PIMS-UBC Math Distinguished Colloquium

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Discovering low-dimensional manifolds in high-dimensional data sets

Diffusion methods help understand and denoise data sets; when there is additional structure (as is often the case), one can use (and get additional benefit from) a fiber bundle model.

This talk reviews diffusion methods to identify low-dimensional manifolds underlying high-dimensional datasets, and illustrates that by pinpointing additional mathematical structure, improved results can be obtained. Much of the talk draws on a case study from a collaboration with biological morphologists, who compare different phenotypical structures to study relationships of living or extinct animals with their surroundings and each other. This is typically done from carefully defined anatomical correspondence points (landmarks) on e.g. bones; such landmarking draws on highly specialized knowledge. To make possible more extensive use of large (and growing) databases, algorithms are required for automatic morphological correspondence maps, without any preliminary marking of special features or landmarks by the user.

For more information and session details, visit *https://www.pims.math.ca/scientific-event/230331-umdcid*