BAYESIAN HIERARCHICAL SPATIALLY CORRELATED FUNCTIONAL DATA ANALYSIS WITH APPLICATION TO COLON CARCINOGENESIS

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We focus on methods to analyze data from an experiment using rodent models to investigate the effect of diet on colon cancer development. In our experiment, various regulatory proteins (biomarkers), known to be precursors of early colon carcinogenesis, are assayed on animals in different diet/treatment groups at various time-points. The biological goals are to understand the relationship among the biomarkers up and down-regulation as well as complex interplays among the diets/treatments and the various biomarkers at a cellular level. What lends a special structure to the data is that the responses are inherently functional in nature, consisting of observed profiles over a spatial variable nested within a two-stage hierarchy, which called hierarchical functional data. The problem is cast within the class of hierarchical Bayesian functional models and the question of understanding these up and down-regulatory relationships is viewed as modeling the functional variations and correlations.