

Functional logistic discrimination and its application to the proteomics trajectory data

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We consider functional logistic discrimination which is an extension of the classical method of logistic discriminant analysis to data where predictor variables are functions or curves. The functional logistic discrimination can effectively classify functions into distinct classes by imposing smoothness constraint on the predictor functions and coefficient function by Gaussian basis function expansion and regularization. In order to select the value of a smoothing parameter, we derive an extended Bayesian information criterion which enables us to evaluate model estimated by regularization method. The proposed method is applied to proteomics trajectory data which measures the kinetic trace of protein expression underlying postnatal development of mouse retina.