

A New Approach for Visualization of Dynamic PET Images Employing Diffusion-Map Space

Mohammad Hadi A'arabi^{1,2}, Sikiru Adebileje^{1,2}, Mahdi Shandiz² and Hamidreza Saligheh Rad^{1,2}

¹Quantitative MR Imaging and Spectroscopy Group, Research Center for Cellular and Molecular Imaging, Tehran University of Medical Sciences, Tehran, Iran.

²Department of Medical Physics and Biomedical Engineering, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.

h-salighehrad@tums.ac.ir

1 Introduction

For the sake of study the time–activity distribution of a radiotracer in a tissue of interest, a dynamic emission scan is to be used to get dynamic PET images. In dynamic PET, positron-carrying radiopharmaceutical tracers are injected into the body. Dynamic PET captures the spatial-temporal patterns of the injected tracers.

Dynamic positron emission tomography possesses high dimension and complex structure, so that detecting available pattern information and its analysis based on conventional linear statistics and classification methods become inefficient. In order to facilitate such quantification or visualization of the data, derogating the undesirable properties of high-dimensional spaces, i.e. dimensionality reduction is far-reaching. Dimensionality reduction is based on finding valid structures and geometric characterization of high dimensional data, to be realized with several techniques, which are categorized into linear and nonlinear methods. Linear methods are based on classic approaches, such as principal component analysis (PCA) and multi-dimensional scaling. Although they guarantee acquisition of real data structures lying on or near a linear subspace of high dimensional input space, they cannot deal with complex nonlinear data. This has led to development of nonlinear methods, such as diffusion-map (DM) techniques for biological data with highly nonlinear manifolds. This paper seeks to address a technique for dynamic PET data visualization, based on images with pixels sampled from underlying manifold.

2 Method

Dynamic PET is represented as $f(x): x \in \mathbb{R}^1 \rightarrow \mathbb{R}^n$, where n is the number of the time activity curves (TAC) samples at each voxel. The proposed Diffusion Map approach is composed of three main steps (Fig.1): (1) Measuring dissimilarities between observations is an important step in handling high dimensional data; (2) Calculate Markov Random Walk matrix; (3) Calculate eigen values and eigen vectors of Markov Random Walk matrix.

3 Result

Fig.2 show the results of our proposed algorithm on one selected axial slice of brain. Table.1 shows correlation evaluation between Diffusion Map and Sum of Activity.

4 Conclusion

This study set out to propose a method for visualization of dynamic PET as a robust method to preserving distance in nonlinear data, while keeping low-dimensional space. The proposed analysis suggests that the DM dimensionality reduction improves visualization, while it stays an active research problem. Due to the wide range of research and clinical applications of dynamic PET, we hope that the proposed method will broaden new horizons for exploring the full richness of dynamic PET to realize ways in which such measurements are affected by pathologies and treatments.

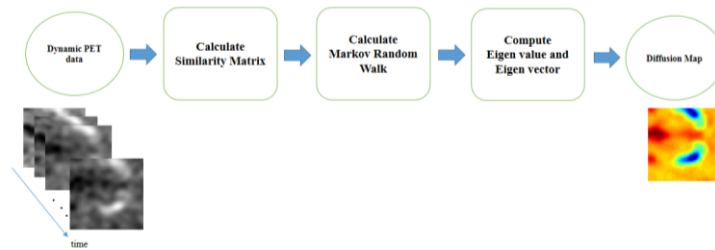


Fig. 1. Overview of Proposed Method

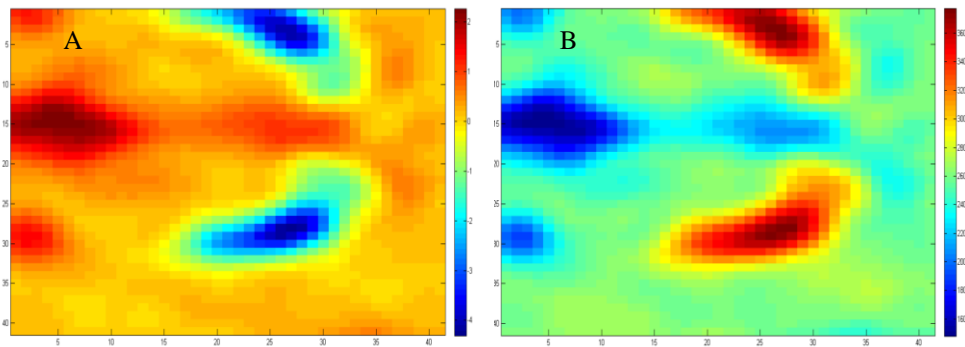


Fig. 2. Left: the Diffusion Map, Right: the Sum of Activity

Table 1. Correlation and p-value of between Diffusion Map and Sum of Activity

Correlation coefficient r	-0.9697
Significance level	P<0.0001