

## **Robust biomarker selection from DNA microarray data with resampling techniques**

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This talk focuses on data analysis techniques for automatically selecting biomarkers from microarray data. The objective is to select biomarkers which are predictive of a clinical outcome such as a positive response to a treatment.

We review here several feature selection methods and we argue in favor of multivariate methods to find genes that are jointly predictive of the clinical response. The interest of embedding the selection method into the classifier estimation is also stressed. We discuss in particular how the stability of the final gene list can be increased with appropriate resampling techniques and a consensus methodology. We report practical results on a private dataset from GSK Biologicals where microarrays were used to predict the clinical activity of the MAGE-A3 Antigen-Specific Cancer Immunotherapeutic. We extend this analysis to several public datasets related to cancer prognosis or diagnosis to illustrate that the consensus approach may improve the classification performance and the stability of the selected markers.