Clustering Patients' Functional Data Based on Spline Functions and Random-Effects Models

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Abstract

Patients' medical records have many valuable functional data, e.g., dose prescriptions over time and diagnostic imaging scans. These data help physicians learn more about metabolic change, disease evolution, etc. One way to turn such data into clinically useful information is through cluster analysis, which aims to separate curves or images among patients into homogeneous subgroups. Various clusters reflect heterogeneity in patients’ characteristics and effectiveness of therapy. However, not all patients were prescribed at regular time points or shared the same sub-area of images as the region of interest. Missing values seems ubiquitous if one aligns measurements at distinct time points or voxel locations. In this talk, the issue is dealt with based on a general framework with spline functions and random-effects models. When outliers are suspected to be present, a simple detection method based on a novel pairwise dissimilarity is also proposed. The detailed implementation of the framework is demonstrated with a methadone dosage maintenance level dataset and a positron emission tomography scan dataset.