Direct Statistical Parametric Image Estimation for Linear Pharmacokinetic Models from Quantitative Positron Emission Tomography Measurements

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ABSTRACT

In dynamic PET studies, the changing activity of the radiotracer is measured through multiple consecutive time frames. Subsequently, the radioactivity distribution for each frame is obtained by a method known as reconstruction. Then, the distribution of the physiological parameter of interest is estimated by applying an appropriate pharmacokinetic model. Thus, the kinetic parameters are obtained indirectly through a two-step process. If the two steps are combined by incorporating the pharmacokinetics of the measured counts into the reconstruction, the directly reconstructed parametric images are expected to be of higher quality and accuracy.

Both indirect and direct parametric estimation methods have been implemented, evaluated and compared for the case where the kinetic model is linear in the pharmacokinetic parameters and displays irreversible behaviour (i.e. Patlak plot). The main aim of this study is the investigation of the statistical properties of different approaches. For the indirect estimation, the tracer distribution during each frame is estimated with filtered back projection (FBP) and ordered subsets expectation maximization (OSEM). Then, the pharmacokinetic parameters are estimated by the Patlak plot. These indirect procedures are compared with a direct parametric reconstruction method which integrates the Patlak plot into the OSEM optimization (POSEM).

The resolution of noiseless reconstructions appeared appreciable lower for the analytically estimated parametric images comparing to those estimated iteratively. In order to investigate other sources of disparities between analytical and iterative methods, the latter were post-filtered to match resolution. The post-filtered images demonstrated similar bias for all methods in the most regions but less standard deviation for OSEM and even less for POSEM. Nevertheless, POSEM converged slowly in some regions and this feature is a general characteristic of this algorithm. Finally, optimization approaches are proposed which may improve the convergence rate and hence the quantification of the pharmacokinetic parameters.

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