Fuzzy Logic for Elimination of Redundant Information of Microarray Data

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Résumé en anglais	Gene subset selection is essential for classification and analysis of microarray data. However, gene selection is known to be a very difficult task since gene expression data not only have high dimensionalities, but also contain redundant information and noises. To cope with these difficulties, this paper introduces a fuzzy logic based pre-processing approach composed of two main steps. First, we use fuzzy inference rules to transform the gene expression levels of a given dataset into fuzzy values. Then we apply a similarity relation to these fuzzy values to define fuzzy equivalence groups, each group containing strongly similar genes. Dimension reduction is achieved by considering for each group of similar genes a single representative based on mutual information. To assess the usefulness of this approach, extensive experimentations were carried out on three well-known public datasets with a combined classification model using three statistic filters and three classifiers.
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