Spring 2016

Mathematical Sciences Colloquium

"Synchronization Problems and the Diffusion Geometry of Shape Spaces"

Kernel-based non-linear dimensionality reduction methods, such as Local Linear Embedding (LLE) and Laplacian Eigenmaps, rely heavily upon pairwise distances or similarity scores, with which one can construct and study a weighted graph associated with the data set. When each individual data object carries structural details, the correspondence relations between these structures provide additional information that can be leveraged for studying the data set using the graph. In this talk, I will introduce the framework of Horizontal Diffusion Maps (HDM), a generalization of Diffusion Maps in manifold learning. This framework models a data set with pairwise structural correspondences as a fibre bundle equipped with a connection. We further demonstrate the advantage of incorporating such additional information and study the asymptotic behavior of HDM on general fibre bundles.

In a broader context, HDM reveals the sub-Riemannian structure of high-dimensional data sets, and provides a nonparametric learning framework for data sets with structural correspondences. Mre generally, it can be viewed as geometric realization of synchronization problems. A synchronization problem for a group G and a graph $\Gamma = \left(V, E\right)$ searches for an assignment of elements in G to edges of Γ so the overall configuration minimizes an energy functional under certain compatibility constraints; it is essentially a generalization to the non-commutative setting of the little Grothendieck problem. In this talk, I will also explain some recent work on the cohomological nature of this type of problems.

Our interest in synchronization and diffusion geometry arises from the emerging field of automated geometric morphometrics. At present, evolutionary anthropologist using physical traits to study evolutionary relationships among living and extinct animals analyze morphological data extracted from carefully defined anatomical landmarks. Identifying and recording these landmarksis time consuming and can be done accurately only by trained morphometricians. This necessity renders these studies inaccessible to non-morphologists and causes phenomics to lag behind genomics in elucidating evolutionary patterns. This talk will also cover the application of our work to the automation of this morphological analysis in a landmark-free manner.

Speaker: Tingran Gao

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Monday, April 18, 2016

Time: 4:00 – 5:00 PM

Location: AE214

Rensselaer

Host: Rongjie Lai