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Clique-Centrality Driven Feature Selection for High-Dimensional Data Classification

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Authors:
Abdelali OUBAOUZINE
Tayeb OUADERHMAN
Hasna CHAMLAL

Department of Mathematics and Informatics, Faculty of Sciences Ain Chock, Hassan II University of Casablanca, Morocco

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Abstract

High-dimensional gene expression data pose a major challenge due to the large number of variables compared to the limited number of samples. The objective is to identify a small informative subset of features without compromising predictive accuracy.

To address this issue, we propose a hybrid feature selection framework structured in three stages. First, a Chi-square test is applied to remove irrelevant features and reduce dimensionality. The remaining features are then represented as a weighted correlation graph, where maximal cliques are extracted to identify strongly related groups of variables. Finally, a centrality measure is used to select the most representative feature from each clique, and a forward selection procedure refines the subset to obtain the final discriminative features.

Experimental results on high-dimensional gene expression datasets demonstrate the robustness and effectiveness of the proposed approach.

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