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Cancer Classification of Microarray Data by Denoising Methods on Graphs. Preliminary report.

We prove results for two denoising methods, local averaging and kernel regression on graphs, adapted from denoising methods for functions in Euclidean space and applied to functions on graphs. These approaches are illustrated in computational biology in the regularization of gene expression feature vectors derived from (typically noisy) cancer microarrays. The microarray feature vectors are viewed as functions on the set of genes, which have the structure of a graph (network) based on gene-gene connections derived from a protein-protein interaction network. A particular property of Euclidean denoising which carries over to these cases is that the accuracy of the denoised function increases to a maximum as a function of the denoising parameter t , and then decreases. (Received August 23, 2011)