A Functional Approach to Deconvolve Dynamic Neuroimaging Data

江其衽
中央研究院統計科學研究所

Abstract

Positron Emission Tomography (PET) is an imaging technique which can be used to investigate chemical changes in human biological processes such as cancer development or neurochemical reactions. Most dynamic PET scans are currently analyzed based on the assumption that linear first order kinetics can be used to adequately describe the system under observation. However, there has recently been strong evidence that this is not the case. In order to provide an analysis of PET data which is free from this compartmental assumption, we propose a nonparametric deconvolution and analysis model for dynamic PET data based on functional principal component analysis. This yields flexibility in the possible deconvolved functions while still performing well when a linear compartmental model setup is the true data generating mechanism. As the deconvolution needs to be performed on only a relative small number of basis functions rather than voxel by voxel in the entire 3-D volume, the methodology is both robust to typical brain imaging noise levels while also being computationally efficient. The new methodology is investigated through simulations in both 1-D functions and 2-D images and also applied to a neuroimaging study whose goal is the quantification of opioid receptor concentration in the brain.