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Efficient Tuning Parameter Selection by Cross-Validated Score in High Dimensional Models

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Abstract : As DNA microarray data contain relatively small sample size compared to the number of genes, high dimensional models are often employed. In high dimensional models, the selection of tuning parameter (or, penalty parameter) is often one of the crucial parts of the modeling. Cross-validation is one of the most common methods for the tuning parameter selection, which selects a parameter value with the smallest cross-validated score. However, selecting a single value as an "optimal" value for the parameter can be very unstable due to the sampling variation since the sample sizes of microarray data are often small. Our approach is to choose multiple candidates of tuning parameter first, then average the candidates with different weights depending on their performance. The additional step of estimating the weights and averaging the candidates rarely increase the computational cost, while it can considerably improve the traditional cross-validation. We show that the selected value from the suggested methods often lead to stable parameter selection as well as improved detection of significant genetic variables compared to the tradition cross-validation via real data and simulated data sets.

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