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Classification of breast cancer subtypes using signaling pathways and persistence homology.

Signaling pathways can be described as graphs that model biological molecular interactions which lead to changes in gene expression. One challenge is to develop a pathway analysis approach that can distinguish cancer subtypes. In our work, we map gene expression data from microarray studies of breast cancer patients with diagnosed subtypes onto the nodes of a pathway to obtain a directed graph G with weighted nodes. We construct a point cloud C from G then use persistence homology to analyze C . (Received September 21, 2015)