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A Bound on the Metric Dimension of Hamming Graphs and Applications in Machine Learning

Many powerful data analysis and data mining techniques require that data be embedded in Euclidean space. When faced with symbolic datasets, including biological sequence data produced by high-throughput sequencing assays, it is not always clear how to generate an effective embedding. In this talk, we discuss low-dimensional representations of symbolic information based on metric dimension. Specifically, we consider an upper bound on the metric dimension of Hamming graphs and how this bound can be used to map biological sequences of arbitrary length to real space.