

Mapping Multi-Class Cancer to Latent Space and Output Prediction Through High-Dimensional Computational Biology

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In the present study, we developed a hierarchical framework of a nonlinear mapping classification for elucidating biology and classify multiclass cancer from microarray data set. It maps the gene expression profiles of multi-class cancer to the visualized latent space and predict the clinical output through high-dimensional computational biology. The proposed method was used to interpret and analyze four leukemia subtypes from microarray data from leukemia patients. The results demonstrate that the proposed method can identify leukemia subtypes on the basis of molecular-level monitoring and improve their interpretability of leukemia clinical outputs for extracting biological insights from microarray data by a high-dimensional nonlinear mapping. Furthermore this nonlinear mapping of subtype cancers is used to establish a relationship between expression-based subclasses of leukemia tumors and leukemia patient treatment outcome.