Many data sets can be viewed as a noisy sampling of an underlying space, and tools from topological data analysis can characterize this structure for the purpose of knowledge discovery. Persistent homology can provide a multiscale description of the homological features within a data set. One useful representation of this homological information is a persistence diagram (PD). Efforts have been made to map PDs into spaces with additional structure valuable to machine learning tasks. In this talk, two approaches to convert a PD, or a sequence of PDs, to a finite-dimensional vector representation will be discussed. The first we call a persistence image, which is a stable transformation of a single PD, and the second is a CROCKER plot which is a representation of Betti numbers as a function of two inputs (such as proximity scale and time). We explore the use of these transformations in machine learning tasks related to dynamical systems such as the linked-twist map and the biological aggregation models of Vicsek et. al. and D'Orsogna et. al.