 components) extracted from EEG and EOG signals recorded during overnight driving simulations of 22 young adults. Short intrusions of sleep during driving, so-called microsleep episodes, were observed in 3216 cases. They form examples of the first class. The second class contains 3216 examples of fatigue states, where driving is still possible. If microsleep episodes happened in typical states of brain activity, the recorded signals should reflect them, and therefore discrimination from signals of the second class, which do not reflect such states, should be possible. SVM and LVQ provide the same generalization ability for the first data set, for the second dataset the SVM perform remarkably better. Optimal kernel parameters of SVM are found by searching minimal test errors with all three validation methods. Results obtained on both different biomedical data sets show different optimal kernel parameters depending on validation method and dataset. It is shown, that the $\xi\alpha$-method is biased and therefore "multiple hold out" or the almost unbiased "leave one out" method should be preferred.

References

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Keywords

SVM, LVQ, HOLD-OUT, LEAVE-ONE-OUT, XI-ALPHA-BOUND