



Feature Filtering Techniques for Biased Microarray Sample Sets

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Condition: New. Publisher/Verlag: VDM Verlag Dr. Müller | Some Thoughts and Solutions | Microarray expression data contain expression levels of a large number of genes and have been used in many scientific research and clinical studies. Due to its high dimensionalities, selecting a small number of genes has shown to be beneficial for many tasks such as building prediction models for a particular disease or gene regulatory network discovery. Traditional gene selection methods, however, fail to take the class distribution into the selection process. In Biomedical science, it is very common to have microarray expression data severely biased having very small number of diseased samples. These biased sample sets require special attention from researchers for identification of genes responsible for a particular disease. In this work, we propose three feature filtering techniques, Higher Weight Relief, Relief with Differential Minority Repeat and Relief with Balanced Minority Repeat to identify genes responsible for fatal diseases from biased microarray expression data. Our solutions will help Bioinformatics, Computer Science and Biomedical Research groups to filter potentially hazardous genes in an efficient way. | Format: Paperback | Language/Sprache: english | 80 pp.



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